



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 164628

TO: Anish Gupta
Art Unit: 1654
Location: REM/3C15/3C18
Serial Number: 10/083768

Friday, September 02, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
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Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

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CP 66

ACCESS DB # 164518
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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: Anush Gupta Examiner #: 73121 Date: 8/31/01
Art Unit: 1654 Phone Number: 2-0965 Serial Number: 10/083,768
Location (Bldg/Room#): Rouse/208 (Mailbox #): Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Peptide & Compounds that bind to a Receptor
Inventors (please provide full names): William Dawes, Ronald Barrett, Steven Cwikla,
David Duffin, Christian Gates, Steven Hazelden, Larry Madecalis, Peter Schatz
Earliest Priority Date: 6/7/96 Christopher Waghorn, Nicholas Wrighton

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

nej Please search seq Id No. 6-13
6 aa 18
7 19
8 19
9 18
10 18
11 19
12 14
13 aa 14

Complete
9/25/01
J.H.

STAFF USE ONLY

Searcher: Beverly C-25-2-8 Type of Search NA Sequence (#)

Searcher Phone #: AA Sequence (#)

Searcher Location: Structure (#)

Date Searcher Picked Up: Bibliographic

Date Completed: Litigation

Searcher Prep & Review Time: Fulltext

Online Time: Other

Vendors and cost where applicable

STN Dialog

Questel/Orbit Lexis/Nexis

Westlaw WWW/Internet

house sequence systems CGN

Commercial Oligomer Score/Length

Interference SPDI Encode/Transl

Other (specify)

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:02 ; Search time 82.7482 Seconds

(without alignments)
84.131 Million cell updates/sec

Title: US-10-083-768-6

Perfect score: 109

Sequence: 1 GCGCAGDPTLRWISFCCG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database: A_Geneseq_16Dec04:*

1: geneseqp19808:*\n2: geneseqp19908:*\n3: geneseqp20008:*\n4: geneseqp20018:*\n5: geneseqp20028:*\n6: geneseqp20038:*\n7: geneseqp20048:*\n8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	18	AAW09456	AAW09456 Thrombopo
2	109	100.0	18	AAW33023	AAW33023 Thrombopo
3	109	100.0	18	AAW17020	AAW17020 TPO-mimet
4	109	100.0	18	AAU25820	AAU25820 Human thr
5	109	100.0	18	ABW72906	ABW72906 TPO mimet
6	109	100.0	18	ADJ73058	ADJ73058 TPO mimet
7	109	100.0	18	ADJ52693	ADJ52693 CHI delet
8	109	100.0	18	ADJ51654	ADJ51654 CHI delet
9	109	100.0	18	AAW09458	AAW09458 Thrombopo
10	109	100.0	19	AAW33025	AAW33025 Thrombopo
11	109	100.0	19	AAU25822	AAU25822 Human thr
12	85	78.0	14	AAW09466	AAW09466 Thrombopo
13	85	78.0	14	AAW09462	AAW09462 Thrombopo
14	85	78.0	14	AAW09465	AAW09465 Thrombopo
15	85	78.0	14	AAW09482	AAW09482 Thrombopo
16	85	78.0	14	AAW33031	AAW33031 Thrombopo
17	85	78.0	14	AAW36633	AAW36633 Thrombopo
18	85	78.0	14	AAW33029	AAW33029 Thrombopo
19	85	78.0	14	AAW35401	AAW35401 Thrombopo
20	85	78.0	14	AAW36647	AAW36647 Thrombopo
21	85	78.0	14	AAW35400	AAW35400 Thrombopo
22	85	78.0	14	AAW33032	AAW33032 Thrombopo
23	85	78.0	14	AAW17014	AAW17014 TPO-mimet
24	85	78.0	14	AAU25826	AAU25826 Human thr
25	85	78.0	14	AAU25852	AAU25852 Human thr

26	85	78.0	14	AAU25866	AAU25866 Human thr
27	85	78.0	14	ABW72900	ABW72900 TPO mimet
28	85	78.0	14	ADJ73051	ADJ73051 TPO mimet
29	85	78.0	14	ADJ52686	ADJ52686 CHI delet
30	85	78.0	14	ADJ51647	ADJ51647 CHI delet
31	76	69.7	13	AAW09467	AAW09467 Thrombopo
32	76	69.7	13	AAW35399	AAW35399 Thrombopo
33	76	69.7	13	AAW5417	AAW5417 Thrombopo
34	76	69.7	13	AAW33033	AAW33033 Thrombopo
35	76	69.7	13	AAW5413	AAW5413 Thrombopo
36	76	69.7	13	AAW5406	AAW5406 Thrombopo
37	76	69.7	13	AAW35422	AAW35422 Thrombopo
38	76	69.7	13	AAW35397	AAW35397 Thrombopo
39	76	69.7	13	AAU25997	AAU25997 Human thr
40	76	69.7	13	AAU25984	AAU25984 Human thr
41	76	69.7	14	AAW53398	AAW53398 Thrombopo
42	76	69.7	14	AAW5336	AAW5336 Thrombopo
43	76	69.7	14	AAW55402	AAW55402 Thrombopo
44	76	69.7	14	AAU25987	AAU25987 Human thr
45	76	69.7	14	AAU25983	AAU25983 Human thr
46	76	69.7	14	AAU25985	AAU25985 Human thr
47	72	66.1	12	AAW5423	AAW5423 Thrombopo
48	72	66.1	12	AAU26000	AAU26000 Human thr
49	67	61.5	13	AAW35405	AAW35405 Thrombopo
50	67	61.5	13	AAW35405	AAW35405 Thrombopo
51	67	61.5	13	AAU25994	AAU25994 Human thr
52	67	61.5	13	AAU25991	AAU25991 Human thr
53	67	61.5	13	AAU25990	AAU25990 Human thr
54	67	61.5	14	AAW35412	AAW35412 Thrombopo
55	67	61.5	14	AAW35407	AAW35407 Thrombopo
56	67	61.5	14	AAW35408	AAW35408 Thrombopo
57	67	61.5	14	AAW35403	AAW35403 Thrombopo
58	67	61.5	14	AAU25993	AAU25993 Human thr
59	67	61.5	14	AAU25989	AAU25989 Human thr
60	67	61.5	14	AAU25995	AAU25995 Human thr
61	67	61.5	14	AAU25992	AAU25992 Human thr
62	67	61.5	14	AAU25986	AAU25986 Human thr
63	67	61.5	14	AAU25988	AAU25988 Human thr
64	67	61.5	25	AAU26042	AAU26042 Human thr
65	67	61.5	25	ADW72531	ADW72531 TPO mimet
66	66	60.6	11	AAW35425	AAW35425 Thrombopo
67	66	60.6	11	AAU26001	AAU26001 Human thr
68	66	60.6	25	ADN59740	ADN59740 Thrombopo
69	65	59.6	13	AAU26041	AAU26041 Human thr
70	64	58.7	14	AAW17017	AAW17017 TPO-mimet
71	64	58.7	14	ABW72903	ABW72903 TPO mimet
72	64	58.7	14	ADJ52689	ADJ52689 CHI delet
73	64	58.7	14	ADJ51650	ADJ51650 CHI delet
74	60	55.0	10	AAW35427	AAW35427 Thrombopo
75	60	55.0	10	AAU26002	AAU26002 Human thr
76	60	55.0	10	ADN59680	ADN59680 Thrombopo
77	59	54.1	22	ADN59839	ADN59839 TWP pepti
78	59	54.1	25	ADN59744	ADN59744 Thrombopo
79	57	52.3	12	ADW72530	ADW72530 TPO mimet
80	57	52.3	13	ADU26039	ADU26039 Human thr
81	57	52.3	13	ADW72529	ADW72529 TPO mimet
82	57	52.3	13	ADW72528	ADW72528 TPO mimet
83	57	52.3	14	AAW66732	AAW66732 Peptide c
84	57	52.3	14	AAU26040	AAU26040 Human thr
85	57	52.3	16	AAW09464	AAW09464 Thrombopo
86	57	52.3	16	AAW33329	AAW33329 Thrombopo
87	57	52.3	16	AAW33029	AAW33029 TPO-mimet
88	57	52.3	16	AAU25829	AAU25829 Human thr
89	57	52.3	16	ABW72905	ABW72905 TPO mimet
90	57	52.3	16	ADJ73057	ADJ73057 TPO mimet
91	57	52.3	16	ADJ52692	ADJ52692 CHI delet
92	57	52.3	16	ADJ51653	ADJ51653 CHI delet
93	56.5	51.8	23	ADN59778	ADN59778 Peptide-v
94	56.5	51.8	41	ADN59816	ADN59816 Peptide-v
95	56.5	51.8	41	ADN59772	ADN59772 Peptide-v
96	56.5	51.8	46	ADN59784	ADN59784 Peptide-v
97	56.5	51.8	46	ADN59784	ADN59784 Peptide-v
98	56	51.4	13	AAW17015	AAW17015 TPO-mimet

AAU25866	Human thr
ABW72900	TPO mimet
ADJ73051	TPO mimet
ADJ52686	CHI delet
ADJ51647	CHI delet
AAW09467	Thrombopo
AAW35399	Thrombopo
AAW5417	Thrombopo
AAW33033	Thrombopo
AAW5413	Thrombopo
AAW5406	Thrombopo
AAW35422	Thrombopo
AAW35397	Thrombopo
AAU25997	Human thr
AAU25984	Human thr
AAW53398	Thrombopo
AAW5336	Thrombopo
AAW55402	Thrombopo
AAU25987	Human thr
AAU25983	Human thr
AAU25985	Human thr
AAW5423	Thrombopo
AAU26000	Human thr
AAW35405	Thrombopo
AAW35405	Thrombopo
AAU25994	Human thr
AAU25991	Human thr
AAU25990	Human thr
AAW35412	Thrombopo
AAW35407	Thrombopo
AAW35408	Thrombopo
AAW35403	Thrombopo
AAU25993	Human thr
AAU25989	Human thr
AAU25995	Human thr
AAU25992	Human thr
AAU25986	Human thr
AAU25988	Human thr
AAU26042	Human thr
ADW72531	TPO mimet
AAW35425	Thrombopo
AAU26001	Human thr
ADN59740	Thrombopo
AAU26041	Human thr
AAW17017	TPO-mimet
ABW72903	TPO mimet
ADJ52689	CHI delet
ADJ51650	CHI delet
AAW35427	Thrombopo
AAU26002	Human thr
ADN59680	Thrombopo
ADN59839	TWP pepti
ADN59744	Thrombopo
ADW72530	TPO mimet
ADU26039	Human thr
ADW72529	TPO mimet
ADW72528	TPO mimet
AAW66732	Peptide c
AAU26040	Human thr
AAW09464	Thrombopo
AAW33329	Thrombopo
AAW33029	TPO-mimet
AAU25829	Human thr
ABW72905	TPO mimet
ADJ73057	TPO mimet
ADJ52692	CHI delet
ADJ51653	CHI delet
ADN59778	Peptide-v
ADN59816	Peptide-v
ADN59772	Peptide-v
ADN59784	Peptide-v
AAW17015	TPO-mimet

99 56 51.4 13 5 ABB72901 TPO mimet
100 56 51.4 13 7 ADJ73054 TPO mimet

ALIGNMENTS

RESULT 1
AAW09456 standard; protein; 18 AA.

AC AAW09456;

DT 10-SEP-1997 (first entry)

DE Thrombopoietin receptor binding compound peptide.

KM Haematology; thrombocytopenia; TPO; TR; proliferation;

KW bone marrow transfusion; chemotherapy; radiation therapy.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 1.18
/note="Preferably linkages are selected from: -CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -C(O)NR6
; -NHC(O)NH- where R is hydrogen or lower alkyl and R6 is lower alkyl"

FT Modified-site

1
/note="Preferably N-terminus is selected from: -NRR1; -NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NHR; succinimide; benzylloxycarbonyl-NH; benzylloxycarbonyl-NH with 1-3 substitutions on the phenyl ring selected from lower alkyl, lower alkoxy, chloro, bromo; where R and R1 are independently selected from hydrogen and lower alkyl"

FT Modified-site

18
/note="Preferably C-terminus is -C(O)R2 where R2 is selected from hydroxy, lower alkoxy, and -NR3R4, where R3 and R4 are independently selected from hydrogen and lower alkyl, and where the nitrogen atom of the -NR3R4 group can optionally be the amine group of the N-terminus of the peptide forming a cyclic peptide"

XX MO640189-A1.

PD 19-DEC-1996.

PF 05-JUN-1996; 96WO-US008998.

PR 07-JUN-1995; 95US-00472371.

PR 07-JUN-1995; 95US-00473604.

PR 07-JUN-1995; 95US-00476168.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00484090.

PR 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

PI Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-051883/05.

PS Claim 18; Page 89; 106pp; English.

CC The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). It has a molecular weight of < 8000 Da, and a binding affinity to TR as expressed by an IC50 of no more than about 100 mM. The compound (especially if modified, see features table) can be used for

CC treating patients suffering from haematological disorders and
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC marrow transfusions. The peptide may also be used to maintain the
CC proliferation and growth of TPO-dependent cell lines and for use in
CC biological research, for detecting TPO receptors on living cells
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 109; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTREWISFCGG 18
1 GGCADGPTREWISFCGG 18

RESULT 2
AAW33023
ID AAW33023 standard; peptide; 18 AA.

AC AAW33023;

DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

KM Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

OS Synthetic.

PN WO640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

PI Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

PS Claim 19; Page 89; 106pp; English.

CC The present peptide binds the thrombopoietin receptor (TR), has a
CC molecular weight of less than 8000 Da and a TR binding affinity as
CC expressed by an IC50 of no more than about 100 microm. It can be used to
CC treat disorders which are susceptible to treatment with a thrombopoietin
CC agonist, preferably haematological disorders and thrombocytopenia
CC resulting from chemotherapy, radiation therapy or bone marrow
CC transfusions. It can also be used diagnostically, e.g. to investigate the
CC mechanism of thrombopoietin signal transduction and receptor activation,
CC or to maintain the proliferation and growth of thrombopoietin dependent
CC cell lines
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 109; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFCGG 18
 DB 1 GGCADGPTLRWISFCGG 18

RESULT 3

AAB17020
 ID AAB17020 standard; peptide; 18 AA.

AC AAB17020;
 XX

DT 31-OCT-2000 (first entry)

DE TPO-mimetic peptide sequence SEQ ID NO:76.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiaesthetic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTUA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.

OS Synthetic.

PN WO200024782-A2.

PD 04-MAY-2000.

PF 25-OCT-1999; 99WO-US025044.

PR 23-OCT-1998; 98US-0105371P.

PR 22-OCT-1999; 99US-00428082.

PA (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheerham J, Boone TC;

XX WPI; 2000-350702/30.

PT Novel composition of matter comprising an Fc domain and pharmacologically
 active peptides, useful for treating cancer and autoimmune diseases.

PS Claim 19; Page 220; 608pp; English.

XX The present invention describes composition of matter (1) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (1) is:
 CC (X1)-a-P1-(X2)-b, where: P1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)-c-P1, -(L1)-c-P1-(L2)-d-P2, -(L1)-c-P1-
 CC (L2)-d-P2-(L3)-e-P3, or -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiaesthetic,
 CC thrombolytic, and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAB69443 to AAB69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention

XX Sequence 18 AA;

Query Match 100.0%; Score 109; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.6e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFCGG 18
 DB 1 GGCADGPTLRWISFCGG 18

RESULT 4
 ID AAV25820
 XX AAV25820 standard; peptide; 18 AA.

AC AAV25820;
 XX

DT 17-DEC-2001 (first entry)

DE Human thrombopoietin receptor (TPO-R) activator peptide #6.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.

OS Homo sapiens.

PN US6251864-B1.

PD 26-JUN-2001.

PF 01-MAR-2000; 2000US-00516704.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PR 07-JUN-1996; 96WO-US009623.

PR 15-AUG-1996; 96US-00699027.

PA (GLAXO) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cwirja SE, Gates CM, Schatz PJ;

XX Balasubramanian P, Wagstrom CR, Hendren RW, Poddaturi S;

XX Yin Q;

XX WPI; 2001-564142/63.

PS Disclosure; Col 65-66; 128pp; English.

XX Sequences AAV25815-AAV26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines

XX Sequence 18 AA;

Query Match 100.0%; Score 109; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.6e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFCGG 18
 DB 1 GGCADGPTLRWISFCGG 18

Db 1 GGCADGPTLRWISFCGG 18

RESULT 5
ABR72906
ID ABR72906 standard; peptide; 18 AA.
XX
AC ABR72906;
XX
DT 05-APR-2002 (first entry)
XX
DE TPO mimetic peptide SEQ ID NO:76.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
KW TPO mimetic peptide; EPO mimetic peptide; EME; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cyclostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antihaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Claim 39; Page 44; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cyclostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antinaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABR72403 to ABR73426 and ABR35695 to ABR35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 109; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFCGG 18
| | | | | | | | | | | | | | | | | |
Db 1 GGCADGPTLRWISFCGG 18

RESULT 6
ADJ73058
ID ADJ73058 standard; peptide; 18 AA.
XX
AC ADJ73058;
XX
DT 06-MAY-2004 (first entry)
XX
DE TPO mimetic peptide sequence SeqID 512.
XX
KW mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
KW immunomodulator; cardiant; antimicrobial; cyclostatic; neuroprotective;
KW TPO.
XX
OS Synthetic.
XX
PN WO2003084477-A2.
XX
PD 16-OCT-2003.
XX
PF 24-MAR-2003; 2003WO-US009139.
XX
PR 29-MAR-2002; 2002US-0368791P.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Heavner GA, Knight DM, Scallion BJ, Ghayeb J;
XX
DR WPI; 2003-804237/75.
XX
PT New CDR mimetibody comprising a portion of a heavy or light chain
PT variable region comprising human framework or ligand binding region,
PT useful for preparing a composition for treating e.g., immune,
PT cardiovascular or neurologic disease.
XX
PS Disclosure; SEQ ID NO 512; 97pp; English.
XX
CC This invention relates to novel mammalian CDR mimetibodies, specific
CC portions or variants thereof. Specifically, it refers to an antibody
CC fragment where a protein has been inserted into, or replaces a portion
CC of, one or more CDR regions, such that each CDR mimetibody comprises at
CC least one portion of a heavy chain or light chain variable region, which
CC itself comprises at least one human framework region and at least one
CC ligand binding region (LBR). The present invention describes human
CC mimetibodies, including modified immunoglobulins and cleavage products
CC that can be useful in gene therapy and the generation of transgenic
CC plants and animals. Furthermore, the CDR mimetibody is useful for
CC preparing compositions for modulating, treating or reducing the symptoms
CC of immune, cardiovascular, infectious, malignant and/or neurologic
CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC cardiant, antimicrobial, cyclostatic and neuroprotective activities. This
CC peptide sequence is a TPO mimetic peptide sequence used to make a
CC mimetibody of the invention.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 109; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFCGG 18
| | | | | | | | | | | | | | | | | |

Db 1 GGCAADGPTLRWISFCGG 18

RESULT 7

ADJ52693
ID ADJ52693 standard; peptide; 18 AA.

XX ADJ52693;

XX 06-MAY-2004 (first entry)

DE CH1 deleted mimetibody-related peptide SegID512.

KW CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiac;
KW hypotensive; neuroprotective; nootropic; antibacterial; virucide;
KW fungicide; gene therapy; immune disorder; cardiovascular disease;
KW arrhythmia; hypertension; heart failure; neurodegenerative;
KW multiple sclerosis; dementia; Alzheimer's disease; anaemia;
KW cancerous condition; infectious disease; bacterial infection;
KW viral infection; fungal infection.

XX Unidentified.
OS Synthetic.

XX WO2004002417-A2.

XX 08-JAN-2004.

XX 27-JUN-2003; 2003WO-US020347.

XX 28-JUN-2002; 2002US-0392431P.

XX (CENZ) CENTOCOR INC.

XX Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
PI Kutolowski KA;

DR WPI; 2004-082870/08.

PT New CH1-deleted mimetibody polypeptides and nucleic acids, useful for
modulating, treating, alleviating, preventing an immune, cardiovascular,
PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
PT diseases.

PS Claim 2; SEQ ID NO 512; 123pp; English.

CC This invention relates to CH1 deleted mimetibodies (and the DNA sequences
CC which encode them), compositions, methods and uses. The invention may be
CC useful for the development of compounds with an immunosuppressive,
CC cardiovascular, cardiac, hypotensive, neuroprotective, nootropic,
CC antibacterial, virucide or fungicide activity. In addition, the disclosed
CC sequences may prove useful for gene therapy. The CH1-deleted mimetibody
CC is useful for diagnosing or treating a disease condition in a cell,
CC tissue, organ or animal, specifically for modulating, treating,
CC alleviating, preventing the incidence or reducing the symptoms of an
CC immune, cardiovascular (for example arrhythmia, hypertension or heart
CC failure), or neurodegenerative (for example multiple sclerosis, dementia
CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
CC conditions, or infectious diseases (for example bacterial, viral or
CC fungal infection). The present sequence is that of a peptide which may be
CC used during the creation of a mimetibody of the invention.

XX Sequence 18 AA;

Query March 100.0%; Score 109; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.6e-09; Mismatches 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCAADGPTLRWISFCGG 18
Db 1 GGCAADGPTLRWISFCGG 18

RESULT 8

ADJ51654
ID ADJ51654 standard; peptide; 18 AA.

XX ADJ51654;

XX 06-MAY-2004 (first entry)

DE CH1 deleted mimetibody-related peptide SegID512.

KW CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
KW dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
KW antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
KW ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
KW TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
KW dental disorder; oral disorder; dermatological disorder; ear disorder;
KW nose disorder; throat disorder; endocrine disorder; metabolic disorder;
KW gastrointestinal disorder; gynaecological disorder; hepatic disorder;
KW obstetric disorder; haematologic disorder; immunologic disorder;
KW allergic disorder; infectious disorder; musculoskeletal disorder;
KW oncological disorder; neurological disorder; nutritional disorder;
KW ophthalmologic disorder; pediatric disorder; psychiatric disorder;
KW renal disorder; pulmonary disorder.

XX Unidentified.
OS Synthetic.

XX WO2004002424-A2.

XX 08-JAN-2004.

XX 30-JUN-2003; 2003WO-US020495.

XX 28-JUN-2002; 2002US-0392431P.

XX 19-SEP-2002; 2002US-0412144P.

XX (CENZ) CENTOCOR INC.

XX Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
PI Kutolowski KA;

DR WPI; 2004-082872/08.

PT New CH1 deleted mimetibody polypeptide and nucleic acid, useful for
PT diagnosing, preventing or treating cardiovascular, dermatologic,
PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
PT nutritional disorders.

PS Claim 15; SEQ ID NO 512; 123pp; English.

CC This invention relates to CH1 deleted mimetibodies (and the DNA sequences
CC which encode them), compositions, methods and uses. The invention may be
CC useful for the development of compounds with an osteopathic,
CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
CC gastroenteric-Gen, gynaecological-Gen, hepatotropic, haemostatic,
CC immunomodulator, antiallergic, muscular-Gen, cytostatic,
CC antiinflammatory, neuroleptic, ophthalmologic, nephrotropic or
CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
CC modulator or cytokine-agonist. The methods and compositions of the
CC present invention are useful for the diagnosis, prevention and/or
CC treatment of diseases or conditions associated with aberrant expression
CC or activity of the CH1 deleted mimetibody, such as a bone or joint,
CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
CC obstetric, haematologic, immunologic, allergic, infectious,
CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
CC pediatric, psychiatric, renal or pulmonary disorders. The present
CC sequence is that of a peptide which may be used during the creation of a
CC mimetibody of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 109; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.6e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGCADGPTLRWISFCGG 18
 1 GGCADGPTLRWISFCGG 18
 Db 1 GGCADGPTLRWISFCGG 18

RESULT 9

AAW09458 standard; protein; 19 AA.

AAW09458;

10-SEP-1997 (first entry)

Thrombopoietin receptor binding compound peptide.

Haematology; thrombocytopenia; TPO; TR; proliferation;
 bone marrow transfusion; chemotherapy; radiation therapy.

Synthetic.

Location/Qualifiers

Key 1.19

/note= "Preferably linkages are selected from: -

CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-; -C(O)NR6

; -NHC(O)NH; where R is hydrogen or lower alkyl and R6 is

lower alkyl"

/note= "Preferably N-terminus is selected from: -NRR1; -

NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NR; succinimide;

benzylloxycarbonyl-NH; benzylloxycarbonyl-NH with 1-3

substitutions on the phenyl ring selected from lower

alkyl, lower alkoxy, chloro, bromo, where R and R1 are

independently selected from hydrogen and lower alkyl"

Modified-site

/note= "Preferably C-terminus is -C(O)R2 where R2 is

selected from hydroxy, lower alkoxy, and -NR3R4, where R3

and R4 are independently selected from hydrogen and lower

alkyl, and where the nitrogen atom of the -NR3R4 group

can optionally be the amine group of the N-terminus of

the peptide forming a cyclic peptide"

MO9640189-A1.

19-DEC-1996.

05-JUN-1996; 96WO-US008998.

07-JUN-1995; 95US-00472371.

07-JUN-1995; 95US-00473604.

07-JUN-1995; 95US-00476168.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00484090.

07-JUN-1995; 95US-00485301.

(GLAX) GLAXO GROUP LTD.

Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

Mattheakis LC, Schatz PU, Wagstrom CR, Wrighton NC;

WPI; 1997-051883/05.

Thrombopoietin receptor-binding/activating peptide(s) and peptide

mimetic(s) - useful in treatment of haematological disorders, esp.

thrombocytopenia resulting from chemotherapy, etc.

Claim 18; Page 89; 106pp; English.

The present sequence is a compound which binds to thrombopoietin (TPO)

receptor (TR). It has a molecular weight of < 8000 Da, and a binding

affinity to TR as expressed by an IC50 of no more than about 100 nM. The
 compound (especially if modified, see features table) can be used for
 treating patients suffering from haematological disorders and
 thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 marrow transfusions. The peptide may also be used to maintain the
 proliferation and growth of TPO-dependent cell lines and for use in
 biological research, for detecting TPO receptors on living cells
 Sequence 19 AA;

Query Match 100.0%; Score 109; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.8e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFCGG 18
 1 GGCADGPTLRWISFCGG 18
 Db 1 GGCADGPTLRWISFCGG 18

RESULT 10

AAW33025 standard; peptide; 19 AA.

AAW33025;

11-MAR-1998 (first entry)

Thrombopoietin receptor binding peptide.

Thrombopoietin receptor; binding peptide; treatment; agonist;

haematological disorder; thrombocytopenia; chemotherapy;

radiation therapy; bone marrow transfusion; diagnosis;

signal transduction; receptor activation; cell culture.

Synthetic.

MO9640750-A1.

19-DEC-1996.

07-JUN-1996; 96WO-US009623.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00485301.

(GLAX) GLAXO GROUP LTD.

Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

Mattheakis LC, Schatz PU, Wagstrom CR, Wrighton NC;

WPI; 1997-052226/05.

Peptides and peptide mimetics which bind to and activate the

thrombopoietin receptor - useful in treatment of haematological

disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

Claim 19; Page 89; 106pp; English.

The present peptide binds the thrombopoietin receptor (TR), has a

molecular weight of less than 8000 Da and a TR binding affinity as

expressed by an IC50 of no more than about 100 microm. It can be used to

treat disorders which are susceptible to treatment with a thrombopoietin

agonist, preferably haematological disorders and thrombocytopenia

resulting from chemotherapy, radiation therapy or bone marrow

transfusions. It can also be used diagnostically, e.g. to investigate the

mechanism of thrombopoietin signal transduction and receptor activation,

or to maintain the proliferation and growth of thrombopoietin dependent

cell lines

Sequence 19 AA;

Query Match 100.0%; Score 109; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.8e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCADGPTLREWISFCGG 18
 |||||
 Db 1 GGCADGPTLREWISFCGG 18

RESULT 11

AAU25822
 ID AAU25822 standard; peptide; 19 AA.

AAU25822;

17-DEC-2001 (first entry)

Human thrombopoietin receptor (TPO-R) activator peptide #8.

Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine; haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA; bone marrow transplantation; haematological disorder; platelet disorder; enzyme-linked immunosorbent assay; in situ staining; biological fluid; tissue homogenate; fluorescence-activated cell sorting; Western blotting; in vitro expansion; megakaryocyte; Headpiece Dimer gene; Iaci gene.

Homo sapiens.

US6251864-B1.

26-JUN-2001.

01-MAR-2000; 2000US-00516704.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00485301.

07-JUN-1996; 96WO-US009623.

15-AUG-1996; 96US-00699027.

(GLAX) GLAXO GROUP LTD.

Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ, Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S; yin Q;

WPI; 2001-564142/63.

Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.

Disclosure; Col 67-68; 128pp; English.

Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines

Sequence 19 AA;

Query Match 100.0%; Score 109; DB 4; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.8e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCADGPTLREWISFCGG 18
 |||||
 Db 1 GGCADGPTLREWISFCGG 18

RESULT 12

AAW09466
 ID AAW09466 standard; protein; 14 AA.

AAW09466;

10-SEP-1997 (first entry)

Thrombopoietin receptor binding compound cyclic peptide.

Haematology; thrombocytopenia; TPO; TR; proliferation; cyclic; bone marrow transfusion; chemotherapy; radiation therapy.

Synthetic.

Location/Qualifiers

Key Disulfide-bond 1..14

Modified-site /note= "In acetyl form"

Modified-site 14 /note= "In amide form"

W09640189-A1.

19-DEC-1996.

05-JUN-1996; 96WO-US008998.

07-JUN-1995; 95US-00472371.

07-JUN-1995; 95US-00473604.

07-JUN-1995; 95US-00476168.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00484090.

07-JUN-1995; 95US-00485301.

(GLAX) GLAXO GROUP LTD.

Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS; Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

WPI; 1997-051883/05.

Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

Claim 30; Page 91; 106pp; English.

The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. The peptide may also be used to maintain the proliferation and growth of TPO-dependent cell lines and for use in biological research, for detecting TPO receptors on living cells

Sequence 14 AA;

Query Match 76.0%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CADGPTLREWISFC 16
 |||||
 Db 1 CADGPTLREWISFC 14

RESULT 13
 AAM09462
 ID AAM09462 standard; protein; 14 AA.
 AC AAM09462;
 DT 10-SEP-1997 (first entry)
 XX
 DE Thrombopoietin receptor binding compound peptide.
 XX
 KW Haematology; thrombocytopenia; TPO; TR; proliferation;
 XX bone marrow transfusion; chemotherapy; radiation therapy.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..14
 FT /note= "Preferably linkages are selected from: -
 FT CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -C(O)NR6
 FT ; -NHC(O)NH; where R is hydrogen or lower alkyl and R6 is
 FT lower alkyl"]
 FT 1
 FT /note= "Preferably N-terminus is selected from: -NRR1;-
 FT NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NHR; succinimide;
 FT benzoyloxycarbonyl-NH; benzoyloxycarbonyl-NH with 1-3
 FT substitutions on the phenyl ring selected from lower
 FT alkyl, lower alkoxy, chloro, bromo; where R and R1 are
 FT independently selected from hydrogen and lower alkyl"
 FT 14
 FT /note= "Preferably C-terminus is -C(O)R2 where R2 is
 FT selected from hydroxy, lower alkoxy, and -NR3R4, where R3
 FT and R4 are independently selected from hydrogen and lower
 FT alkyl, and where the nitrogen atom of the -NR3R4 group
 FT can optionally be the amine group of the N-terminus of
 FT the peptide forming a cyclic peptide"
 XX
 PN WO640189-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US008998.
 XX
 PR 07-JUN-1995; 95US-00472371.
 PR 07-JUN-1995; 95US-00473604.
 PR 07-JUN-1995; 95US-00476168.
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00484090.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 DR WPI; 1997-051883/05.
 XX
 PT Thrombopoietin receptor-binding/activating peptide(s) and peptide
 PT mimetic(s) - useful in treatment of haematological disorders, esp.
 PT thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Claim 18; Page 89; 106pp; English.
 XX
 CC The present sequence is a compound which binds to thrombopoietin (TPO)
 CC receptor (TR). It has a molecular weight of < 8000 Da, and a binding
 CC affinity to TR as expressed by an IC50 of no more than about 100 mM. The
 CC compound (especially if modified, see features table) can be used for
 CC treating patients suffering from haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. The peptide may also be used to maintain the
 CC proliferation and growth of TPO-dependent cell lines and for use in
 CC biological research, for detecting TPO receptors on living cells

XX
 SQ Sequence 14 AA;
 Query Match 78.0%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CADGPTLRWISFC 16
 DB 1 CADGPTLRWISFC 14
 RESULT 14
 AAM09465
 ID AAM09465 standard; protein; 14 AA.
 AC AAM09465;
 DT 10-SEP-1997 (first entry)
 XX
 DE Thrombopoietin receptor binding compound cyclic peptide.
 XX
 KW Haematology; thrombocytopenia; TPO; TR; proliferation; cyclic;
 XX bone marrow transfusion; chemotherapy; radiation therapy.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..14
 FT 14
 FT /note= "Preferably C-terminus is -C(O)R2 where R2 is
 FT selected from hydroxy, lower alkoxy, and -NR3R4, where R3
 FT and R4 are independently selected from hydrogen and lower
 FT alkyl, and where the nitrogen atom of the -NR3R4 group
 FT can optionally be the amine group of the N-terminus of
 FT the peptide forming a cyclic peptide"
 XX
 PN WO640189-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US008998.
 XX
 PR 07-JUN-1995; 95US-00472371.
 PR 07-JUN-1995; 95US-00473604.
 PR 07-JUN-1995; 95US-00476168.
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00484090.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 DR WPI; 1997-051883/05.
 XX
 PT Thrombopoietin receptor-binding/activating peptide(s) and peptide
 PT mimetic(s) - useful in treatment of haematological disorders, esp.
 PT thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Claim 30; Page 91; 106pp; English.
 XX
 CC The present sequence is a compound which binds to thrombopoietin (TPO)
 CC receptor (TR). The compound can be used for treating patients suffering
 CC from haematological disorders and thrombocytopenia resulting from
 CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide
 CC may also be used to maintain the proliferation and growth of TPO-
 CC dependent cell lines and for use in biological research, for detecting
 CC TPO receptors on living cells
 XX
 SQ Sequence 14 AA;
 Query Match 78.0%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CADGPTLRWISFC 16
 DB 1 CADGPTLRWISFC 14

RESULT 15

AAW09482

ID AAW09482 standard; protein; 14 AA.

XX AAW09482;

XX 10-SEP-1997 (first entry)

XX Thrombopoietin receptor binding peptide.

XX Hematology; thrombocytopenia; TPO; TR; proliferation;

XX bone marrow transfusion; chemotherapy; radiation therapy.

XX Synthetic.

XX WO9640189-A1.

XX 19-DEC-1996.

XX 05-JUN-1996; 96WO-US008998.

XX 07-JUN-1995; 95US-00472371.

XX 07-JUN-1995; 95US-00473504.

XX 07-JUN-1995; 95US-00476168.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00484090.

XX 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

XX Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-051883/05.

XX Thrombopoietin receptor-binding/activating peptide(s) and peptide

XX mimetic(s) - useful in treatment of haematological disorders, esp.

XX thrombocytopenia resulting from chemotherapy, etc.

XX Disclosure; Page 26; 106pp; English.

XX Sequence 14 AA;

XX Query Match 78.0%; Score 85; DB 2; Length 14;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-05;

XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 3 CADGPTLRWISFC 16

XX 1 CADGPTLRWISFC 14

RESULT 16

ID AAW33031 standard; peptide; 14 AA.

XX AAW33031;

XX 11-MAR-1998 (first entry)

XX Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.

XX Synthetic.

XX Key Location/Qualifiers

XX Disulfide-bond 1..14

XX WO9640750-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009623.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

XX Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

XX Peptides and peptide mimetics which bind to and activate the

XX thrombopoietin receptor - useful in treatment of haematological

XX disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX Claim 30; Page 91; 106pp; English.

XX The present peptide binds the thrombopoietin receptor (TR), has a

XX molecular weight of less than 800 Da and a TR binding affinity as

XX expressed by an IC₅₀ of no more than about 100 microm. It can be used to

XX treat disorders which are susceptible to treatment with a thrombopoietin

XX agonist, preferably haematological disorders and thrombocytopenia

XX resulting from chemotherapy, radiation therapy or bone marrow

XX transfusions. It can also be used diagnostically, e.g. to investigate the

XX mechanism of thrombopoietin signal transduction and receptor activation,

XX or to maintain the proliferation and growth of thrombopoietin dependent

XX cell lines

XX Sequence 14 AA;

XX Query Match 78.0%; Score 85; DB 2; Length 14;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-05;

XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 3 CADGPTLRWISFC 16

XX 1 CADGPTLRWISFC 14

XX 11-MAR-1998 (first entry)

XX Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

XX haematological disorder; thrombocytopenia; chemotherapy;

XX radiation therapy; bone marrow transfusion; diagnosis;

XX signal transduction; receptor activation; cell culture.

XX Synthetic.

XX WO9640750-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009623.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barret RM, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX
 DR WPI; 1997-052226/05.
 XX
 PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Disclosure; Page 26; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 XX
 SQ Sequence 14 AA;
 Query Match 78.0%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CADGPTLRWISFC 16
 Db 1 CADGPTLRWISFC 14
 RESULT 18
 AAW33029
 ID AAW33029 standard; peptide; 14 AA.
 XX
 AC AAW33029;
 XX
 DT 11-MAR-1998 (first entry)
 XX
 DE Thrombopoietin receptor binding peptide.
 XX
 KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 PN WO9640750-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009623.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barret RM, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX
 DR WPI; 1997-052226/05.
 XX
 PT Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Claim 19; Page 89; 106pp; English.
 XX
 CC The present peptide binds the thrombopoietin receptor (TR), has a
 CC molecular weight of less than 8000 Da and a TR binding affinity as
 CC expressed by an IC50 of no more than about 100 microm. It can be used to
 CC treat disorders which are susceptible to treatment with a thrombopoietin
 CC agonist, preferably haematological disorders and thrombocytopenia
 CC resulting from chemotherapy, radiation therapy or bone marrow
 CC transfusions. It can also be used diagnostically, e.g. to investigate the
 CC mechanism of thrombopoietin signal transduction and receptor activation,
 CC or to maintain the proliferation and growth of thrombopoietin dependent
 CC cell lines
 XX
 SQ Sequence 14 AA;
 Query Match 78.0%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CADGPTLRWISFC 16
 Db 1 CADGPTLRWISFC 14
 RESULT 19
 AAW35401
 ID AAW35401 standard; peptide; 14 AA.
 XX
 AC AAW35401;
 XX
 DT 11-MAR-1998 (first entry)
 XX
 DE Thrombopoietin receptor binding peptide.
 XX
 KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH Disulfide-bond 1. 14
 FT Modified-site 14
 FT /note= "NH2-D-Cys"
 XX
 PN WO9640750-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009623.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barret RM, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX
 DR WPI; 1997-052226/05.
 XX
 PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Example 6; Page 63; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a

CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

XX Sequence 14 AA;

Query Match 78.0%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFC 16
 Db 1 CADGPTLRWISFC 14

RESULT 20

AAW36647 ID AAW36647 standard; peptide; 14 AA.

AC AAW36647;

XX 11-MAR-1998 (first entry)

DT Thrombopoietin receptor binding peptide.

DE Thrombopoietin receptor; binding peptide; treatment; agonist;

XX haematological disorder; thrombocytopenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KM signal transduction; receptor activation; cell culture.

XX Synthetic.

PN WO9640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

DR Peptides and peptide mimetics which bind to and activate the

XX thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX Disclosure; Page 26; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be

XX used to treat disorders which are susceptible to treatment with a

XX thrombopoietin agonist, preferably haematological disorders and

XX thrombocytopenia resulting from chemotherapy, radiation therapy or bone

XX marrow transfusions. It can also be used diagnostically, e.g. to

XX investigate the mechanism of thrombopoietin signal transduction and

XX receptor activation, or to maintain the proliferation and growth of

XX thrombopoietin dependent cell lines

QY 3 CADGPTLRWISFC 16
 Db 1 CADGPTLRWISFC 14

Query Match 78.0%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CADGPTLRWISFC 14

RESULT 21

AAW35400 ID AAW35400 standard; peptide; 14 AA.

XX AAW35400;

XX 11-MAR-1998 (first entry)

DT Thrombopoietin receptor binding peptide.

DE Thrombopoietin receptor; binding peptide; treatment; agonist;

XX haematological disorder; thrombocytopenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KM signal transduction; receptor activation; cell culture.

XX Synthetic.

PN WO9640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

DR Peptides and peptide mimetics which bind to and activate the

XX thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX Example 6; Page 63; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be

XX used to treat disorders which are susceptible to treatment with a

XX thrombopoietin agonist, preferably haematological disorders and

XX thrombocytopenia resulting from chemotherapy, radiation therapy or bone

XX marrow transfusions. It can also be used diagnostically, e.g. to

XX investigate the mechanism of thrombopoietin signal transduction and

XX receptor activation, or to maintain the proliferation and growth of

XX thrombopoietin dependent cell lines

XX Sequence 14 AA;

QY 3 CADGPTLRWISFC 16
 Db 1 CADGPTLRWISFC 14

Query Match 78.0%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 22
 AAW33032 ID AAW33032 standard; peptide; 14 AA.

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XX AAW3032;
AC
XX
XX 11-MAR-1998 (first entry)
DT
XX
DE Thrombopoietin receptor binding peptide.
XX
XX Thrombopoietin receptor; binding peptide; treatment; agonist;
KW haematological disorder; thrombocytopenia; chemotherapy;
KM radiation therapy; bone marrow transfusion; diagnosis;
KM signal transduction; receptor activation; cell culture.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Disulfide-bond 1. .14
FT Modified-site 1 /note= "acylated"
FT Modified-site 14 /note= "amidated"
FT
FT
XX MO9640750-A1.
XX
XX 19-DEC-1996.
PD
XX
XX 07-JUN-1996; 96WO-US009623.
PF
XX
XX 07-JUN-1995; 95US-00478128.
PR
XX 07-JUN-1995; 95US-00485301.
XX
XX (GLAXO ) GLAXO GROUP LTD.
PA
XX
XX Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
PI Mathiakakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX
XX WPI; 1997-052226/05.
DR
XX
XX Peptides and peptide mimetics which bind to and activate the
PT thrombopoietin receptor - useful in treatment of haematological
PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX
XX Claim 30; Page 91; 106pp; English.
XX
XX The present peptide binds the thrombopoietin receptor (TR), has a
CC molecular weight of less than 8000 Da and a TR binding affinity as
CC expressed by an IC50 of no more than about 100 microm. It can be used to
CC treat disorders which are susceptible to treatment with a thrombopoietin
CC agonist, preferably haematological disorders and thrombocytopenia
CC resulting from chemotherapy, radiation therapy or bone marrow
CC transplants. It can also be used diagnostically, e.g. to investigate the
CC mechanism of thrombopoietin signal transduction and receptor activation,
CC or to maintain the proliferation and growth of thrombopoietin dependent
CC cell lines
CC
XX
XX Sequence 14 AA;
SQ
XX
XX Query Match 78.0%; Score 85; DB 2; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-05;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CADGPTLRWISFC 16
DB 1 CADGPTLRWISFC 14

```

```

DE TPO-mimetic peptide sequence SEQ ID NO:70.
XX
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTR44; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
XX thrombolysis; pharmaceutical.
XX
XX Synthetic.
OS
XX
XX MO200024782-A2.
XX
XX 04-MAY-2000.
PD
XX
XX 25-OCT-1999; 99WO-US025044.
PF
XX
XX 23-OCT-1998; 98US-0105371P.
PR
XX 22-OCT-1999; 99US-00428082.
XX
XX (AMGEN-) AMGEN INC.
PA
XX
XX Feige U, Liu C, Cheatham J, Boone TC;
PI
XX
XX WPI; 2000-350702/30.
DR
XX
XX Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
XX Claim 19; Page 218; 608pp; English.
XX
XX The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)-C-P1, -(L1)-C-P1-(L2)-d-P2, -(L1)-C-P1-
CC -(L2)-d-P2-(L3)-e-P3, or -(L1)-C-P1-(L2)-d-P2-(L3)-e-P3-(L4)-F-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombolysis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions, and
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
CC
XX
XX Sequence 14 AA;
SQ
XX
XX Query Match 78.0%; Score 85; DB 3; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-05;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CADGPTLRWISFC 16
DB 1 CADGPTLRWISFC 14

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RESULT 24
AAU25826
ID AAU25826 standard; peptide; 14 AA.
XX
XX AAU25826;
AC
XX 17-DEC-2001 (first entry)
DT
XX Human thrombopoietin receptor (TPO-R) activator peptide #12.
DE
XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; cytokine;
XX

```

KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ,
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Poddaturi S;
 PI Yin Q;
 DR WPI; 2001-564142/63.
 XX
 DR Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 PS Disclosure; Col 67-68; 128pp; English.
 XX
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX
 SO Sequence 14 AA;
 Query Match 78.0%; Score 85; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CADGPTLREWISFC 16
 DB 1 CADGPTLREWISFC 14
 RESULT 25
 AAU25852
 ID AAU25852 standard; peptide; 14 AA.
 XX
 AC AAU25852;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #38.
 XX

KW peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ,
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Poddaturi S;
 PI Yin Q;
 DR WPI; 2001-564142/63.
 XX
 DR Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 PS Disclosure; Col 20; 128pp; English.
 XX
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX
 SO Sequence 14 AA;
 Query Match 78.0%; Score 85; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CADGPTLREWISFC 16
 DB 1 CADGPTLREWISFC 14
 RESULT 26
 AAU25866
 ID AAU25866 standard; peptide; 14 AA.
 XX
 AC AAU25866;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #52.
 XX

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
XX haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
XX bone marrow transplantation; haematological disorder; platelet disorder;
XX enzyme-linked immunosorbent assay; in situ staining; biological fluid;
XX tissue homogenate; fluorescence-activated cell sorting; Western blotting;
XX in vitro expansion; megakaryocyte; Headpiece Dimer gene; IacI gene.
OS Homo sapiens.
XX US6251864-B1.
XX 26-JUN-2001.
XX 01-MAR-2000; 2000US-00516704.
XX 07-JUN-1995; 95US-00478128.
XX 07-JUN-1995; 95US-00485301.
XX 07-JUN-1996; 96WO-US0009623.
XX 15-AUG-1996; 96US-00699027.
XX (GLAXO) GLAXO GROUP LTD.
XX Dower WJ, Barrett RM, Cwiria SE, Gates CM, Schatz PJ;
XX Balasubramanian P, Wagstrom CR, Hendren RM, Depirince RB, Poddaturi S;
XX Yin Q;
XX WPI; 2001-564142/63.
XX Activating thrombopoietin receptors in cells, used to treat
XX thrombocytopenia and hematological disorders, comprises contacting cells
XX with peptides and peptide mimetics attached to hydrophilic polymers.
XX Disclosure; Col 20; 128pp; English.
XX Sequences AM25815-AM26049 represent peptides and peptide mimetics that
XX bind to and activate the human thrombopoietin receptor (TPO-R). Methods
XX of activating thrombopoietin receptors in cells comprise contacting the
XX cells with effective amounts of peptides and peptide mimetics attached to
XX hydrophilic polymers. The methods are used to treat thrombocytopenia such
XX as that due to chemotherapy, radiation therapy or bone-marrow
XX transplantation and to prevent thrombocytopenia in patients at risk. The
XX sequences are used to treat and prevent haematological disorders
XX including thrombocytopenia and platelet disorders. They are used in vitro
XX as unique tools for understanding the biological role of thrombopoietin
XX (TPO) and to develop other compounds that bind to and activate the TPO
XX receptor. The peptides can be used to detect TPO receptors on living
XX cells and fixed cells, in biological fluids, in tissue homogenates, and
XX in purified or natural biological materials. They may also be used for in
XX situ staining, fluorescence-activated cell sorting, Western blotting and
XX enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
XX be used for in vitro expansion of megakaryocytes and their committed
XX progenitors alone or in conjunction with additional cytokines
XX Sequence 14 AA;
XX
XX Query Match 78.0%; Score 85; DB 4; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-05;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CADGPTLRWISFC 16
DB 1 CADGPTLRWISFC 14
RESULT 27
ABR72900
ID ABR72900 standard; peptide; 14 AA.
XX
XX AC ABR72900;
XX
XX DT 05-APR-2002 (first entry)

DE TPO mimetic peptide SEQ ID NO:70.
XX Modified peptide, mimetic; Fe domain; fusion; immunoglobulin G; IgG; EPO;
XX erythropoietin; TPO; tumor necrosis factor alpha inhibitor;
XX TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
XX TPO mimetic peptide; EPO mimetic peptide; EGF; VEGF antagonist;
XX MMP inhibitor; antiinflammatory; antitumor; immunosuppressive;
XX cytostatic; antineutlastic; antirheumatic; antidiabetic; ophthalmological;
XX antianemic; anorectic; antifertility; haemostatic; dermatological;
XX neuroprotective; inflammatory disease; autoimmune disease; tumor growth;
XX cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
XX sleep disorder; neurological degenerative disease; anaemia;
XX thrombocytopenia; metastatic tumor; systemic lupus erythematosus;
XX Fanconi's syndrome.
XX Homo sapiens.
XX Synthetic.
XX WO200183525-A2.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US014310.
XX 03-MAY-2000; 2000US-00563286.
XX (AMGE-) AMGEN INC.
XX Feige U, Liu C, Cheatham JC, Boone TC, Gudae JM;
XX WPI; 2002-130313/17.
XX Novel vehicle-peptide molecule or its multimers useful for treating
XX inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
XX diabetic retinopathy, obesity, sleep disorders and infertility.
XX Claim 39; Page 44; 176pp; English.
XX The present invention describes a vehicle-peptide molecule (I) or its
XX multimers. (I) can have antiinflammatory, antitumor, immunosuppressive,
XX cytostatic, anorectic, antirheumatic, antidiabetic, ophthalmological,
XX antianemic, anorectic, antifertility, haemostatic, dermatological and
XX neuroprotective activities. (I) can be used as a therapeutic or
XX prophylactic agent as well as for screening purposes. (I) is useful for
XX diagnosing diseases characterised by dysfunction of their associated
XX protein of interest, for identifying normal or abnormal proteins of
XX interest, as a part of diagnostic kit to detect the presence of their
XX proteins of interest in a biological sample. Additionally, (I) is useful
XX for treating inflammatory and autoimmune diseases, tumor growth, cancer,
XX rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
XX infertility, and neurological degenerative diseases. (I), comprising EPO-
XX mimetic compounds are useful for treating disorders characterised by low
XX red blood cell levels such as anaemia. The TPO-mimetic comprising
XX compounds are useful for treating conditions that involve an existing
XX megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
XX deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
XX tumor which result in thrombocytopenia, systemic lupus erythematosus,
XX CC represent amino acid and nucleic acid sequences used in the
XX exemplification of the present invention
XX Sequence 14 AA;
XX
XX Query Match 78.0%; Score 85; DB 5; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-05;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CADGPTLRWISFC 16
DB 1 CADGPTLRWISFC 14
RESULT 28

ADJ73051	standard; peptide; 14 AA.
ID	
XX	
AC	ADJ73051;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	TPO mimetic peptide sequence Segid 505.
XX	
KW	mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KW	cardiovascular; infectious; malignant; neurologic disease; anaemia;
KW	immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
XX	TPO.
XX	
OS	Synthetic.
XX	
PN	WO2003084477-A2.
XX	
PD	16-OCT-2003.
XX	
PF	24-MAR-2003; 2003WO-US009139.
XX	
PR	29-MAR-2002; 2002US-0368791P.
XX	
PA	(CENZ) CENTOCOR INC.
XX	
PI	Heavner GA, Knight DM, Scallion BJ, Grayeb J;
XX	
DR	WPI; 2003-804237/75.
XX	
PT	New CDR mimetibody comprising a portion of a heavy or light chain
PT	variable region comprising human framework or ligand binding region,
PT	useful for preparing a composition for treating e.g., immune,
PT	cardiovascular or neurologic disease.
XX	
PS	Disclosure; SEQ ID NO 505; 97pp; English.
XX	
CC	This invention relates to novel mammalian CDR mimetibodies, specific
CC	portions or variants thereof. Specifically, it refers to an antibody
CC	fragment where a protein has been inserted into, or replaces a portion
CC	of, one or more CDR regions, such that each CDR mimetibody comprises at
CC	least one portion of a heavy chain or light chain variable region, which
CC	itself comprises at least one human framework region and at least one
CC	ligand binding region (LBR). The present invention describes human
CC	mimetibodies, including modified immunoglobulins and cleavage products
CC	that can be useful in gene therapy and the generation of transgenic
CC	plants and animals. Furthermore, the CDR mimetibody is useful for
CC	preparing compositions for modulating, treating or reducing the symptoms
CC	of immune, cardiovascular, infectious, malignant and/or neurologic
CC	diseases, as well as anemia. Accordingly, they exhibit immunomodulator,
CC	cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC	peptide sequence is a TPO mimetic peptide sequence used to make a
CC	mimetibody of the invention.
XX	
SQ	Sequence 14 AA:
XX	
QY	3 CADGPTLRMISFC 16
DB	1 CADGPTLRMISFC 14
XX	
Query Match	78.0%; Score 85; DB 7; Length 14;
Best Local Similarity	100.0%; Pred. No. 1.3e-05;
Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
XX	
RESULT 29	
ADJ52686	
ID	ADJ52686 standard; peptide; 14 AA.
XX	
AC	ADJ52686;
XX	
DT	06-MAY-2004 (first entry)
XX	

[illegible]

XX	dermatological-gen; auditory; endocrine-gen; gastrointestinal-gen;
KW	gynaecological-gen; hepatotropic; haemostatic; immunomodulator;
KW	antiallergic; muscular-gen; cytosolic; antiinflammatory; neuroleptic;
KW	ophthalmologic; nephrotropic; respiratory-gen; tumour necrosis factor;
KW	TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
KW	dental disorder; oral disorder; dermatological disorder; ear disorder;
KW	nose disorder; throat disorder; endocrine disorder; metabolic disorder;
KW	gastrointestinal disorder; gynaecological disorder; hepatic disorder;
KW	osteotic disorder; haematologic disorder; immunological disorder;
KW	allergic disorder; infectious disorder; musculoskeletal disorder;
KW	oncological disorder; neurological disorder; nutritional disorder;
KW	ophthalmologic disorder; pediatric disorder; psychiatric disorder;
KW	renal disorder; pulmonary disorder.
XX	Unidentified.
OS	Synthetic.
XX	WO2004002424-A2.
PN	08-JAN-2004.
PD	08-JAN-2004.
XX	30-JUN-2003; 2003WO-US020495.
XX	28-JUN-2002; 2002US-0392431P.
PR	19-SEP-2002; 2002US-0412144P.
XX	(CENZ) CENTOCOR INC.
PA	Heavner GA, Knight DM, Ghirayev J, Scallion EJ, Nessor TC,
PI	Kutolooski KA,
PI	WPI; 2004-082872/08.
DR	
XX	New CH1 deleted mimetibody polypeptide and nucleic acid, useful for
PT	diagnosing, preventing or treating cardiovascular, dermatologic,
PT	endocrine, gastrointestinal, gynecologic, infectious, neurologic and
PT	nutritional disorders.
XX	
PS	Claim 15; SEQ ID NO 505; 123pp; English.
XX	
XX	This invention relates to CH1 deleted mimetibodies (and the DNA sequences
CC	which encode them), compositions, methods and uses. The invention may be
CC	useful for the development of compounds with an osteopathic,
CC	cardiovascular-gen, dermatological-gen, auditory, endocrine-gen,
CC	gastrointestinal-gen, gynaecological-gen, hepatotropic, haemostatic,
CC	immunomodulator, antiallergic, muscular-gen, cytosolic,
CC	antiinflammatory, neuroleptic, ophthalmologic, nephrotropic or
CC	respiratory-gen activity acting as a tumour necrosis factor (TNF)-
CC	modulator or cytokine-agonist. The methods and compositions of the
CC	present invention are useful for the diagnosis, prevention and/or
CC	treatment of diseases or conditions associated with aberrant expression
CC	or activity of the CH1 deleted mimetibody, such as a bone or joint,
CC	cardiovascular, dental or oral, dermatological, ear, nose or throat,
CC	endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
CC	osteotic, haematologic, immunological, allergic, infectious,
CC	musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
CC	pediatric, psychiatric, renal or pulmonary disorders. The present
CC	sequence is that of a peptide which may be used during the creation of a
CC	mimetibody of the invention.
CC	
XX	
XX	Sequence 14 AA;
XX	
XX	Query Match 78.0%; Score 85; DB 8; Length 14;
XX	Best Local Similarity 100.0%; Pred. No. 1,3e-05;
XX	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
QY	3 CADGPTLRWISFC 16
QY	
QY	
QY	
QY	
QY	1 CADGPTLRWISFC 14
QY	Db
QY	RESULT 31
QY	AA090467

ID		AAW09467 standard; protein; 13 AA.
XX		
AC	AAW09467;	
DT	10-SEP-1997	(first entry)
XX		
DE	Thrombopoietin receptor binding compound cyclic peptide.	
XX		
KM	Haematology; thrombocytopenia; TPO; TR; proliferation; cyclic; bone marrow transfusion; chemotherapy; radiation therapy.	
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers 1
FT	Modified-site	/note= "The Ala is linked with the modified Cys at position 13"
FT		14
FT	Modified-site	/label= OTHER
FT		/note= "S-carboxymethyl-L-cysteine alpha-carboxamide; forming a linkage onto the Ala at position one with the delta C of this residue"
PN	WO9640189-A1.	
PD	19-DEC-1996.	
PJ		
PF	05-JUN-1996;	96WO-US0088998.
PR	07-JUN-1995;	95US-00472371.
PR	07-JUN-1995;	95US-00473604.
PR	07-JUN-1995;	95US-00476168.
PR	07-JUN-1995;	95US-00478128.
PR	07-JUN-1995;	95US-00484090.
PA	07-JUN-1995;	95US-00485301.
	(GLAXO) GLAXO GROUP LTD.	
XK	Dower WJ, Barrett RM, Cairla SE, Duffin DJ, Gatee CM, Johnson SS; Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;	
PI	MPI, 1997-051883/05.	
DR		
XX	Thrombopoietin receptor-binding/activating peptide(s) and peptide mimetic(s) - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.	
PS	Claim 30; Page 91; 106pp; English.	
CC	The present sequence is a compound which binds to thrombopoietin (TPO) receptor (TR). The compound can be used for treating patients suffering from haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transusions. The peptide may also be used to maintain the proliferation and growth of TPO- dependent cell lines and for use in biological research, for detecting TPO receptors on living cells	
CC		
CC		
XX	Sequence 13 AA;	
QQ		
Query Match	69.7%; Score 76; DB 2; Length 13;	
Best Local Similarity	100.0%; Pred. No. 0.00025;	
Matches 13; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	4 ADGPTLRHWISFC 16 	
Db	1 ADGPTLRHWISFC 13	
RESULT 32		
AAW35399		
ID	AAW35399 standard; peptide; 13 AA.	
XX		
AC	AAW35399;	

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XX 11-MAR-1998 (first entry)
DT Thrombopoietin receptor binding peptide.
DE
XX Thrombopoietin receptor; binding peptide; treatment; agonist;
XX haematological disorder; thrombocytopenia; chemotherapy;
KM radiation therapy; bone marrow transfusion; diagnosis;
KW signal transduction; receptor activation; cell culture.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "COCH2-alanine linked via CH2 group to Cys13"
FT Modified-site 13 /note= "NH2-cytosine linked via sulphoxidised thiol group
FT to Ala1"
XX
XX WO9640750-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US009623.
XX
XX 07-JUN-1995; 95US-00478128.
XX 07-JUN-1995; 95US-00485301.
XX
XX (GLAXO ) GLAXO GROUP LTD.
XX
XX Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX
XX WPI; 1997-052226/05.
XX
XX Peptides and peptide mimetics which bind to and activate the
PT thrombopoietin receptor - useful in treatment of haematological
PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX
XX Example 6; Page 63; 106pp; English.
XX
XX The present peptide, which binds the thrombopoietin receptor (TR), can be
CC used to treat disorders which are susceptible to treatment with a
CC thrombopoietin agonist, preferably haematological disorders and
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC marrow transfusions. It can also be used diagnostically, e.g. to
CC investigate the mechanism of thrombopoietin signal transduction and
CC receptor activation, or to maintain the proliferation and growth of
CC thrombopoietin dependent cell lines
XX
XX Sequence 13 AA;
SQ
Query Match 69.7%; Score 76; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ADGPTLRWISFC 16
DB 1 ADGPTLRWISFC 13

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KM radiation therapy; bone marrow transfusion; diagnosis;
KW signal transduction; receptor activation; cell culture.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Cross-links 1 /note= "linked via disulfide bond to Cys1 of identical
FT peptide"
FT Modified-site 13 /note= "NH2-Phe"
XX
XX WO9640750-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US009623.
XX
XX 07-JUN-1995; 95US-00478128.
XX 07-JUN-1995; 95US-00485301.
XX
XX (GLAXO ) GLAXO GROUP LTD.
XX
XX Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX
XX WPI; 1997-052226/05.
XX
XX Peptides and peptide mimetics which bind to and activate the
PT thrombopoietin receptor - useful in treatment of haematological
PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX
XX Example 9; Page 73; 106pp; English.
XX
XX The present peptide, which binds the thrombopoietin receptor (TR), can be
CC used to treat disorders which are susceptible to treatment with a
CC thrombopoietin agonist, preferably haematological disorders and
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC marrow transfusions. It can also be used diagnostically, e.g. to
CC investigate the mechanism of thrombopoietin signal transduction and
CC receptor activation, or to maintain the proliferation and growth of
CC thrombopoietin dependent cell lines
XX
XX Sequence 13 AA;
SQ
Query Match 69.7%; Score 76; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CADGPTLRWISF 15
DB 1 CADGPTLRWISF 13

```

```

RESULT 33
AAW35417
ID AAW35417 standard; peptide; 13 AA.
XX
XX AAW35417;
AC
XX
XX 11-MAR-1998 (first entry)
DT
XX
XX Thrombopoietin receptor binding peptide.
DE
XX
XX Thrombopoietin receptor; binding peptide; treatment; agonist;
KW haematological disorder; thrombocytopenia; chemotherapy;
KM signal transduction; receptor activation; cell culture.

```

```

RESULT 34
AAW33033
ID AAW33033 standard; peptide; 13 AA.
XX
XX AAW33033;
AC
XX
XX 11-MAR-1998 (first entry)
DT
XX
XX Thrombopoietin receptor binding peptide.
DE
XX
XX Thrombopoietin receptor; binding peptide; treatment; agonist;
KW haematological disorder; thrombocytopenia; chemotherapy;
KW radiation therapy; bone marrow transfusion; diagnosis;
KW signal transduction; receptor activation; cell culture.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1

```

FT	Modified-site	/note= "COCH2-alanine linked via CH2 group to Cys13"
FT	13	
FT	/note= "NH2-cytosine linked via thiol group to Ala1"	
XX		
XX	WO9640750-A1.	
XX		
XX	19-DEC-1996.	
PD		
XX		
XX	07-JUN-1996;	96WO-US0009623.
PF		
XX		
PR	07-JUN-1995;	95US-00478128.
PR	07-JUN-1995;	95US-00485301.
XX		
XX	(GLAX) GLAXO GROUP LTD.	
PA		
XX		
PI	Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;	
PI	Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;	
XX		
DR	WPI: 1997-052226/05.	
XX		
XX		
PT	Peptides and peptide mimetics which bind to and activate the	
PT	thrombopoietin receptor - useful in treatment of haematological	
PT	disorders, esp. thrombocytopenia resulting from chemotherapy, etc.	
XX		
PS	Claim 30; Page 91; 106pp; English.	
XX		
XX		
CC	The present peptide binds the thrombopoietin receptor (TR), has a	
CC	molecular weight of less than 8000 Da and a TR binding affinity as	
CC	expressed by an IC50 of no more than about 100 microm. It can be used to	
CC	treat disorders which are susceptible to treatment with a thrombopoietin	
CC	agonist, preferably haematological disorders and thrombocytopaenia	
CC	resulting from chemotherapy, radiation therapy or bone marrow	
CC	transfusions. It can also be used diagnostically, e.g. to investigate the	
CC	mechanism of thrombopoietin signal transduction and receptor activation,	
CC	or to maintain the proliferation and growth of thrombopoietin dependent	
CC	cell lines	
XX		
XX		
SQ	Sequence 13 AA;	
	Query Match	69.7%; Score 76; DB 2; Length 13;
	Best local Similarity	100.0%; Pred. No. 0.00025;
	Matches 13; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	4 ADGPTLRWISFC 16	
	1 ADGPTLRWISFC 13	
DB		
	RESULT 35	
	AAW35413	
ID	AAW35413 standard; peptide; 13 AA.	
XX		
XX	AAW35413;	
AC		
XX		
DT	11-MAR-1998 (first entry)	
XX		
DE		
XX	Thrombopoietin receptor binding peptide.	
XX		
KW	Thrombopoietin receptor; binding peptide; treatment; agonist;	
KW	haematological disorder; thrombocytopaenia; chemotherapy;	
KW	radiation therapy; bone marrow transfusion; diagnosis;	
KW	signal transduction; receptor activation; cell culture.	
XX		
OS	Synthetic.	
XX		
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	1
FT	/note= "Br-Ala"	
FT	Modified-site	13
FT	/note= "NH2-Cys"	
XX		
XX	WO9640750-A1.	
XX		

[illegible]

XX	Dover WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI	Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX	
DR	WPI, 1997-052226/05.
XX	
PT	Peptides and peptide mimetics which bind to and activate the
PT	thrombopoietin receptor - useful in treatment of haematological
PT	disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX	
PS	Example 6; Page 64; 106pp; English.
XX	
CC	The present peptide, which binds the thrombopoietin receptor (TR), can be
CC	used to treat disorders which are susceptible to treatment with a
CC	thrombopoietin agonist, preferably haematological disorders and
CC	thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC	marrow transfusions. It can also be used diagnostically, e.g. to
CC	investigate the mechanism of thrombopoietin signal transduction and
CC	receptor activation, or to maintain the proliferation and growth of
CC	thrombopoietin dependent cell lines
XX	
SO	Sequence 13 AA;
Query Match	69.7%; Score 76; DB 2; Length 13;
Best Local Similarity	100.0%; Pred. No. 0.00025;
Matches 13; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	4 ADGPTLRWISFC 16
DB	1 ADGPTLRWISFC 13
RESULT 37	
AAW35422	
ID	AAW35422 standard; peptide; 13 AA.
XX	
AC	AAW35422;
XX	
DT	11-MAR-1998 (first entry)
XX	
DE	Thrombopoietin receptor binding peptide.
XX	
KW	Thrombopoietin receptor; binding peptide; treatment; agonist;
KW	haematological disorder; thrombocytopenia; chemotherapy;
KW	radiation therapy; bone marrow transfusion; diagnosis;
XX	signal transduction; receptor activation; cell culture.
XX	
OS	Synthetic.
XX	
PH	Key
FT	Modified-site
FT	Location/Qualifiers
FT	1
FT	/note= "optionally acylated"
FT	13
FT	/note= "linked via disulfide bond to Cys13 of identical
FT	peptide"
XX	
PN	WO9640750-A1.
XX	
PD	19-DEC-1996.
XX	
PF	07-JUN-1996; 96WO-US009623.
XX	
PR	07-JUN-1995; 95US-00478128.
XX	
PR	07-JUN-1995; 95US-00485301.
XX	
PA	(GLAX) GLAXO GROUP LTD.
XX	
PI	Dover WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI	Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX	
DR	WPI, 1997-052226/05.
XX	

PT	thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX	
PS	Example 9; Page 74; 106pp; English.
XX	
CC	The present peptide, which binds the thrombopoietin receptor (TR), can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and thrombocytopenia resulting from chemotherapy, radiation therapy or bone marrow transfusions. It can also be used diagnostically, e.g. to investigate the mechanism of thrombopoietin signal transduction and receptor activation, or to maintain the proliferation and growth of thrombopoietin dependent cell lines
CC	
CC	Sequence 13 AA;
SQ	
Query Match	69.7%; Score 76; DB 2; Length 13;
Best Local Similarity	100.0%; Pred. No. 0.00025; Mismatches 0; Indels 0; Gaps 0
Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	4 ADGPTLRWISFC 16 1 ADGPTLRWISFC 13
Db	
RESULT 38	
AAM35397	
ID	AAM35397 standard; peptide; 13 AA.
XX	
AC	AAM35397;
XX	
DT	11-MAR-1998 (first entry)
XX	
DE	Thrombopoietin receptor binding peptide.
XX	
KM	Thrombopoietin receptor; binding peptide; treatment; agonist; haematological disorder; thrombocytopenia; chemotherapy; radiation therapy; bone marrow transfusion; diagnosis; signal transduction; receptor activation; cell culture.
KW	
OS	Synthetic.
XX	
FH	Key
FT	Modified-site
FT	Location/Qualifiers
FT	1
FT	/note= "COCN2-alanine linked via CH2 group to Cys13"
FT	Modified-site
FT	13
FT	/note= "NH2-cytosine linked via thiol group to Ala1"
XX	
PN	WO9640750-A1.
XX	
PD	19-DEC-1996.
XX	
PF	07-JUN-1996; 96WO-US009623.
XX	
PR	07-JUN-1995; 95US-00478128.
PR	07-JUN-1995; 95US-00485301.
XX	
PA	(GLAXO) GLAXO GROUP LTD.
XX	
PI	Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS; Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX	
DR	WPI; 1997-052226/05.
XX	
PT	Peptides and peptide mimetics which bind to and activate the thrombopoietin receptor - useful in treatment of haematological disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX	
PS	Example 6; Page 63; 106pp; English.
XX	
CC	The present peptide, which binds the thrombopoietin receptor (TR), can be used to treat disorders which are susceptible to treatment with a thrombopoietin agonist, preferably haematological disorders and

CC thrombocytopaenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transplants. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

SQ Sequence 13 AA;

Query Match 69.7%; Score 76; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 ADGPTLRWISFC 16
 |||||
 Db 1 ADGPTLRWISFC 13

RESULT 39

AAU25997

ID AAU25997 standard; peptide; 13 AA.

AC AAU25997;

DT 17-DEC-2001 (first entry)

DE Human thrombopoietin receptor (TPO-R) activator peptide #183.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 XX haemostatic; thrombocytopaenia; chemotherapy; radiation therapy; ELISA;
 XX bone marrow transplantation; haematological disorder; platelet disorder;
 XX enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 XX tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 XX in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.

OS Homo sapiens.

PN US6251864-B1.

PD 26-JUN-2001.

PF 01-MAR-2000; 2000US-00516704.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PR 07-JUN-1996; 96WO-US009623.

PR 15-AUG-1996; 96US-00699027.

PA (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ,
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;
 PI Yin Q;

DR WPI; 2001-564142/63.

PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopaenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.

PS Disclosure; Col 143-144; 128pp; English.

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopaenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopaenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopaenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living

CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines

SQ Sequence 13 AA;

Query Match 69.7%; Score 76; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CADGPTLRWISF 15
 |||||
 Db 1 CADGPTLRWISF 13

RESULT 40

AAU25984

ID AAU25984 standard; peptide; 13 AA.

AC AAU25984;

DT 17-DEC-2001 (first entry)

DE Human thrombopoietin receptor (TPO-R) activator peptide #170.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 XX haemostatic; thrombocytopaenia; chemotherapy; radiation therapy; ELISA;
 XX bone marrow transplantation; haematological disorder; platelet disorder;
 XX enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 XX tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 XX in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.

OS Homo sapiens.

PN US6251864-B1.

PD 26-JUN-2001.

PF 01-MAR-2000; 2000US-00516704.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PR 07-JUN-1996; 96WO-US009623.

PR 15-AUG-1996; 96US-00699027.

PA (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ,
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;
 PI Yin Q;

DR WPI; 2001-564142/63.

PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopaenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.

PS Disclosure; Col 137; 128pp; English.

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopaenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopaenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopaenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO

receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for in situ staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can be used for in vitro expansion of megakaryocytes and their committed progenitors alone or in conjunction with additional cytokines

XX Sequence 13 AA;

Query Match 69.7%; Score 76; DB 4; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00025; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 ADGPTLRWISFC 16
1 ADGPTLRWISFC 13

RESULT 41

AAW35398 standard; peptide; 14 AA.

AAW35398;

11-MAR-1998 (first entry)

Thrombopoietin receptor binding peptide.

Thrombopoietin receptor; binding peptide; treatment; agonist;

haematological disorder; thrombocytopenia; chemotherapy;

radiation therapy; bone marrow transplantation; diagnosis;

signal transduction; receptor activation; cell culture.

Synthetic.

Key Location/Qualifiers

Disulfide-bond 1..14 /note= "Homocysteine"

Modified-site 14 /note= "NH2-Cys"

Modified-site 14

MO9640750-A1.

19-DEC-1996.

07-JUN-1996; 96WO-US009623.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00485301.

(GLAXO) GLAXO GROUP LTD.

Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

Mattheakis LC, Schatz PJ, Westrom CR, Wrighton NC;

WP1; 1997-052226/05.

Peptides and peptide mimetics which bind to and activate the

thrombopoietin receptor - useful in treatment of haematological

disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

Example 6; Page 63; 106pp; English.

The present peptide, which binds the thrombopoietin receptor (TR), can be

used to treat disorders which are susceptible to treatment with a

thrombopoietin agonist, preferably haematological disorders and

thrombocytopenia resulting from chemotherapy, radiation therapy or bone

marrow transplants. It can also be used diagnostically, e.g. to

investigate the mechanism of thrombopoietin signal transduction and

receptor activation, or to maintain the proliferation and growth of

thrombopoietin dependent cell lines

XX Sequence 14 AA;

Query Match 69.7%; Score 76; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00027; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 ADGPTLRWISFC 16
2 ADGPTLRWISFC 14

RESULT 42

AAW35396 standard; peptide; 14 AA.

AAW35396;

11-MAR-1998 (first entry)

Thrombopoietin receptor binding peptide.

Thrombopoietin receptor; binding peptide; treatment; agonist;

haematological disorder; thrombocytopenia; chemotherapy;

radiation therapy; bone marrow transplantation; diagnosis;

signal transduction; receptor activation; cell culture.

Synthetic.

Key Location/Qualifiers

Disulfide-bond 1..14 /note= "Penicillamine"

Modified-site 14 /note= "NH2-Cys"

Modified-site 14

MO9640750-A1.

19-DEC-1996.

07-JUN-1996; 96WO-US009623.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00485301.

(GLAXO) GLAXO GROUP LTD.

Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

Mattheakis LC, Schatz PJ, Westrom CR, Wrighton NC;

WP1; 1997-052226/05.

Peptides and peptide mimetics which bind to and activate the

thrombopoietin receptor - useful in treatment of haematological

disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

Example 6; Page 63; 106pp; English.

The present peptide, which binds the thrombopoietin receptor (TR), can be

used to treat disorders which are susceptible to treatment with a

thrombopoietin agonist, preferably haematological disorders and

thrombocytopenia resulting from chemotherapy, radiation therapy or bone

marrow transplants. It can also be used diagnostically, e.g. to

investigate the mechanism of thrombopoietin signal transduction and

receptor activation, or to maintain the proliferation and growth of

thrombopoietin dependent cell lines

QY 4 ADGPTLREWISFC 16
 |||||
 DB 2 ADGPTLREWISFC 14

RESULT 43

AAW35402
 ID AAW35402 standard; peptide; 14 AA.

AC AAW35402;

DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.

OS Synthetic.

FT Key Location/Qualifiers

FT Disulfide-bond 1. .14

FT Modified-site /note= "D-form residue, Penicillamine"

FT Modified-site 14

FT /note= "NH2-D-Cys"

PN WO9640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PA (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barrett RW, Cwirila SE, Duffin DJ, Gates CM, Johnson SS;
 PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

WP1; 1997-052226/05.

PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

PS Example 6; Page 64; 106pp; English.

CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

SQ Sequence 14 AA;

Query Match 69.7%; Score 76; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00077;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ADGPTLREWISFC 16
 |||||
 DB 2 ADGPTLREWISFC 14

RESULT 44
 AAU25987

ID AAU25987 standard; peptide; 14 AA.

AC AAU25987;

DT 18-DEC-2001 (first entry)

DE Human thrombopoietin receptor (TPO-R) activator peptide #173.

KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.

OS Homo sapiens.

PN US6251864-B1.

PD 26-JUN-2001.

PF 01-MAR-2000; 2000US-00516704.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PR 07-JUN-1996; 96WO-US009623.

PR 15-AUG-1996; 96US-00699027.

PA (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barrett RW, Cwirila SE, Gates CM, Schatz PJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Depirince RB, Poddaturi S;
 PI Yin Q;

WP1; 2001-564142/63.

PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.

PS Disclosure; Col 139; 128pp; English.

CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines

SQ Sequence 14 AA;

Query Match 69.7%; Score 76; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00027;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CADGPTLREWISF 15
 |||||
 DB 1 CADGPTLREWISF 13

RESULT 45

Search completed: September 1, 2005, 16:12:08
Job time : 84.7482 secs

AAU25983
ID AAU25983 standard; peptide, 14 AA.
AC AAU25983;
XX
XX
XX
DT 18-DEC-2001 (first entry)
XX
XX
DE Human thrombopoietin receptor (TPO-R) activator peptide #169.
XX
XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
KM haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
KM bone marrow transplantation; haematological disorder; platelet disorder;
KM enzyme-linked immunosorbent assay; in situ staining; biological fluid;
KM tissue homogenate; fluorescence-activated cell sorting; Western blotting;
KM in vitro expansion; megakaryocyte; Headpiece Dimer gene; Iaci gene.
XX
XX Homo sapiens.
OS
XX
XX US6251864-B1.
PN
XX 26-JUN-2001.
PD
XX
XX 01-MAR-2000; 2000US-00516704.
PF
XX
XX 07-JUN-1995; 95US-00478128.
PR 07-JUN-1995; 95US-00485301.
PR 07-JUN-1996; 96WO-US009623.
PR 15-AUG-1996; 96US-00699027.
XX
XX (GLAXO) GLAXO GROUP LTD.
PA
XX
XX Dower WJ, Barrett RM, Cwiria SE, Gates CM, Schatz PJ,
PI Balasubramanian P, Wagstrom CR, Hendren RM, Deprince RB, Podduturi S;
PI Yin Q;
XX
XX WPI; 2001-564142/63.
DR
XX
XX Activating thrombopoietin receptors in cells, used to treat
PT thrombocytopenia and hematological disorders, comprises contacting cells
PT with peptides and peptide mimetics attached to hydrophilic polymers.
XX
XX
PS Disclosure; Col 135-137, 128pp; English.
XX
XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
CC of activating thrombopoietin receptors in cells comprise contacting the
CC cells with effective amounts of peptides and peptide mimetics attached to
CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
CC as that due to chemotherapy, radiation therapy or bone-marrow
CC transplantation and to prevent thrombocytopenia in patients at risk. The
CC sequences are used to treat and prevent haematological disorders
CC including thrombocytopenia and platelet disorders. They are used in vitro
CC as unique tools for understanding the biological role of thrombopoietin
CC (TPO) and to develop other compounds that bind to and activate the TPO
CC receptor. The peptides can be used to detect TPO receptors on living
CC cells and fixed cells, in biological fluids, in tissue homogenates, and
CC in purified or natural biological materials. They may also be used for in
CC situ staining, fluorescence-activated cell sorting, Western blotting and
CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
CC be used for in vitro expansion of megakaryocytes and their committed
CC progenitors alone or in conjunction with additional cytokines
XX
XX
SQ Sequence 14 AA;
Query Match 69.7%; Score 76; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ADGPTLRWISFC 16
DB 2 ADGPTLRWISFC 14

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2005, 15:57:33 ; Search time 13.7266 Seconds
(without alignments)
126.171 Million cell updates/sec

Title: US-10-083-768-6

Perfect score: 109
Sequence: 1 GGCAGDPTLRWISFCGG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

1: PIR.79:*
2: PIR2:*
3: PIR3:*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	45.0	245	2	T47701
2	47	43.1	475	2	T33943
3	45	41.3	108	2	T49731
4	45	41.3	180	2	T4944
5	45	41.3	421	2	T22969
6	45	41.3	499	2	S51089
7	44	40.4	346	2	T19008
8	44	40.4	346	2	A58583
9	44	40.4	371	2	D75266
10	44	40.4	490	2	T09084
11	44	40.4	526	2	A86440
12	44	40.4	974	2	S34189
13	44	40.4	1022	1	S00503
14	44	40.4	1023	2	A24414
15	43.5	39.9	376	2	T39685
16	43.5	39.9	1499	2	A89813
17	43	39.4	113	2	D72595
18	43	39.4	115	2	T15386
19	43	39.4	230	2	I48685
20	43	39.4	233	2	A82768
21	43	39.4	246	2	T19988
22	43	39.4	247	2	T01012
23	43	39.4	268	2	D97548
24	43	39.4	276	2	A38654
25	43	39.4	953	2	S54478
26	43	39.4	1010	2	B37227
27	43	39.4	1013	1	S00801
28	43	39.4	1013	2	C24639
29	43	39.4	1017	2	A37227

30	43	39.4	1020	2	A34474	Na+/K+-exchanging
31	43	39.4	1020	2	B24639	Na+/K+-exchanging
32	43	39.4	1021	1	PMSHNA	Na+/K+-exchanging
33	43	39.4	1021	1	S04630	Na+/K+-exchanging
34	43	39.4	1021	2	A28139	Na+/K+-exchanging
35	43	39.4	1021	2	B24862	Na+/K+-exchanging
36	43	39.4	1022	2	S49127	Na+/K+-exchanging
37	43	39.4	1023	1	A24639	Na+/K+-exchanging
38	43	39.4	1023	1	S24650	Na+/K+-exchanging
39	43	39.4	1025	2	A60444	Na+/K+-exchanging
40	43	39.4	1027	1	PMCCNM	Na+/K+-exchanging
41	43	39.4	1038	1	S03632	Na+/K+-exchanging
42	42.5	39.0	353	2	T32638	Na+/K+-exchanging
43	42.5	39.0	1004	2	JH0470	Na+/K+-exchanging
44	42.5	39.0	1302	2	T00038	Na+/K+-exchanging
45	42	38.5	141	2	AH2829	Na+/K+-exchanging
46	42	38.5	141	2	F97607	Na+/K+-exchanging
47	42	38.5	192	1	A24902	Na+/K+-exchanging
48	42	38.5	192	1	S28148	Na+/K+-exchanging
49	42	38.5	312	2	F86876	Na+/K+-exchanging
50	42	38.5	440	2	F81555	Na+/K+-exchanging
51	42	38.5	440	2	B86508	Na+/K+-exchanging
52	42	38.5	440	2	G72114	Na+/K+-exchanging
53	42	38.5	473	2	T31717	Na+/K+-exchanging
54	42	38.5	522	2	D69226	Na+/K+-exchanging
55	42	38.5	522	2	S62941	Na+/K+-exchanging
56	42	38.5	725	2	A11544	Na+/K+-exchanging
57	42	38.5	842	2	T11201	Na+/K+-exchanging
58	41.5	38.1	108	2	G82991	Na+/K+-exchanging
59	41	37.6	132	1	G69256	Na+/K+-exchanging
60	41	37.6	189	2	S07755	Na+/K+-exchanging
61	41	37.6	245	2	JC7273	Na+/K+-exchanging
62	41	37.6	273	2	H70849	Na+/K+-exchanging
63	41	37.6	274	2	A45754	Na+/K+-exchanging
64	41	37.6	275	2	C35863	Na+/K+-exchanging
65	41	37.6	298	2	T23362	Na+/K+-exchanging
66	41	37.6	410	1	DBPSXA	Na+/K+-exchanging
67	41	37.6	410	2	C83365	Na+/K+-exchanging
68	41	37.6	473	2	B84853	Na+/K+-exchanging
69	41	37.6	494	2	H82489	Na+/K+-exchanging
70	41	37.6	576	2	C88950	Na+/K+-exchanging
71	41	37.6	593	2	S45281	Na+/K+-exchanging
72	41	37.6	618	2	T48193	Na+/K+-exchanging
73	41	37.6	929	2	S75098	Na+/K+-exchanging
74	41	37.6	955	2	T10947	Na+/K+-exchanging
75	41	37.6	966	1	PHPOAG	Na+/K+-exchanging
76	41	37.6	971	2	T09210	Na+/K+-exchanging
77	41	37.6	1000	2	S47243	Na+/K+-exchanging
78	41	37.6	1313	2	B96509	Na+/K+-exchanging
79	41	37.6	1522	2	C96578	Na+/K+-exchanging
80	41	37.6	1616	2	T17884	Na+/K+-exchanging
81	40.5	37.2	1363	2	T43320	Na+/K+-exchanging
82	40	36.7	98	2	A70301	Na+/K+-exchanging
83	40	36.7	152	2	S21826	Na+/K+-exchanging
84	40	36.7	155	2	S23629	Na+/K+-exchanging
85	40	36.7	157	2	B83066	Na+/K+-exchanging
86	40	36.7	169	1	ICMS2	Na+/K+-exchanging
87	40	36.7	169	2	S37289	Na+/K+-exchanging
88	40	36.7	169	2	B95908	Na+/K+-exchanging
89	40	36.7	188	2	T33623	Na+/K+-exchanging
90	40	36.7	206	2	E45315	Na+/K+-exchanging
91	40	36.7	206	2	T22345	Na+/K+-exchanging
92	40	36.7	217	2	S46354	Na+/K+-exchanging
93	40	36.7	226	2	G87518	Na+/K+-exchanging
94	40	36.7	241	2	B83447	Na+/K+-exchanging
95	40	36.7	252	2	B97072	Na+/K+-exchanging
96	40	36.7	357	2	T37154	Na+/K+-exchanging
97	40	36.7	360	2	S25561	Na+/K+-exchanging
98	40	36.7	361	2	F91207	Na+/K+-exchanging
99	40	36.7	361	2	H86053	Na+/K+-exchanging
100	40	36.7	361	2	C65171	Na+/K+-exchanging

ALIGNMENTS

RESULT 1

T47701 translation initiation factor eif-6-like protein [imported] - Arabidopsis thaliana

N/Alternate names: protein F116.30

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C/Accession: T47701

R/Sense, V.: Wurmback, E.; Drzonek, H.; Anseorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.

submitted to the Protein Sequence Database, March 2000

A/Reference number: Z24473

A/Accession: T47701

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1245 <BEN>

A/Cross-references: UNIPROT:Q9M060; EMBL:AL161667

A/Experimental source: cultivar Columbia; BAC clone F116

C/Genetics:

A/Map position: 3

A/Introns: 4/1; 36/2; 65/1; 80/1; 123/3; 160/3

A/Note: F116.30

C/Superfamily: conserved hypothetical protein YP016c

Query Match

45.0%; Score 49; DB 2; Length 245;

Best Local Similarity 57.1%; Pred. No. 8.2;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 ADGPTLRWISFCG 17

DB 194 AAGMTVNDWTSFCG 207

RESULT 2

T33943 hypothetical protein C01B4.7 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C/Accession: T33943

R/Smith, A.; Wamley, P.; Fromick, W.

submitted to the EMBL Data Library, February 1999

A/Description: The sequence of C. elegans cosmid C01B4.

A/Reference number: Z21443

A/Accession: T33943

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1475 <SMT>

A/Cross-references: UNIPROT:Q9UAT5; EMBL:AF125952; PIDD:AA014699.1; GSPDB:GN00023; CESP:

A/Experimental source: strain Bristol N2; clone C01B4

C/Genetics:

A/Map position: 5

A/Introns: 45/2; 80/1; 118/2; 189/3; 239/2; 340/3; 433/3

Query Match 43.1%; Score 47; DB 2; Length 475;

Best Local Similarity 50.0%; Pred. No. 30;

Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFCG 18

DB 268 CTDRCVLSAWVSFLDG 283

RESULT 3

T49731 hypothetical protein B24B19.30 [imported] - Neurospora crassa

C/Species: Neurospora crassa

C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C/Accession: T49731

R/Schulte, U.; Aign, V.; Hobeisel, J.; Brandt, P.; Fattmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, May 2000

A/Reference number: Z25022

A/Accession: T49731

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1108 <SCH>

A/Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.30

A/Experimental source: BAC clone B24B19; strain OR74A

C/Genetics:

A/Map position: 6

A/Supersfamily: Neurospora crassa hypothetical protein B24B19.30

Query Match 41.3%; Score 45; DB 2; Length 108;

Best Local Similarity 50.0%; Pred. No. 15;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFC 16

DB 70 CCGQPTLRWLSMC 83

RESULT 4

T44944 hypothetical protein 5 [imported] - Natronobacterium pharaonis

C/Species: Natronobacterium pharaonis

C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C/Accession: T44944

R/Mattar, S.; Engelhard, M.

Eur. J. Biochem. 250, 332-341, 1997

A/Title: Cytochrome b3 from Natronobacterium pharaonis: An archaeal four-subunit cyto

A/Reference number: Z22876; PMID:9808958; PMID:9428682

A/Accession: T44944

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1180 <MAT>

A/Cross-references: UNIPROT:O07291; EMBL:Y10500; PIDD:CAA71527.1

A/Experimental source: strain SP1/28

C/Genetics:

A/Note: OR15

C/Superfamily: conserved hypothetical protein AF1745

Query Match 41.3%; Score 45; DB 2; Length 180;

Best Local Similarity 77.8%; Pred. No. 24;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 LREWISFCG 17

DB 116 LLEWLSFCG 124

RESULT 5

T22969 hypothetical protein F59A1.13 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T22969

R/Mortimore, B.

submitted to the EMBL Data Library, November 1996

A/Reference number: Z19644

A/Accession: T22969

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1421 <WIL>

A/Cross-references: UNIPROT:Q9XUV7; EMBL:Z01557; PIDD:CAB04538.1; GSPDB:GN00023; CESP:

A/Experimental source: clone F59A1

C/Genetics:

A/Map position: 13

A/Introns: 27/1; 116/1; 245/3; 286/3; 340/3; 381/3

Query Match 41.3%; Score 45; DB 2; Length 421;

Best Local Similarity 50.0%; Pred. No. 53;

Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Oy 3 CADGPTLRWISFCG 18
 Db 214 CTDGTVLWGLSVFVG 229

RESULT 6

ammonium transport protein MEP2 - yeast (Saccharomyces cerevisiae)
 N/Alternate names: NH3 permease; protein JTA499; protein NI207; protein NI820; protein Y
 C/Species: Saccharomyces cerevisiae
 C/Date: 10-May-1995 #sequence revision 19-Oct-1995 #text_change 09-Jul-2004
 C/Accession: S51089, S55142, S59247, S63087
 R/Martin, A.M.; Andre, B.
 Submitted to the EMBL Data Library, December 1994
 A/Reference number: S51089
 A/Accession: S51089
 A/Molecule type: DNA
 A/Residues: 1-499 <MAR>
 A/Cross-references: UNIPROT:P41948, EMBL:X83608, NID:G619513, PIDN:CAA58587.1, PID:G6195
 R/Mallet, L.; Buserreau, F.; Jacquet, M.
 Submitted to the EMBL Data Library, November 1994
 A/Description: A 43.5 kb fragment of the chromosome XIV.
 A/Reference number: S55136
 A/Accession: S55142
 A/Molecule type: DNA
 A/Residues: 1-499 <MAL>
 A/Cross-references: EMBL:Z46843, NID:G861113, PIDN:CAA66884.1, PID:G854496
 R/Mallet, L.; Buserreau, F.; Jacquet, M.
 Yeast 11, 1195-1209, 1995
 A/Title: A 43.5 kb segment of yeast chromosome XIV, which contains MPA2, MEP2, CAP/SRV2,
 A/Reference number: S59241, MUID:96109932, PMID:8619318
 A/Accession: S59247
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-499 <MAW>
 A/Cross-references: EMBL:Z46843, NID:G861113, PIDN:CAA66884.1, PID:G854496
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994
 R/Mallet, L.; Buserreau, F.; Jacquet, M.
 Submitted to the Protein Sequence Database, April 1996
 A/Reference number: S63069
 A/Accession: S63087
 A/Molecule type: DNA
 A/Residues: 1-499 <MAF>
 A/Cross-references: EMBL:Z71418, NID:G1302090, PIDN:CAA96025.1, PID:G1302091, MIBS:YNL14
 A/Experimental source: strain S288C
 C/Genetics:
 A/Gene: SGD:MEP2
 A/Cross-references: SGD:S0005086; MIPS:YNL142w
 A/Map position: 14L
 C/Function:
 A/Description: ammonium transport
 C/Superfamily: ammonium transport protein
 C/Keywords: ammonium transport; transmembrane protein
 F/35-51/Domain: transmembrane #status predicted <TM1>
 F/62-78/Domain: transmembrane #status predicted <TM2>
 F/123-139/Domain: transmembrane #status predicted <TM3>
 F/154-170/Domain: transmembrane #status predicted <TM4>
 F/228-244/Domain: transmembrane #status predicted <TM5>
 F/288-304/Domain: transmembrane #status predicted <TM6>
 F/306-332/Domain: transmembrane #status predicted <TM7>
 F/397-413/Domain: transmembrane #status predicted <TM8>

Query Match 41.3%; Score 45; DB 2; Length 499;
 Best Local Similarity 38.5%; Pred. No. 61;
 Matches 10; Conservative 1; Mismatches 7; Indels 8; Gaps 1;

Oy 1 GGCAAGPTLRWISF-----CGG 18
 Db 247 GGSAGNATIRAWYSIMSTNLAAACGG 272

RESULT 7
 T19008

hypothetical protein C06C6.2 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T19008
 R/McMurray, A.
 Submitted to the EMBL Data Library, March 1997
 A/Reference number: Z19059
 A/Accession: T19008
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-346 <WIL>
 A/Cross-references: UNIPROT:O62030, EMBL:Z93374, PIDN:CAB07554.1, GSPDB:GN00023; CESP:C
 A/Experimental source: clone C06C6
 C/Genetics:
 A/Gene: CESP:C06C6.2
 A/Map position: 5
 A/Intons: 109/1; 135/2; 160/2; 310/1
 C/Superfamily: Caenorhabditis hypothetical protein C49G7.2

Query Match 40.4%; Score 44; DB 2; Length 346;
 Best Local Similarity 56.2%; Pred. No. 61;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 2 CADGPTLRWISFCG 17
 Db 183 GLADGTTIMWDSFIC 198

RESULT 8

A58583
 testosterone-resistant immunity-associated protein IAP38 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
 C/Accession: A58583
 R/Kruceken, J.; Schmitt-Wrede, H.P.; Markmann-Mullisch, U.; Wunderlich, F.
 Biochem. Biophys. Res. Commun. 230, 167-170, 1997
 A/Title: Novel gene expressed in spleen cells mediating acquired testosterone-resistant
 A/Reference number: A58583; MUID:97148595; PMID:9020038
 A/Accession: A58583
 A/Molecule type: mRNA
 A/Residues: 1-346 <KRU>
 A/Cross-references: UNIPROT:P70224; GB:Y08026; NID:G1550784; PIDN:CAA69283.1, PID:G1550
 A/Experimental source: spleen cell
 C/Comment: This protein is a plasma membrane protein with two membrane-spanning domains
 chabaudi malaria.
 C/Genetics:
 A/Gene: iap38
 F/148-167/Domain: transmembrane #status predicted <TM1>
 F/320-335/Domain: transmembrane #status predicted <TM2>

Query Match 40.4%; Score 44; DB 2; Length 346;
 Best Local Similarity 43.8%; Pred. No. 61;
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 3 CADGPTLRWISFCG 18
 Db 213 CTDNRALRDVVAECGG 228

RESULT 9
 D15266
 cell division protein, FtsW/RodA/SpoVE family - Deinococcus radiodurans (strain R1)
 C/Species: Deinococcus radiodurans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: D15266
 R/White, O.; Eissen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; M
 Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A/Reference number: A75250; MUID:20036896; PMID:10567266
 A/Accession: D15266
 A/Status: preliminary

A;Molecule type: DNA
A;Residues: 1-371 <MHI>
A;Cross-references: UNIPROT:Q9RRJ3; GB:AE002079; GB:AE000513; NID:96460315; PIDN:AAF1203
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2497
A;Map position: 1
C;Superfamily: rod shape-determining protein

Query Match 40.4%; Score 44; DB 2; Length 371;
Best Local Similarity 43.8%; Pred. No. 66;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 GCADGPTLRWISFCG 17
Db 77 GSDSPGVRWLSIAG 92

RESULT 10
T09084 phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)

C;Species: Chlamydomonas reinhardtii

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: T09084

R;Molendijk, A.J.; Irvine, R.P.

Plant Mol. Biol. 37, 53-66, 1998

A;Title: Inositolide signalling in Chlamydomonas: Characterization of a phosphatidylinositol

A;Reference number: Z16411; MUID:98281574; PMID:9620264

A;Accession: T09084

A;Status: preliminary; translated from GB/EMBL/DDB

A;Molecule type: DNA

A;Residues: 1-490 <MOL>

A;Cross-references: UNIPROT:Q04270; EMBL:U97663; NID:92109290; PIDN:AAC50018.1; PID:9210

A;Experimental source: strain cw-15

C;Genetics:

A;Introns: 265/3; 331/3; 370/3; 455/1; 481/3

Query Match 40.4%; Score 44; DB 2; Length 490;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 10; Conservative 3; Mismatches 3; Indels 4; Gaps 2;

QY 1 GGCA--DGPTLR--EWISFC 16
Db 244 GSSPGDGSTARWDLWTF 263

RESULT 11

A86440 58.5K hypothetical protein - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: A86440

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

amann, N.P.; Hughes, B.; Huizart, L.

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon,

Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A86440

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-526 <STO>

A;Cross-references: UNIPROT:Q9C868; GB:AE005172; NID:91054679; PIDN:AA627899.1; GSPDB:Q

C;Genetics:

A;Map position: 1

Query Match 40.4%; Score 44; DB 2; Length 526;
Best Local Similarity 44.4%; Pred. No. 91;

Matches 8; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
QY 1 GCADGPT--LRWISFC 16
Db 395 GGRVGGPSPLINQWIEFC 412

RESULT 12

S34189 starch phosphorylase (EC 2.4.1.1) L - potato

C;Species: Solanum tuberosum (potato)

C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: S53489; S34189

R;Somewald, U.; Baesner, A.; Greve, B.; Steup, M.

Plant Mol. Biol. 27, 567-576, 1995

A;Title: A second L-type isozyme of potato glucan phosphorylase: cloning, antisense inh

A;Reference number: S53489; MUID:95201249; PMID:7894019

A;Accession: S53489

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-974 <SO2>

A;Cross-references: UNIPROT:P53535; EMBL:X73684; NID:9313346; PIDN:CAA52036.1; PID:9313

C;Superfamily: glucan phosphorylase

C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphat

F;820/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 40.4%; Score 44; DB 2; Length 974;
Best Local Similarity 58.3%; Pred. No. 1,6e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 DGPTLRWISFC 16
Db 619 NGVTPRRWLSFC 630

RESULT 13

S00503 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - Pacific electric ray

C;Species: Torpedo californica (Pacific electric ray)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C;Accession: S00503; S28885; S29880

R;Kawakami, K.; Noguchi, S.; Node, M.; Takahashi, H.; Ohta, T.; Kawamura, M.; Nojima, H

Nature 316, 733-736, 1985

A;Title: Primary structure of the alpha-subunit of Torpedo californica Na(+)K(+)ATPa

A;Reference number: S00503; MUID:85296307; PMID:2893505

A;Accession: S00503

A;Molecule type: mRNA

A;Residues: 1-1022 <KAW1>

A;Cross-references: UNIPROT:P05025; EMBL:X02810; NID:964399; PIDN:CAA26578.1; PID:96440

A;Accession: S28885

A;Molecule type: protein

A;Residues: 228-240/431-438;535-550;671-690;1011-1022 <KAW2>

R;Ohta, T.; Nagano, K.; Yoshida, M.

Proc. Natl. Acad. Sci. U.S.A. 83, 2071-2075, 1986

A;Title: The active site structure of Na(+)K(+)ATPase: location of the 5

A;Reference number: S29880; MUID:86177549; PMID:3008150

A;Accession: S29880

A;Molecule type: protein

A;Residues: 386-402;502-512;671-689;887-906 <OHT>

C;Superfamily: Na+/+-transporting ATPase alpha chain; ATPase nucleotide-binding domain

C;Keywords: ATP; heterodimer; hydrolyase; ion transport; phosphoprotein; potassium trans

F;96-110/Domain: transmembrane #status predicted <TM1>

F;130-149/Domain: transmembrane #status predicted <TM2>

F;150-290/Domain: intracellular #status predicted <INT2>

F;320-348/Domain: transmembrane #status predicted <TM4>

F;349-785/Domain: intracellular #status predicted <INT3>

F;586-782/Domain: ATPase nucleotide-binding domain homology <ATN>

F;786-809/Domain: transmembrane #status predicted <TM5>

F;848-873/Domain: transmembrane #status predicted <TM6>

F;874-951/Domain: intracellular #status predicted <INT4>

F;952-977/Domain: transmembrane #status predicted <TM7>

F;978-1022/Domain: extracellular #status predicted <EXT>

F:376/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:507/Binding site: ATP (lys) #status predicted
 F:716,720,725/Active site: Asp, Asp, Lys #status predicted

Query Match 40.4%; Score 44; DB 1; Length 1022;
 Best Local Similarity 70.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16
 |||
 Db 84 PTPPEWIKFC 93

RESULT 14

A24414
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - human
 N:Alternate names: sodium pump; sodium/potassium transporting ATPase alpha-A chain
 C/Species: Homo sapiens (hmn)
 C/Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 09-Jul-2004
 C/Accession: A24414; A27795; A39910; I60116; S09171
 R/Kawakami, K.; Ohta, T.; Nojima, H.; Nagano, K.
 J. Biochem. 100, 389-397, 1986
 A>Title: Primary structure of the alpha-subunit of human Na,K-ATPase deduced from cDNA
 A/Reference number: A24414; MUID:87057096; PMID:2430951

A/Accession: A24414
 A/Molecule type: mRNA
 A/Residues: 1-1023 <RAW>
 A/Cross-references: UNIPROT:P05023; EMBL:X04297; NID:g28926; PIDN:CAA27840.1; PID:g28927
 R/Shull, M.M.; Lingrel, J.B.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
 A>Title: Multiple genes encode the human Na,K-ATPase catalytic subunit.
 A/Reference number: A94158; MUID:87231946; PMID:3035563
 A/Accession: A27795

A/Molecule type: DNA
 A/Residues: 168-189,213-214, 'X', 216-244 <SHU>
 R/Chehab, F.F.; Kan, Y.W.; Law, M.L.; Hartz, J.; Kao, F.T.; Blostein, R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7901-7905, 1987
 A>Title: Human placental Na,K-ATPase alpha subunit: cDNA cloning, tissue expression, D
 A/Reference number: A39910; MUID:8806506; PMID:2891135
 A/Accession: A39910

A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 199-942 <CHE>
 A/Cross-references: GB:U03007
 R/Shull, M.M.; Pugh, D.G.; Lingrel, J.B.
 Genomics 6, 451-460, 1990
 A>Title: The human Na,K-ATPase alpha 1 gene: characterization of the 5'-flanking region
 A/Reference number: I60116; MUID:90228961; PMID:1970326
 A/Accession: I60116

A/Status: translation not shown; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-61 <RES>
 A/Cross-references: GB:M0310; NID:g179206; PIDN:AAA51801.1; PID:g179208
 C/Genetics:
 A/Gene: GDB:ATP1A1
 A/Cross-references: GDB:119711; OMIM:182310
 A/Map position: 1p13-1p11

C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C/Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
 F:6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>
 F:6-95/Domain: intracellular #status predicted <INT1>
 F:96-120/Domain: transmembrane #status predicted <TM1>
 F:130-149/Domain: transmembrane #status predicted <TM2>
 F:150-200/Domain: intracellular #status predicted <INT2>
 F:291-313/Domain: transmembrane #status predicted <TM3>
 F:320-348/Domain: transmembrane #status predicted <TM4>
 F:349-766/Domain: intracellular #status predicted <INT3>
 F:587-783/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:787-810/Domain: transmembrane #status predicted <TM5>
 F:849-874/Domain: transmembrane #status predicted <TM6>
 F:875-952/Domain: intracellular #status predicted <INT4>
 F:953-978/Domain: transmembrane #status predicted <TM7>
 F:979-1023/Domain: extracellular #status predicted <EXT>

F:376/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:508/Binding site: ATP (lys) #status predicted
 F:717,721,726/Active site: Asp, Asp, Lys #status predicted

Query Match 40.4%; Score 44; DB 2; Length 1023;
 Best Local Similarity 70.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16
 |||
 Db 84 PTPPEWIKFC 93

RESULT 15

T39685
 conserved hypothetical protein SPBC1778.03c - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T39685
 R/Oliver, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, March 1998
 A/Reference number: Z21869
 A/Accession: T39685

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-376 <OLI>
 A/Cross-references: UNIPROT:Q9Y7J0; EMBL:AL049489; PIDN:CB339798.1; GSPDB:GN00067; SPDB
 A/Experimental source: strain 972h-; cosmid cl778
 C/Genetics:
 A/Gene: SPDB:SPBC1778.03c
 A/Map position: 2
 A/Introns: 11/2

Query Match 39.9%; Score 43.5; DB 2; Length 376;
 Best Local Similarity 42.9%; Pred. No. 79;
 Matches 9; Conservative 3; Mismatches 6; Indels 3; Gaps 1;
 QY 1 GGCAAGTLEWIS--FCGG 18
 |||
 Db 164 GACAFARSITDWSRYPFG 184

RESULT 16

A89813
 glutamate synthase large subunit [imported] - Staphylococcus aureus (strain N315)
 C/Species: Staphylococcus aureus
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 16-Aug-2004
 C/Accession: A89813
 R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
 ma, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; MUID:21311952; PMID:11418146
 A/Accession: A89813
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1499 <RUR>
 A/Cross-references: UNIPROT:Q99WD1; GB:BA000018; PID:g13700362; PIDN:BA041660.1; GSPDB
 A/Experimental source: strain N315
 C/Genetics:
 A/Gene: gltB

C/Superfamily: Glutamate synthase, large subunit

Query Match 39.9%; Score 43.5; DB 2; Length 1499;
 Best Local Similarity 64.3%; Pred. No. 2.8e+02;
 Matches 9; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 5 DGPTLRWISFCGG 18
 |||
 Db 339 DGPTM--ISFCNG 149

```

RESULT 17
D72595
hypothetical protein ABE1229 - Aeropyrum permix (strain K1)
C:Species: Aeropyrum permix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: D72595
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahara, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999
A>Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A/Reference number: A72450; MID:9310339; PMID:10382966
A/Accession: D72595
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-113 <RAM>
A/Cross-references: UNIPROT:Q9YCM9; DDBJ:AP000061; NID:G5104821; PIDN:BAA80218.1; PID:dl
A/Experimental source: strain K1
A/Genetics:
A/Gene: ABE1229

Query Match          39.4%; Score 43; DB 2; Length 113;
Best Local Similarity 61.5%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 GPTLRWISFCG 18
    ||| ||| |||
    21 GEARLGMPSFCRG 33

RESULT 18
T15386
hypothetical protein C03B1.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15386
R:Martin, J.
Submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid C03B1.
A/Reference number: Z18340
A/Accession: T15386
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-115 <MAR>
A/Cross-references: UNIPROT:Q11110; EMBL:U04952; NID:G1072237; PID:G1072244; PIDN:AAA817
A/Genetics:
A/Gene: CESP:C03B1.3
A/Introns: 80/1

Query Match          39.4%; Score 43; DB 2; Length 115;
Best Local Similarity 46.7%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CADPTLRWISFCG 17
    ||| ||| |||
    68 CASGEVHYHMACFCG 82

RESULT 19
I48685
mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I48685; S43172
R:Huang, R.; Hellman, L.
Immunogenetics 40, 397-414, 1994
A>Title: Genes for mast-cell serine protease and their molecular evolution.
A/Reference number: I48684; MUID:95048582; PMID:7959952
A/Accession: I48685
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-230 <RSS>
A/Cross-references: UNIPROT:P21845; EMBL:X78542; NID:9468809; PIDN:CAA55288.1; PID:94688
A/Superfamily: trypsin; trypsin homology

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C/Keywords: hydrolase; serine proteinase
F:32-230/Domain: trypsin homology #status atypical <TRY>

Query Match          39.4%; Score 43; DB 2; Length 230;
Best Local Similarity 70.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 LBEWISFCG 18
    ||| ||| |||
    53 LNMVHIFCG 62

RESULT 20
AB2768
lipoate biosynthesis protein B [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AB2768
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.E.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AB2768
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-233 <KUR>
A/Cross-references: UNIPROT:Q8UF44; GB:AE008688; PIDN:AAL42560.1; PID:G17739983; GSPDB:A
A/Experimental source: strain C58 (Dupont)
A/Genetics:
A/Map position: circular chromosome
C/Superfamily: Escherichia coli lipoate-protein ligase lipB

Query Match          39.4%; Score 43; DB 2; Length 233;
Best Local Similarity 43.5%; Pred. No. 60;
Matches 10; Conservative 3; Mismatches 4; Indels 6; Gaps 1;

QY 1 GGCAD-----GPTLRWISFCG 17
    ||| : ||| : ||| : |||
    148 GGMABDKIALGIRLKNWVSFHG 170

RESULT 21
T19988
hypothetical protein C47B2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T19988
R:Kershaw, J.
Submitted to the EMBL Data Library, October 1997
A/Reference number: Z19208
A/Accession: T19988
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-246 <WIL>
A/Cross-references: UNIPROT:O62106; EMBL:Z99709; PIDN:CAB16860.1; GSPDB:GN00019; CESP:C
A/Experimental source: clone C47B2
A/Genetics: CESP:C47B2.5
A/Map position: 1
A/Introns: 91/3; 127/3
C/Superfamily: conserved hypothetical protein YP016c

Query Match          39.4%; Score 43; DB 2; Length 246;
Best Local Similarity 41.7%; Pred. No. 63;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 GPTLRWISFCG 17
    ||| : ||| : |||

```


Db 196 GMVNDWVAFCG 207

RESULT 22
T01012

Probable translation initiation factor [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004

C/Accession: T01012; H84821

R/Roundley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, November 1997

A/Description: Arabidopsis thaliana chromosome II BAC T517 genomic sequence.

A/Reference number: Z14162

A/Accession: T01012

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-247 <R0U>

A/Cross-references: UNIPROT:Q022290; EMBL:AC003000; NID:g2642152; PIDN:AA87131.1; PID:g2

A/Experimental source: cultivar Columbia

R/Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.

euens, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ventner, J

Nature 402: 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: H84821

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-247 <S0U>

A/Cross-references: GB:AE002093; NID:g2642164; PIDN:AA87131.1; GSPDB:GN00139

C/Genetics:

A/Map position: 2

A/Introns: 4/1; 38/2; 82/1; 162/3

C/Superfamily: conserved hypothetical protein YPR016c

Query Match

Best Local Similarity 39.4%; Score 43; DB 2; Length 247;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

6 GPTLRWISFCG 17

198 GLTVNDWVAFCG 209

RESULT 23

D97548

Lipidate-protein ligase b (lipidate biosynthesis protein b) [imported] - Agrobacterium tum

C/Species: Agrobacterium tumefaciens

C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C/Accession: D97548

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Mollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: D97548

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-268 <KUR>

A/Cross-references: UNIPROT:Q8UF44; GB:AE007869; PIDN:AAK87341.1; PID:g15156641; GSPDB:G

C/Genetics:

A/Map position: circular chromosome

C/Superfamily: Escherichia coli lipase-protein ligase lipb

Query Match

Best Local Similarity 39.4%; Score 43; DB 2; Length 268;

Matches 10; Conservative 3; Mismatches 4; Indels 6; Gaps 1;

1 GGCAD-----GPTLRWISFCG 17

Db 183 GMAEDKIALGIRLRKWSFHG 205

RESULT 24

A38654

mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 21-Feb-1992 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004

C/Accession: A38654; B38654; D35646; I59478

R/Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serrafin, W.E.

U. Biol. Chem. 266, 3847-3853, 1991

A/Title: Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription by P

A/Reference number: A38654; MUID:91139682; PMID:1995638

A/Accession: A38654

A/Molecule type: DNA

A/Residues: 1-276 <REY>

A/Cross-references: UNIPROT:P21845; GB:M57625; NID:g200506; PIDN:AAA39987.1; PID:g20050

A/Note: the authors translated the codon GCG for residue 24 as Ala, GAG for residue 37

s Gly, GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly

A/Accession: B38654

A/Molecule type: mRNA

A/Residues: 1-276 <RE2>

A/Cross-references: GB:M57626; NID:g200508; PIDN:AAA39988.1; PID:g200509

R/Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serrafin, W.E.

Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990

A/Title: Different mouse mast cell populations express various combinations of at least

A/Accession: D35646

A/Molecule type: protein

A/Residues: 32-54 <RE3>

R/Huang, R.; Ahrink, M.; Gobl, A.E.; Nilsson, G.; Aveskogh, M.; Larsson, L.G.; Nilsson,

Scand. J. Immunol. 38, 359-367, 1993

A/Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and

A/Accession: I59478; MUID:94023807; PMID:8210998

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-276 <RES>

A/Cross-references: GB:U31853; NID:g473480; PIDN:AAA39725.1; PID:g473481

C/Genetics:

A/Introns: 24/1; 79/2; 168/1; 222/3

C/Superfamily: trypsin, trypsin homology

C/Keywords: hydrolase, serine proteinase, zymogen

F/1-21/Domain: signal sequence #status predicted <SIG>

F/22-31/Domain: activation peptide #status predicted <ACT>

F/32-276/Product: mast cell proteinase 6 #status experimental <MAT>

F/33-268/Domain: trypsin homology <TRY>

F/75,122,225/Active site: His, Asp, Ser #status predicted

Query Match

Best Local Similarity 39.4%; Score 43; DB 2; Length 276;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

9 LRWISFCG 18

53 LNWIMHFCG 62

RESULT 25

S54478

probable membrane protein YMR266w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein YMR156.08

C/Species: Saccharomyces cerevisiae

C/Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C/Accession: S54478

R/Lye, G.; Churcher, C.M.

submitted to the EMBL Data Library, May 1995

A/Reference number: S54478

A/Accession: S54478

A/Molecule type: DNA

A/Residues: 1-953 <LYE>

A/Cross-references: UNIPROT:Q03516; EMBL:Z49260; NID:g809081; PID:g809089; GSPDB:GN0001

A:Experimental source: strain AB972
 C:Genetic8:
 A:Gene: SGD:RSN1; MIPS:YMR266w
 A:Reference number: S0004879
 A:Cross-references: SGD:S0004879
 A:Map position: 13R
 C:Superfamily: yeast probable membrane protein Y0I084w
 C:Keywords: transmembrane protein
 F:12-48/Domain: transmembrane #status predicted <TM1>
 F:106-122/Domain: transmembrane #status predicted <TM2>
 F:152-168/Domain: transmembrane #status predicted <TM3>
 F:195-411/Domain: transmembrane #status predicted <TM4>
 F:335-451/Domain: transmembrane #status predicted <TM5>
 F:345-561/Domain: transmembrane #status predicted <TM6>
 F:599-615/Domain: transmembrane #status predicted <TM7>
 F:646-662/Domain: transmembrane #status predicted <TM8>
 F:668-684/Domain: transmembrane #status predicted <TM9>

Query Match 39.4%; Score 43; DB 2; Length 953;
 Best Local Similarity 41.2%; Pred. No. 2.2e+02;
 Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFC 17
 DB 558 GAFIDGTVRKRMKRFCS 574

RESULT 26
 B37227
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
 C:Accession: B37227; I50395
 R:Takeyasu, K.; Lemas, V.; Fambrough, D.M.
 Am. J. Physiol. 259, C619-C630, 1990
 A:Title: Stability of Na(+)-K(+) ATPase alpha-subunit isoforms in evolution.
 A:Reference number: A37227; PMID:91023019; PMID:2171348
 A:Accession: B37227
 A:Molecule type: mRNA
 A:Residues: 1-1010 <TAA>
 A:Cross-references: UNIPROT:P24798; GB:M5960; NID:G212407; PIDN:AAA48982.1; PID:G212408
 C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C:Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium tr
 F:574-770/Domain: ATPase nucleotide-binding domain homology <ATP>
 F:202-470/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:363/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:495/Binding site: ATP (Lys) #status predicted

Query Match 39.4%; Score 43; DB 2; Length 1010;
 Best Local Similarity 60.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLRWISFC 16
 DB 71 PTPPEWVKFC 80

RESULT 27
 S00801
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C:Accession: S00801; S04019; A27397; S02275
 R:Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Melkov, A.M.; S
 dyanov, N.N.; Sverdlov, E.D.
 FEBS Lett. 233, 87-94, 1988
 A:Title: Family of human Na,K-ATPase genes. Structure of the gene for the catalytic subu
 A:Reference number: S00801; PMID:88255304; PMID:2838329
 A:Accession: S00801
 A:Molecule type: DNA
 A:Residues: 1-1013 <OVC>
 A:Cross-references: UNIPROT:P13637; EMBL:M37456
 R:Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Melkov, A.M.; Smir
 ov, N.N.; Ovchinnikov, Y.A.

Dokl. Biochem. 297, 426-431, 1987
 A:Title: Family of human Na(+),K(+)-ATPase genes. Structure of the gene of isoform alph
 A:Reference number: S04019
 A:Accession: S04019
 A:Molecule type: DNA
 A:Residues: 1, 'EIH', 3-1013 <SVEI>
 A:Cross-references: EMBL:X12910; NID:G28963
 A>Note: the authors translated the codon TTC for residue 283 as Ser and TCT for residue
 A>Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk;
 R:Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Alimkhet, R.L.; I
 lina, M.B.; Sverdlov, V.E.; Modyanov, N.N.; Ovchinnikov, Y.A.
 FEBS Lett. 217, 275-278, 1987
 A:Title: The family of human Na+, K+-ATPase genes. No less than five genes and/or pseudo
 A:Reference number: A27397; PMID:87247232; PMID:3036582
 A:Accession: A27397
 A:Molecule type: mRNA
 A:Residues: 243-434 <SVE2>
 A:Cross-references: GB:M27570
 C:Genetic8:
 A:Gene: GDB:ATP1A3
 A:Cross-references: GDB:119713; OMIM:182350
 A:Map position: 19q13.2-19q13.2
 A:Introns: 2/3; 31/3; 51/3; 119/3; 157/3; 202/3; 242/1; 331/3; 398/1; 435/2; 479/3; 544/
 C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans
 F:86-110/Domain: transmembrane #status predicted <TM1>
 F:120-139/Domain: transmembrane #status predicted <TM2>
 F:140-280/Domain: intracellular #status predicted <TM3>
 F:281-303/Domain: transmembrane #status predicted <TM4>
 F:310-338/Domain: transmembrane #status predicted <TM5>
 F:339-776/Domain: intracellular #status predicted <TM3>
 F:577-773/Domain: ATPase nucleotide-binding domain homology <ATP>
 F:839-864/Domain: transmembrane #status predicted <TM6>
 F:865-942/Domain: intracellular #status predicted <TM7>
 F:943-968/Domain: transmembrane #status predicted <EXT>
 F:969-1013/Domain: extracellular #status predicted
 F:366/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:498/Binding site: ATP (Lys) #status predicted
 F:707, 711, 716/Active site: Asp, Asp, Lys #status predicted

Query Match 39.4%; Score 43; DB 1; Length 1013;
 Best Local Similarity 60.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLRWISFC 16
 DB 74 PTPPEWVKFC 83

RESULT 28
 C24639
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - rat
 N:Alternate names: Na+/K+-transporting ATPase alpha (III) chain
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1988 #sequence_revision 23-Apr-1993 #text_change 09-Jul-2004
 C:Accession: C24639; S00514; B27180; A60470
 R:Shull, G.E.; Greeb, J.; Lingrel, J.B.
 Biochemistry 25, 8125-8132, 1986
 A:Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit f
 A:Reference number: A90512; PMID:87128908; PMID:3028470
 A:Accession: C24639
 A:Molecule type: mRNA
 A:Residues: 1-1013 <SHU>
 A:Cross-references: UNIPROT:P06687; EMBL:M4513; NID:G203030; PIDN:AAA40777.1; PID:G203
 A>Note: in the authors' translation 405-Ser is shown after residue 409 and, consequentl
 R:Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Ohta, T.;
 U. Biochem. 102, 43-58, 1987
 A:Title: Primary structures of two types of alpha-subunit of rat brain Na(+),K(+)-ATP
 A:Reference number: S00460; PMID:88032933; PMID:2822682
 A:Accession: S00514
 A:Molecule type: mRNA
 A:Residues: 1-907, 'C', 909-1013 <HAR>

A;Cross-references: EMBL:X05883; NID:955769; PDB:CAA29307.1; PID:955770
 R;Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard, B.
 J. Cell Biol. 105, 1855-1865, 1987
 A;Title: Three differentially expressed Na,K-ATPase alpha subunit isoforms: structural
 A;Reference number: A92749; MUID:88033255; PMID:2822726
 A;Accession: B27180
 A;Molecule type: mRNA
 A;Residues: 1,'N','4'-103,'R',105-113,'E',115-127,'G',129-148,'Q',150-151,'T',153-165,'D'
 A;Cross-references: EMBL:M8648; NID:9205633; PDB:AAA1672.1; PID:9205634
 A;Note: the authors translated the codon CAG for residue 149 as Glu, GGC for residue 194
 R;Hau, Y.M.; Guidotti, G.
 Biochemistry 28, 569-573, 1989
 A;Title: Rat brain has the alpha3 form of the (Na,K)-ATPase.
 A;Reference number: A60470; MUID:8923049; PMID:2540801
 A;Accession: A60470
 A;Molecule type: protein
 A;Residues: 117-132;586-595,'X',597-601 <HSU>
 A;Comment: The alpha-3 form appears to be highly ouabain-inhibitable, as is alpha-2 but
 C;Genetics:
 A;Gene: NKAA3
 C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
 F;86-110/Domain: transmembrane #status predicted <TM1>
 F;120-139/Domain: transmembrane #status predicted <TM2>
 F;140-280/Domain: intracellular #status predicted <INT7>
 F;281-303/Domain: transmembrane #status predicted <TM3>
 F;310-338/Domain: transmembrane #status predicted <TM4>
 F;339-776/Domain: intracellular #status predicted <INT3>
 F;577-773/Domain: ATPase nucleotide-binding domain homology <ATN>
 F;777-800/Domain: transmembrane #status predicted <TM5>
 F;839-864/Domain: transmembrane #status predicted <TM6>
 F;865-942/Domain: intracellular #status predicted <INT4>
 F;943-968/Domain: transmembrane #status predicted <TM7>
 F;969-1013/Domain: extracellular #status predicted <EXT>
 F;366/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F;488/Binding site: ATP (Lys) #status predicted
 F;707,711,716/Active site: Asp, Asp, Lys #status predicted

Query Match 39.4%; Score 43; DB 2; Length 1013;
 Best Local Similarity 60.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16
 DB 74 PTLPEWVKFC 83

RESULT 29
 A37227
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 16-Sep-1992 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C;Accession: I50394; A37227
 R;Takeyasu, K.; Lemas, M.; Fambrough, D.M.
 Am. J. Physiol. 259, 619-630, 1991
 A;Title: Stability of the Na,K-ATPase alpha-subunit isoforms in evolution.
 A;Reference number: I50394
 A;Accession: I50394
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1017 <TMX>
 A;Cross-references: UNIPROT:P24797; GB:M59959; NID:9212405; PDB:AAA48981.1; PID:9212406
 R;Takeyasu, K.; Lemas, V.; Fambrough, D.M.
 Am. J. Physiol. 259, 619-630, 1990
 A;Title: Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms in evolution.
 A;Reference number: A37227; MUID:91023019; PMID:2171348
 A;Accession: A37227
 A;Molecule type: mRNA
 A;Residues: 3-1017 <TA2>
 C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C;Keywords: ATP; glycoprotein; hydrolase; phosphoprotein
 F;581-777/Domain: ATPase nucleotide-binding domain homology <ATN>
 F;210,478/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;371/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 39.4%; Score 43; DB 2; Length 1017;
 Best Local Similarity 60.0%; Pred. No. 2.3e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16
 DB 79 PTLPEWVKFC 88

RESULT 30
 A34474
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - human
 A;Alternate names: Na+/K+-exchanging ATPase alpha chain-4; sodium/potassium transp
 C;Species: Homo sapiens (man)
 C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
 C;Accession: A34474; B27795; D27397
 R;Shull, M.M.; Pugh, D.G.; Lingrel, J.B.
 J. Biol. Chem. 264, 17532-17543, 1989
 A;Title: Characterization of the human Na,K-ATPase alpha2 gene and identification of in
 A;Reference number: A34474; MUID:9008924; PMID:2477373
 A;Accession: A34474
 A;Molecule type: DNA
 A;Residues: 1-1020 <SHU>
 A;Cross-references: UNIPROT:P50993; GB:J05096; NID:9179164; PDB:AAA51797.1; PID:917916
 R;Shull, M.M.; Lingrel, J.B.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
 A;Title: Multiple genes encode the human Na,K-ATPase catalytic subunit.
 A;Reference number: A94158; MUID:87231946; PMID:3035563
 A;Accession: B27795
 A;Molecule type: DNA
 A;Residues: 211-249 <SH2>
 A;Cross-references: GB:M16795; NID:9179196; PDB:AAA51799.1; PID:9553194
 R;Sverdlov, E.D.; Monastyrskaya, G.S.; Brode, N.E.; Ushkaryov, Y.A.; Allikmeets, R.L.;
 Lina, M.B.; Sverdlov, V.E.; Modyanov, N.N.; Ovchinnikov, Y.A.
 FEBS Lett. 217, 275-278, 1987
 A;Title: The family of human Na,K-ATPase genes. No less than five genes and/or pseudo
 A;Reference number: A27397; MUID:87247232; PMID:3036582
 A;Accession: D27397
 A;Molecule type: DNA
 A;Residues: 251-442 <SVE>
 A;Cross-references: GB:M27571
 C;Genetics:
 A;Gene: GDB:ATP1A2
 A;Cross-references: GDB:119712; OMIM:182340
 A;Map position: 1q21-q23
 C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans
 F;6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MAT>
 F;6-93/Domain: intracellular #status predicted <INT1>
 F;94-118/Domain: transmembrane #status predicted <TM1>
 F;128-147/Domain: transmembrane #status predicted <TM2>
 F;148-288/Domain: intracellular #status predicted <INT2>
 F;289-311/Domain: transmembrane #status predicted <TM3>
 F;318-346/Domain: transmembrane #status predicted <TM4>
 F;347-783/Domain: intracellular #status predicted <INT3>
 F;584-780/Domain: ATPase nucleotide-binding domain homology <ATN>
 F;784-807/Domain: transmembrane #status predicted <TM5>
 F;846-871/Domain: transmembrane #status predicted <TM6>
 F;872-949/Domain: intracellular #status predicted <INT4>
 F;950-975/Domain: transmembrane #status predicted <TM7>
 F;976-1020/Domain: extracellular #status predicted <EXT>
 F;376/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F;505/Binding site: ATP (Lys) #status predicted
 F;714,718,723/Active site: Asp, Asp, Lys #status predicted

Query Match 39.4%; Score 43; DB 2; Length 1020;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16

Db 82 PTPPEWVKFC 91

RESULT 31

B24639
Na+/K+-exchanging ATPase (BC 3.6.3.9) alpha-2 chain - rat
N/Alternate names: Na+/K+-transporting ATPase alpha-plus chain
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C/Accession: B24639
R/Shull, G.E.; Greeb, J.; Lingrel, J.B.
Biochemistry 25, 8125-8132, 1986
A/Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit from
A/Reference number: A90512; MUID:87128908; PMID:3028470
A/Accession: B24639
A/Molecule type: mRNA
A/Residues: 1-1020 <SHU>
A/Cross-references: UNIPROT:P06686; EMBL:M14512; NID:G203028; PIDN:AAA40776.1; PID:G203028
C/Genetics:
A/Gene: NKA2
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F/6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MAT>
F/6-93/Domain: intracellular #status predicted <INT1>
F/94-119/Domain: transmembrane #status predicted <TM1>
F/128-147/Domain: transmembrane #status predicted <TM2>
F/148-288/Domain: intracellular #status predicted <INT2>
F/289-311/Domain: transmembrane #status predicted <TM3>
F/318-346/Domain: transmembrane #status predicted <TM4>
F/347-783/Domain: intracellular #status predicted <INT3>
F/584-780/Domain: ATPase nucleotide-binding domain homology <ATN>
F/784-807/Domain: transmembrane #status predicted <TM5>
F/846-871/Domain: transmembrane #status predicted <TM6>
F/872-949/Domain: intracellular #status predicted <INT4>
F/950-975/Domain: transmembrane #status predicted <TM7>
F/976-1020/Domain: extracellular #status predicted <EXT>
F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/505/Binding site: ATP (Lys) #status predicted
F/714,718,723/Active site: Asp, Asp, Lys #status predicted

Query Match 39.4%; Score 43; DB 2; Length 1020;

Best Local Similarity 60.0%; Pred. No. 2.4e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTPPEWVKFC 16

Db 82 PTPPEWVKFC 91

RESULT 32

PMSINA
Na+/K+-exchanging ATPase (BC 3.6.3.9) alpha chain precursor - sheep
N/Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha chain
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C/Accession: A01074; A35426
R/Shull, G.E.; Schwartz, A.; Lingrel, J.B.
Nature 316, 691-695, 1985
A/Title: Amino-acid sequence of the catalytic subunit of the (Na(+) + K(+)) ATPase deduced
A/Reference number: A01074; MUID:85296229; PMID:2993903
A/Accession: A01074
A/Molecule type: mRNA
A/Residues: 1-1021 <SHU>
A/Cross-references: UNIPROT:P04074; GB:X02813; NID:G1205; PIDN:CAA36581.1; PID:G1206
R/Hinz, H.R.; Kierley, T.L.
J. Biol. Chem. 265, 10260-10265, 1990
A/Title: Lysine 480 is an essential residue in the putative ATP site of lamb kidney (Na,
A/Reference number: A35426; MUID:90285144; PMID:2162343
A/Accession: A35426
A/Status: preliminary
A/Molecule type: protein
A/Residues: 475-492 <HN>
C/Comment: This is the catalytic component of the active enzyme, which catalyzes the hyd

reates the electrochemical gradient of sodium and potassium, providing the energy for a
n function.

C/Comment: This enzyme is specifically inhibited by cardiac glycosides such as digoxin.
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; hydrolase; phosphoprotein; potassium transport; sodium transport; tran
F/6-1021/Product: Na+/K+-transporting ATPase alpha chain #status predicted <MAT>
F/94-115/Domain: transmembrane #status predicted <TM1>
F/128-144/Domain: transmembrane #status predicted <TM2>
F/289-311/Domain: transmembrane #status predicted <TM3>
F/318-346/Domain: transmembrane #status predicted <TM4>
F/585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
F/785-808/Domain: transmembrane #status predicted <TM5>
F/847-872/Domain: transmembrane #status predicted <TM6>
F/951-976/Domain: transmembrane #status predicted <TM7>
F/977-1021/Domain: extracellular #status predicted <EXT>
F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/506/Binding site: ATP (Lys) #status predicted

Query Match 39.4%; Score 43; DB 1; Length 1021;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTPPEWVKFC 16

Db 82 PTPPEWVKFC 91

RESULT 33

S04630
Na+/K+-exchanging ATPase (BC 3.6.3.9) alpha-1 chain - horse
C/Species: Equus caballus (domestic horse)
C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C/Accession: S04630
R/Kano, I.; Nagai, F.; Satoh, K.; Ushiyama, K.; Nakao, T.; Kano, K.
FEBS Lett. 250, 91-98, 1989
A/Title: Structure of the alpha(1) subunit of horse Na,K-ATPase gene.
A/Reference number: S04630; MUID:89290042; PMID:2544461
A/Accession: S04630
A/Molecule type: DNA
A/Residues: 1-1021 <KAN>
A/Cross-references: UNIPROT:P18907; EMBL:X16773; NID:G1010; PIDN:CAA34716.1; PID:G87102

C/Genetics:
A/Intons: 4/3; 39/3; 59/3; 127/3; 165/3; 210/3; 250/1; 339/3; 406/1; 442/3; 487/3; 552/
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium tran
F/6-1021/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>
F/6-93/Domain: intracellular #status predicted <INT1>
F/94-118/Domain: transmembrane #status predicted <TM1>
F/128-147/Domain: transmembrane #status predicted <TM2>
F/148-288/Domain: intracellular #status predicted <INT2>
F/289-311/Domain: transmembrane #status predicted <TM3>
F/318-346/Domain: transmembrane #status predicted <TM4>
F/347-784/Domain: intracellular #status predicted <INT3>
F/585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
F/785-808/Domain: transmembrane #status predicted <TM5>
F/847-872/Domain: transmembrane #status predicted <TM6>
F/873-950/Domain: intracellular #status predicted <INT4>
F/951-976/Domain: transmembrane #status predicted <TM7>
F/977-1021/Domain: extracellular #status predicted <EXT>
F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/506/Binding site: ATP (Lys) #status predicted
F/715,719,724/Active site: Asp, Asp, Lys #status predicted

Query Match 39.4%; Score 43; DB 1; Length 1021;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTPPEWVKFC 16

Db 82 PTPPEWVKFC 91

RESULT 34

A28199
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - chicken
C:Species: Gallus gallus (chicken)
C>Date: 21-Sep-1988 #sequence_revision 21-Sep-1988 #text_change 09-Jul-2004
C:Accession: A28199
R:Keywords: K.; Tamkun, M.M.; Renaud, K.J.; Fambrough, D.M.
J. Biol. Chem. 265, 4347-4354, 1988
A>Title: Ouabain-sensitive (Na⁺) + K⁺)-ATPase activity expressed in mouse L cells by
A:Reference number: A28199; MUID:88153759; PMID:2831227
A:Accession: A28199
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1021 <TRK>
A:Cross-references: UNIPROT:P09572; GB:J03230; NID:g211219; PIDN:AAA48607.1; PID:g211220
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein
F:586-781/Domain: ATPase nucleotide-binding domain homology <ATN>
F:213,481/Binding site: carboxylate (Asn) (covalent) #status predicted
F:374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:506/Binding site: ATP (Lys) #status predicted

Query Match 39.4%; Score 43; DB 2; Length 1021;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16
DB 82 PTPREWVFC 91

RESULT 35
B24862
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - pig
N:Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha chain
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C:Accession: B24862; I46572; A35504; S00011; S00502; S02569; S29762
R:Ovchinnikov, Y.A.; Modyanov, N.N.; Broude, N.E.; Petrakhin, K.E.; Grishin, A.V.; Arzam
FEBS Lett. 201, 237-245, 1986
A>Title: Pig kidney Na⁺, K⁺-ATPase. Primary structure and spatial organization.
A:Reference number: A91361; MUID:86220813; PMID:2423371
A:Accession: B24862
A:Molecule type: mRNA
A:Residues: 1-1021 <OVCL>
A:Cross-references: UNIPROT:P05024; EMBL:X03938; NID:g1897; PIDN:CAA27576.1; PID:g1898
A>Note: The authors translated the codon TCC for residue 391 as Phe, TCG for residue 723
R:Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Arsenyan, S.G.; Broude, N.E.; Petrakhin, K.E.;
Dokl. Biochem. 283, 270-272, 1995
A>Title: Amino acid sequence of the 17-kilodalton fragment of the cytoplasmic region of
A:Reference number: I46572
A:Accession: I46572
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 469-617 <OVCL>
A:Cross-references: GB:M32512; NID:g164385; PIDN:AAA31004.1; PID:g164386
R:Karliel, S.J.D.; Goldshleger, R.; Stein, W.D.
Proc. Natl. Acad. Sci. U.S.A. 87, 4566-4570, 1990
A>Title: A 19-kDa C-terminal tryptic fragment of the alpha chain of Na⁺/K⁺-ATPase is esser
A:Reference number: A35504; MUID:90280416; PMID:2162048
A:Accession: A35504
A:Molecule type: Protein
A:Residues: 836-845, 'R', 847-851 <KAR>
R:Ovchinnikov, Y.A.; Arzamazova, N.M.; Arystarkhova, E.A.; Gevondyan, N.M.; Aldanova, N.
FEBS Lett. 217, 265-274, 1987
A>Title: Detailed structural analysis of exposed domains of membrane-bound Na⁺, K⁺-ATPase
A:Reference number: S00011; MUID:8724731; PMID:3036581
A:Contents: annotation; membrane topology
R:Ovchinnikov, Y.A.; Luneva, N.M.; Arystarkhova, E.A.; Gevondyan, N.M.; Arzamazova, N.M.
FEBS Lett. 227, 230-234, 1988
A>Title: Topology of Na⁺, K⁺-ATPase: identification of the extra- and intracellular hydrog
A:Reference number: S02569; MUID:88112252; PMID:2448169
A:Contents: annotation; membrane topology

C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans
F:6-1021/Product: Na+/K+-transporting ATPase alpha chain #status experimental <MAT>
F:6-93/Domain: intracellular #status predicted <INT1>
F:94-118/Domain: transmembrane #status predicted <TM1>
F:128-147/Domain: transmembrane #status predicted <TM2>
F:148-288/Domain: intracellular #status predicted <INT2>
F:289-311/Domain: transmembrane #status predicted <TM3>
F:318-336/Domain: transmembrane #status predicted <TM4>
F:347-784/Domain: intracellular #status predicted <INT3>
F:585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
F:785-808/Domain: transmembrane #status predicted <TM5>
F:847-872/Domain: transmembrane #status predicted <TM6>
F:873-950/Domain: intracellular #status predicted <INT4>
F:951-976/Domain: transmembrane #status predicted <TM7>
F:977-1021/Domain: extracellular #status predicted <EXT>
F:374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:506/Binding site: ATP (Lys) #status predicted
F:715,719,724/Active site: Asp, Asp, Lys #status predicted

Query Match 39.4%; Score 43; DB 2; Length 1021;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16
DB 82 PTPREWVFC 91

RESULT 36
S49127
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - European eel
C:Species: Anguilla anguilla (European eel)
C>Date: 01-Feb-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
C:Accession: S49127
R:Cutler, C.; Sanders, I.L.; Cramb, G.
submitted to the EMBL Data Library, November 1993
A:Reference number: S45093
A:Accession: S49127
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1022 <CVL>
A:Cross-references: UNIPROT:Q92030; EMBL:X76108; NID:g509405; PIDN:CAA53714.1; PID:g509
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; transmem
F:586-782/Domain: ATPase nucleotide-binding domain homology <ATN>
F:214,482/Binding site: carboxylate (Asn) (covalent) #status predicted
F:375/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:507/Binding site: ATP (Lys) #status predicted

Query Match 39.4%; Score 43; DB 2; Length 1022;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16
DB 83 PTPREWVFC 92

RESULT 37
A24639
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain [validated] - rat
N:Alternate names: Na+/K+-transporting ATPase alpha chain; kidney-type
N:Contents: Na+/K+-transporting ATPase alpha-S chain
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: A24639; S00460; A27180; S11020; A25171; S29877; S10758
R:Shull, G.E.; Greb, J.; Lingrel, J.B.
Biochemistry 25, 8125-8132, 1986
A>Title: Molecular cloning of three distinct forms of the Na⁺, K⁺-ATPase alpha-subunit f
A:Reference number: A90512; MUID:87128908; PMID:3028470
A:Accession: A24639
A:Molecule type: mRNA

A;Residues: 1-1023 <SHU>
A;Cross-references: UNIPROT:P06685; EMBL:M4511; NID:G203026; PIDD:AAA40775.1; PID:G2030
R;Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamine, H.; Kojima, T.; Ohka, T.; N
J. Biochem. 102, 43-58, 1987
A;Title: Primary structures of two types of alpha-subunit of rat brain Na(+), K(+)-ATPase
A;Reference number: S00460; MUID:86032933; PMID:2622682
A;Accession: S00460
A;Molecule type: mRNA
A;Residues: 1-1023 <HAR>
A;Cross-references: EMBL:X05882; NID:G55771; PIDD:CAA29306.1; PID:G55772
R;Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard, B.
J. Cell Biol. 105, 1855-1865, 1987
A;Title: Three differentially expressed Na,K-ATPase alpha subunit isoforms: structural a
A;Reference number: A92749; MUID:88033255; PMID:2822726
A;Accession: A27180
A;Molecule type: mRNA
A;Residues: 1-67, 'PV', 70-174, 'E', 176-187, 'V', 189-334, 'V', 336-1023 <HER>
A;Cross-references: EMBL:M8644; NID:G205631; PIDD:AAA41671.1; PID:G205632
R;Tagawa, Y.; Kawakami, K.; Nagano, K.
Biochim. Biophys. Acta 1049, 286-292, 1990
A;Title: Cloning and analysis of the 5'-flanking region of rat Na(+)/K(+)-ATPase alpha-1
A;Reference number: S11020; MUID:90344872; PMID:2166579
A;Accession: S11020
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-41 <YAG>
A;Cross-references: EMBL:X53233
R;Schneider, J.W.; Mercer, R.W.; Caplan, M.; Emanuel, J.R.; Sweadner, K.J.; Benz Jr., E.
Proc. Natl. Acad. Sci. U.S.A. 82, 6357-6361, 1985
A;Title: Molecular cloning of rat brain Na,K-ATPase alpha-subunit cDNA.
A;Reference number: A25171; MUID:85298352; PMID:2994074
A;Accession: A25171
A;Molecule type: mRNA
A;Residues: 489-533 <SCH>
R;Lytton, J.
Biochem. Biophys. Res. Commun. 132, 764-769, 1985
A;Title: The catalytic subunits of the (Na(+), K(+))-ATPase alpha and alpha(+) isozymes
A;Reference number: S29877; MUID:8650667; PMID:2998384
A;Accession: S29877
A;Status: preliminary
A;Molecule type: protein
A;Residues: 6-19 <LTV>
R;Kurihara, K.; Hosoi, K.; Kodama, A.; Ueha, T.
Biochim. Biophys. Acta 1039, 234-240, 1990
A;Title: A new electrophoretic variant of alpha subunit of Na(+)/K(+)-ATPase from the su
A;Reference number: S10758; MUID:90304196; PMID:2163680
A;Accession: S10758
A;Molecule type: protein
A;Residues: 6, 'X', 8-10, 'X', 12-16 <KUR>
A;Experimental source: submandibular gland
A;Note: designated alpha-S form; thought to arise from alpha-1 chain by post-translation
C;Genetics:
A;Gene: NKXAL
A;Intons: 4/3
A;Note: the list of introns may be incomplete
C;Superfamily: Na(+)/K(+)-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F;6-1023/Product: Na(+)/K(+)-transporting ATPase alpha-1 chain #status experimental <MAT>
F;6-95/Domain: intracellular #status predicted <INT1>
F;96-110/Domain: transmembrane #status predicted <TM1>
F;110-149/Domain: transmembrane #status predicted <TM2>
F;150-290/Domain: intracellular #status predicted <INT2>
F;291-313/Domain: transmembrane #status predicted <TM3>
F;320-348/Domain: transmembrane #status predicted <TM4>
F;349-786/Domain: intracellular #status predicted <INT3>
F;587-783/Domain: ATPase nucleotide-binding domain homology <ATN>
F;787-810/Domain: transmembrane #status predicted <TM5>
F;849-874/Domain: transmembrane #status predicted <TM6>
F;885-952/Domain: intracellular #status predicted <INT4>
F;953-978/Domain: transmembrane #status predicted <TM7>
F;979-1023/Domain: extracellular #status predicted <EXT>
F;376/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;508/Binding site: ATP (Lys) #status predicted

F;717,721,726/Active site: Asp, Asp, Lys #status predicted
Query Match 39.4%; Score 43; DB 1; Length 1023;
Best Local Similarity 60.0%; Pred. No. 2,4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 7 PTLREWISFC 16
DB 84 PTLREWVKFC 93
RESULT 38
Na(+)/K(+)-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - giant toad
C;Species: Bufo marinus (giant toad)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #ext_change 09-Jul-2004
C;Accession: A43451; S24650
R;Baisner, F.; Canessa, C.M.; Horisberger, J.D.; Rossier, B.C.
J. Biol. Chem. 267, 16895-16903, 1992
A;Title: Primary sequence and functional expression of a novel ouabain-resistant Na,K-A
A;Reference number: A43451; MUID:92380991; PMID:1380956
A;Accession: A43451
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1023 <JAI>
A;Cross-references: UNIPROT:P30714; EMBL:Z11798; NID:G62491; PIDD:CAA77842.1; PID:G6249
A;Experimental source: urinary bladder cell line TBM 18-23
A;Note: submitted to the EMBL Data Library, March 1992
C;Superfamily: Na(+)/K(+)-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F;6-1023/Product: Na(+)/K(+)-transporting ATPase alpha-1 chain #status predicted <MAT>
F;6-95/Domain: intracellular #status predicted <INT1>
F;96-120/Domain: transmembrane #status predicted <TM1>
F;130-149/Domain: transmembrane #status predicted <TM2>
F;150-290/Domain: intracellular #status predicted <INT2>
F;291-313/Domain: transmembrane #status predicted <TM3>
F;320-348/Domain: transmembrane #status predicted <TM4>
F;349-786/Domain: intracellular #status predicted <INT3>
F;587-783/Domain: ATPase nucleotide-binding domain homology <ATN>
F;787-810/Domain: transmembrane #status predicted <TM5>
F;849-874/Domain: transmembrane #status predicted <TM6>
F;885-952/Domain: intracellular #status predicted <INT4>
F;953-978/Domain: transmembrane #status predicted <TM7>
F;979-1023/Domain: extracellular #status predicted <EXT>
F;376/Active site: Asp (aspartylphosphate intermediate) #status predicted
F;508/Binding site: ATP (Lys) #status predicted
F;717,721,726/Active site: Asp, Asp, Lys #status predicted
Query Match 39.4%; Score 43; DB 1; Length 1023;
Best Local Similarity 60.0%; Pred. No. 2,4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 7 PTLREWISFC 16
DB 84 PTLREWVKFC 93
RESULT 39
Na(+)/K(+)-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - African clawed frog
N;Alternate names: sodium pump alpha chain
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #ext_change 09-Jul-2004
C;Accession: A60444
R;Verrey, F.; Kairouz, P.; Schaefer, E.; Fuentes, P.; Geering, K.; Rossier, B.C.; Kraeh
Am. J. Physiol. 256, F1034-F1043, 1989
A;Title: Primary sequence of Xenopus laevis Na(+)-K(+)-ATPase and its localization in A
A;Reference number: A60444; MUID:89285429; PMID:2544104
A;Accession: A60444
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1025 <VER>

RESULT 43

JH0470
 Na+/K+-exchanging ATPase (BC 3.6.3.9) alpha chain (clone pAATNa136) - brine shrimp
 C:/Species: Artemia franciscana (brine shrimp)
 C:/Date: 30-Jan-1992 #sequence_revision 30-Jan-1992 #text_change 09-Jul-2004
 C:/Accession: JH0470; S24196
 R:/Macias, M.T.; Palmero, I.; Sastre, L.
 Gene 105, 197-204, 1991
 A:/Title: Cloning of a cDNA encoding an Artemia franciscana Na/K ATPase alpha-subunit.
 A:/Reference number: JH0470; MID:92039032; PMID:1657719
 A:/Accession: JH0470
 A:/Molecule type: mRNA
 A:/Residues: 1-1004 <MAC>
 A:/Cross-references: UNIPROT:P28774; EMBL:X56650; NID:910933; PIDN:CAA39972.1; PID:910934
 C:/Superfamily: Na+/K+-transferring ATPase alpha chain; ATPase nucleotide-binding domain
 C:/Keyword: ATP, heterodimer, hydrolyase, ion transport, phosphoprotein, potassium transp
 F:/2-1004/Product: Na+/K+-transferring ATPase alpha chain #status predicted <MAT>
 F:/2-75/Domain: intracellular #status predicted <INT1>
 F:/76-97/Domain: transmembrane #status predicted <TM1>
 F:/111-130/Domain: transmembrane #status predicted <TM2>
 F:/322-396/Domain: transmembrane #status predicted <TM3>
 F:/301-329/Domain: transmembrane #status predicted <TM4>
 F:/330-367/Domain: intracellular #status predicted <INT>
 F:/568-764/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:/768-791/Domain: transmembrane #status predicted <TM5>
 F:/830-855/Domain: transmembrane #status predicted <TM6>
 F:/856-936/Domain: intracellular #status predicted <INT4>
 F:/937-955/Domain: transmembrane #status predicted <TM7>
 F:/956-1004/Domain: extracellular #status predicted <EXT>
 F:/557/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:/489/Binding site: ATP (lys) #status predicted
 F:/598,702,707/Active site: Asp, Asp, Lys #status predicted

Query Match 39.0%; Score 42.5; DB 2; Length 1004;
 Best Local Similarity 47.4%; Pred. No. 2.7e+02;
 Matches 9; Conservative 0; Mismatches 3; Indels 7; Gaps 1;
 QY 5 DGP-----TLREWISFC 16
 DB 55 DGNCLTPKPTPEWIKFC 73

RESULT 44

T00038
 hypothetical protein KIAA0289 - human (fragment)
 C:/Species: Homo sapiens (man)
 C:/Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
 C:/Accession: T00038
 R:/Ohara, O.; Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Nomura, N.
 submitted to the EMBL Data Library, August 1997
 A:/Description: Prediction of the coding sequences of unidentified human genes.
 A:/Reference number: Z14073
 A:/Accession: T00038
 A:/Status: preliminary; translated from GB/EMBL/DBJ
 A:/Molecule type: mRNA
 A:/Residues: 1-1302 <OHA>
 A:/Cross-references: EMBL:AB006627; NID:d1170680; PIDN:BA422958.1; PID:d1023834
 A:/Experimental source: brain
 C:/Genetics:
 A:/Note: KIAA0289

Query Match 39.0%; Score 42.5; DB 2; Length 1302;
 Best Local Similarity 35.7%; Pred. No. 3.5e+02;
 Matches 10; Conservative 1; Mismatches 6; Indels 11; Gaps 1;
 QY 1 GGC-----ADGPTLRWISFCG 17
 DB 666 GGCCEQLCLQOMAPFPDDPTLYNIMFCG 693

RESULT 45

AH2829

conserved hypothetical protein Atu2063 [imported] - Agrobacterium tumefaciens (strain C
 C:/Species: Agrobacterium tumefaciens
 C:/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:/Accession: AH2829
 R:/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J
 erige, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavlin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, W.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:/Reference number: AB2577; MID:21608550; PMID:11743193
 A:/Accession: AH2829
 A:/Status: preliminary
 A:/Molecule type: DNA
 A:/Residues: 1-141 <KUR>
 A:/Cross-references: UNIPROT:O8UD08; GB:AE008688; PIDN:AA143054.1; PID:g17740521; GSPDB:
 A:/Experimental source: strain C58 (Dupont)
 C:/Genetics:
 A:/Gene: Atu2063
 A:/Map position: circular chromosome

Query Match 38.5%; Score 42; DB 2; Length 141;
 Best Local Similarity 47.1%; Pred. No. 53;
 Matches 8; Conservative 2; Mismatches 3; Indels 4; Gaps 1;
 QY 2 GCADGPTLRWISFCG 18
 DB 60 GAADAP----WLAFIGG 72

Search completed: September 1, 2005, 16:22:47
 Job time : 17.7266 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:37 ; Search time 66.9496 Seconds
(without alignments)
137.677 Million cell updates/sec

Title: US-10-083-768-6
Perfect score: 109
Sequence: 1 GGCADGPTLRKRWISFCGG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database: UniProt 03:*
1: uniprot_sprot:*
2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	51.4	297	Q7UG64	Q7UG64 rhodopirell
2	54.5	50.0	934	Q9NEX6	Q9NEX6 caenorhabdi
3	50.5	46.3	387	Q98A97	Q98A97 rhizobium 1
4	50.5	46.3	389	Q8KJF9	Q8KJF9 rhizobium 1
5	50	45.9	386	Q8KJF9	Q8KJF9 rhizobium 1
6	50	45.9	386	Q8KJF9	Q8KJF9 rhizobium 1
7	49.5	45.4	405	Q9KIE9	Q9KIE9 streptomyc
8	49	45.0	245	Q9M060	Q9M060 arabidopsis
9	49	45.0	349	Q7V2B2	Q7V2B2 prochloroco
10	48	44.0	319	Q9RKM5	Q9RKM5 streptomyc
11	48	44.0	342	Q6VME4	Q6VME4 streptomyc
12	48	44.0	461	Q7J2W7	Q7J2W7 mycobacteri
13	48	44.0	1123	Q7QCE3	Q7QCE3 atropheles g
14	47.5	43.6	283	Q7ULR5	Q7ULR5 rhodopirell
15	47.5	43.6	283	Q82CW2	Q82CW2 streptomyc
16	47	43.1	94	Q6MX73	Q6MX73 azoarcus sp
17	47	43.1	129	Q8DHX7	Q8DHX7 synecococc
18	47	43.1	271	Q89PR8	Q89PR8 bradyrhizob
19	47	43.1	475	Q9UAT5	Q9UAT5 caenorhabdi
20	47	43.1	821	Q96BD4	Q96BD4 caenorhabdi
21	47	43.1	956	Q6C1J9	Q6C1J9 kluyveromyc
22	47	43.1	1926	Q9Y8B3	Q9Y8B3 paracoccidi
23	46.5	42.7	166	Q6KGG9	Q6KGG9 bacterioph
24	46.5	42.7	425	Q89HD8	Q89HD8 bradyrhizob
25	46	42.2	97	Q8FPC4	Q8FPC4 corynebacte
26	46	42.2	117	Q7MVA9	Q7MVA9 porphyromon
27	46	42.2	159	Q8N852	Q8N852 homo sapien
28	46	42.2	162	Q63KH8	Q63KH8 burkholderi
29	46	42.2	196	Q7VWWS	Q7VWWS bordetella
30	46	42.2	196	Q7W9K1	Q7W9K1 bordetella
31	46	42.2	245	Q8GVFS	Q8GVFS oryza sativ

32	46	42.2	275	013090	013090 pleurodeles
33	46	42.2	347	Q7PPP6	Q7PPP6 anopheles g
34	46	42.2	403	Q88NU2	Q88NU2 pseudomonas
35	46	42.2	443	Q9P858	Q9P858 phaeosphaer
36	46	42.2	482	Q6AIT0	Q6AIT0 desulfocale
37	46	42.2	926	1 AASS HUMAN	Q9u4t5 homo sapien
38	46	42.2	1902	Q9Y878	Q9Y878 coccidioid
39	45.5	41.7	309	Q8XZNS	Q8XZNS ralsconia s
40	45	41.3	108	Q7RUN5	Q7RUN5 neurospora
41	45	41.3	146	Q6ZTT4	Q6ZTT4 homo sapien
42	45	41.3	173	Q8C4M6	Q8C4M6 mus musculu
43	45	41.3	180	Q07291	Q07291 natronomona
44	45	41.3	209	Q6N1X5	Q6N1X5 rhodopseudo
45	45	41.3	290	Q89JRS	Q89JRS bradyrhizob
46	45	41.3	338	Q82CX1	Q82CX1 streptomyc
47	45	41.3	379	Q7SKV0	Q7SKV0 brachydanio
48	45	41.3	410	Q623V1	Q623V1 burkholderi
49	45	41.3	410	Q63H26	Q63H26 burkholderi
50	45	41.3	421	Q9XUV7	Q9XUV7 caenorhabdi
51	45	41.3	499	1 MEP2 YEAST	P41948 saccharomyc
52	45	41.3	540	Q82L10	Q82L10 streptomyc
53	45	41.3	594	Q7SHC4	Q7SHC4 neurospora
54	45	41.3	769	Q70804	Q70804 et virus. 1
55	44.5	40.8	175	Q7XQ02	Q7XQ02 oryza sativ
56	44.5	40.8	248	Q7PXF4	Q7PXF4 anopheles g
57	44.5	40.8	282	Q7QCK2	Q7QCK2 chemus the
58	44.5	40.8	429	Q8AVB0	Q8AVB0 brachydanio
59	44.5	40.8	485	Q08SC10	Q08SC10 propionibac
60	44.5	40.8	497	Q7QIK7	Q7QIK7 anopheles g
61	44.5	40.8	497	Q6PBA6	Q6PBA6 brachydanio
62	44.5	40.8	818	Q6M209	Q6M209 aspergillus
63	44.5	40.8	1067	Q81TL2	Q81TL2 trypanosoma
64	44.5	40.8	1142	Q7NLE9	Q7NLE9 gloeobacter
65	44.5	40.8	173	Q6ZAD7	Q6ZAD7 oryza sativ
66	44	40.4	173	Q6QHD2	Q6QHD2 gallid herp
67	44	40.4	178	Q6PL14	Q6PL14 gallid herp
68	44	40.4	197	Q6R8A0	Q6R8A0 sodalis glo
69	44	40.4	209	Q9L059	Q9L059 streptomyc
70	44	40.4	210	Q69PA9	Q69PA9 oryza sativ
71	44	40.4	238	Q70KX0	Q70KX0 anopheles g
72	44	40.4	277	1 IMP1 MOUSE	P70224 mus musculu
73	44	40.4	292	Q67642	Q67642 gallid herp
74	44	40.4	298	Q86653	Q86653 gallid herp
75	44	40.4	310	Q678H2	Q678H2 lymphocyti
76	44	40.4	346	Q62030	Q62030 caenorhabdi
77	44	40.4	371	Q9RRJ3	Q9RRJ3 deinococcus
78	44	40.4	385	Q7XMK0	Q7XMK0 oryza sativ
79	44	40.4	404	Q7QFA0	Q7QFA0 anopheles g
80	44	40.4	425	Q8PD03	Q8PD03 xenomomas
81	44	40.4	450	Q75211	Q75211 abhya goss
82	44	40.4	490	Q04270	Q04270 chlamydomon
83	44	40.4	519	Q7Y1N9	Q7Y1N9 oryza sativ
84	44	40.4	524	Q66GJ0	Q66GJ0 arabidopsis
85	44	40.4	524	Q84WJ3	Q84WJ3 arabidopsis
86	44	40.4	524	Q9C868	Q9C868 arabidopsis
87	44	40.4	537	Q63M37	Q63M37 burkholderi
88	44	40.4	613	Q7YGT5	Q7YGT5 dirosophila
89	44	40.4	613	Q9VGR8	Q9VGR8 dirosophila
90	44	40.4	742	Q8SRJ4	Q8SRJ4 encephalit
91	44	40.4	926	1 AASS MOUSE	Q99K67 mus musculu
92	44	40.4	946	Q9UE55	Q9UE55 dictyosteli
93	44	40.4	974	1 PHS2 SOLTU	P53535 solanum tub
94	44	40.4	997	Q6B126	Q6B126 debaryomyce
95	44	40.4	1008	Q8AY57	Q8AY57 fundulus he
96	44	40.4	1011	Q6VYV7	Q6VYV7 oncorhynch
97	44	40.4	1022	1 ATIA TORCA	P05025 torpido cal
98	44	40.4	1023	Q7ZYK8	Q7ZYK8 homo sapien
99	44	40.4	1025	Q7ZYK8	Q7ZYK8 xenopus lae
100	44	40.4			

ALIGNMENTS

```

RESULT 1
SQ 07U0E4 PRELIMINARY; PRT; 297 AA.
AC 07U0E4;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
DE Hypoetical protein.
GN OrderedlocusNames=RB6375;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxId=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294144; CAD74759.1; -.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR PROSITE; PS00152; ATPase_ALPHA_BETA; UNKNOWN_1.
DR PROSITE; PS50829; GYP; 1.
KW Complete proteome; Hypoetical protein.
SQ SEQUENCE 297 AA; 31805 MW; 475F670F02C78B9B CRC64;

Query Match 51.4%; Score 56; DB 2; Length 297;
Best local Similarity 69.2%; Pred. No. 2.2;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCADGPTLRW 14
Db 173 GPADGPTMKQWIS 185

RESULT 2
SQ 09NEX6 PRELIMINARY; PRT; 934 AA.
AC 09NEX6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)
DE Hypoetical protein Y105E8A.21.
GN ORFNames=Y105E8A.21;
OS Caenorhabditis elegans.
OC Bukariota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditicoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132876; CAC48140.1; -.
DR WormBase; WBGenome00013679; Y105E8A.21.
DR WormPep; Y105E8A.21; CR25162.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; C:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.

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KW Hypoetical protein.
SQ SEQUENCE 934 AA; 104855 MW; 5ED4E1D03DB06F24 CRC64;

Query Match 50.0%; Score 54.5; DB 2; Length 934;
Best local Similarity 58.8%; Pred. No. 12;
Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 3 CADGPTLRW-ISFCGG 18
Db 899 CVDGTSRDMVPSFTGG 915

RESULT 3
SQ 098A97 PRELIMINARY; PRT; 387 AA.
AC 098A97;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, last annotation update)
DE M16096 protein.
GN OrderedlocusNames=m16096;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxId=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Iessawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsuno M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakasaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003008; BAB52440.1; -.
DR HSSP; P77407; 1POY.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR003673; CAIR_BAIF.
DR Pfam; PF02515; CoA_transf_3; 1.
KW Complete proteome.
SQ SEQUENCE 387 AA; 42226 MW; 64643BEBCE8F25518 CRC64;

Query Match 46.3%; Score 50.5; DB 2; Length 387;
Best local Similarity 42.9%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 2; Indels 7; Gaps 1;

QY 3 CADGPTLRW-----REMISFC 16
Db 237 CADGKEIVFSVQNDREVMVNC 257

RESULT 4
SQ 08KJF9 PRELIMINARY; PRT; 389 AA.
AC 08KJF9;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, last annotation update)
DE PUTATIVE RACEMASE/DEHYDRATASE PROTEIN.
GN Name=m81181;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxId=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R7A;
RX MEDLINE=21999272; PubMed=12003951;
RX DOI=10.1128/JB.184.11.3086-3095.2002;
RA Sullivan J.T., Trzciatkowski J.R., Crutickbank R.W., Gouzy J.,

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RA Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rosbach U.,
 RA Stuart G.S., Weaver J.B., Webby R.J., de Bruijn F.J., Ronson C.W.,
 RT "Comparative sequence analysis of the symbiosis island of
 RT Mesorhizobium loti strain R7A."
 RL J. Bacteriol. 184:3086-3095 (2002).
 DR EMBL: AL672113; CAD31586.1; -
 DR HSSP: P77407.1PQY.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR003673; CA1B_BAIF.
 DR Pfam: PF02515; COA_transf_3; 1.
 SQ SEQUENCE 389 AA; 42703 MW; 6678D2C96A7E5204 CRC64;
 Query Match 46.3%; Score 50.5; DB 2; Length 389;
 Best Local Similarity 42.9%; Pred. No. 21;
 Matches 9; Conservative 3; Mismatches 2; Indels 7; Gaps 1;
 Oy 3 CADGPTL-----REMISFC 16
 Db 243 CADGKEVIFSVQNDREWNFC 263
 RESULT 5
 ETR1_CANTR STANDARD; PRT; 386 AA.
 AC Q8WZM3;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Enoyl-[acyl-carrier protein] reductase [NADPH, B-specific] 1,
 DE mitochondrial precursor (EC 1.3.1.10).
 GN Name=ETR1;
 OS Candida tropicalis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5482;
 [1]
 RN SEQUENCE FROM N.A., SEQUENCE OF 23-29, FUNCTION, SUBUNIT, AND
 RP SUBCELLULAR LOCATION.
 RC STRAIN=ATCC 20336;
 RX PubMed=12890667; DOI=10.1074/jbc.M307664200;
 RX MEDLINE=21400968; PubMed=11509667;
 RX DOI=10.1128/MCB.21.18.6243-6253.2001;
 RA Torckko J.M., Kolivuranta K.T., Minalainen I.J., Yagi A.I., Schmitz W.,
 RA Kaatanen A.J., Airenne T.T., Gurvitz A., Hiltunen J.K.;
 RT "Candida tropicalis Etr1p and Saccharomyces cerevisiae Ydr26p
 RT (Mfi1p), 2-enoil thioester reductases essential for mitochondrial
 RT respiratory competence.";
 RL Mol. Cell. Biol. 21:6243-6253 (2001).
 [2]
 RN SUBUNIT.
 RP STRAIN=ATCC 20336;
 RC PubMed=12890667; DOI=10.1074/jbc.M307664200;
 RA Torckko J.M., Kolivuranta K.T., Kaatanen A.J., Airenne T.T.,
 RA Glumoff T., Ilves M., Hartig A., Gurvitz A., Hiltunen J.K.;
 RT "Candida tropicalis expresses two mitochondrial 2-enoil thioester
 RT reductases that are able to form both homodimers and heterodimers.";
 RL J. Biol. Chem. 278:41213-41220 (2003).
 [3]
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS), AND MUTAGENESIS OF TYR-79.
 RP PubMed=12614607; DOI=10.1016/S0022-2836(03)00038-X;
 RA Airenne T.T., Torckko J.M., Van den Plas S., Sotomunen R.T.,
 RA Kaatanen A.J., Wierenga R.K., Hiltunen J.K.;
 RT "Structure-function analysis of enoyl thioester reductase involved in
 RT mitochondrial maintenance.";
 RL J. Mol. Biol. 327:47-59 (2003).
 CC -1- FUNCTION: Required for respiration and the maintenance of the
 CC mitochondrial compartment. May have a role in the mitochondrial
 CC synthesis of fatty acids.
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NADP(+) = trans-
 CC 2,3-dehydroacyl-[acyl-carrier protein] + NADPH.
 CC -1- SUBUNIT: Homodimer and heterodimer with etr2.
 CC -1- SUBCELLULAR LOCATION: Mitochondrion.
 CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family. Quinone oxidoreductase subfamily.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL: U94997; AAL55472.1; -
 DR PDB: 1GU7; X-ray; A/B=23-386.
 DR PDB: 1GUP; X-ray; A/B=23-386.
 DR PDB: 1GYR; X-ray; A/B/C=23-386.
 DR InterPro: IPR002085; Adh_zn_family.
 DR InterPro: IPR011032; GroES_Like.
 DR Pfam: PF00107; Adh_zinc_N; 1.
 KW 3D-structure; Direct protein sequencing; Fatty acid biosynthesis;
 KW Mitochondrion; NADP; Oxidoreductase; Transit peptide.
 FT TRANSIT 1 22
 FT CHAIN 23 386
 FT MUTAGEN 79 79
 FT SEQUENCE 386 AA; 42160 MW; FCBC174A240742D8 CRC64;
 SQ
 Query Match 45.9%; Score 50; DB 1; Length 386;
 Best Local Similarity 61.5%; Pred. No. 25;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 6 GPTLEWIMISPCGG 18
 Db 254 GPTLEWIMISPCGG 266
 RESULT 6
 ETR2_CANTR STANDARD; PRT; 386 AA.
 AC Q8WZM4;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Enoyl-[acyl-carrier protein] reductase [NADPH, B-specific] 2,
 DE mitochondrial precursor (EC 1.3.1.10).
 GN Name=ETR2;
 OS Candida tropicalis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5482;
 [1]
 RN SEQUENCE FROM N.A., FUNCTION, AND SUBUNIT.
 RP STRAIN=ATCC 20336;
 RC PubMed=12890667; DOI=10.1074/jbc.M307664200;
 RA Torckko J.M., Kolivuranta K.T., Kaatanen A.J., Airenne T.T.,
 RA Glumoff T., Ilves M., Hartig A., Gurvitz A., Hiltunen J.K.;
 RT "Candida tropicalis expresses two mitochondrial 2-enoil thioester
 RT reductases that are able to form both homodimers and heterodimers.";
 RL J. Biol. Chem. 278:41213-41220 (2003).
 [2]
 RN X-RAY CRYSTALLOGRAPHY (2.11 ANGSTROMS).
 RP Airenne T.T., Torckko J.M., Hiltunen J.K.;
 RT "Crystal structure of enoyl thioester reductase 2.";
 RL Submitted (JUN-2002) to the PDB data bank.
 CC -1- FUNCTION: Required for respiration and the maintenance of the
 CC mitochondrial compartment. May have a role in the mitochondrial
 CC synthesis of fatty acids.
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NADP(+) = trans-
 CC 2,3-dehydroacyl-[acyl-carrier protein] + NADPH.
 CC -1- SUBUNIT: Homodimer and heterodimer with ETR1.
 CC -1- SUBCELLULAR LOCATION: Mitochondrion (By similarity).
 CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 CC family. Quinone oxidoreductase subfamily.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC -----

DR EMBL; U94996; AAL55471.1; -

DR PDB; 1HOK; X-ray; A/B=23-386.

DR InterPro; IPR002085; Adh zn family.

DR InterPro; IPR011032; GroES like.

DR Pfam; PF00107; ADH_zinc_N; 1

KW 3D-structure; fatty acid biosynthesis; Mitochondrion; NADP;

KW Oxidoreductase; Transist peptide.

FT TRANSIT 1 Mitochondrion (potential)

FT CHAIN 23 386 Enoyl-[acyl-carrier protein] reductase

FT [NADPH, B-specific] 2.

SEQUENCE 386 AA; 42116 MW; 91ABB00831F0C28 CRC64;

Query Match 45.9%; Score 50; DB 1; Length 386;

Best Local Similarity 61.5%; Pred. No. 25;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 GPTLRWISRCG 18

DB 254 GPTKEWIKQSG 266

RESULT 7

Q9KIE9 PRELIMINARY; PRT; 405 AA.

AC Q9KIE9;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Pkde.

GN Name=FKBE;

OS Streptomyces hygroscopicus subsp. ascomyceticus.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycinae; Streptomycetaceae; Streptomycetes.

OX NCBI_TaxID=132248;

RN (1)

SEQUENCE FROM N.A.

RX MEDLINE=20323220; PubMed=10863099; DOI=10.1016/S0378-1119(00)00171-2;

RA Wu K., Chung L., Revill W.P., Katz L., Reeves C.D.;

RT "The FK520 gene cluster of Streptomyces hygroscopicus var. ascomyceticus (ATCC 14891) contains genes for biosynthesis of unusual polyketide extender units.";

RT polyketide extender units.";

RL Gene 251:81-90(2000).

DR EMBL; AF235504; AAF8384.1; -

DR HSSP; P77407; 1POY.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR003673; CAIB BAIF.

DR Pfam; PF02515; CoA_transf_3; 1.

SEQUENCE 405 AA; 43696 MW; DC2569DFC914AD6F CRC64;

QY

Query Match 45.4%; Score 49.5; DB 2; Length 405;

Best Local Similarity 50.0%; Pred. No. 31;

Matches 10; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 5 DGPTL-----RWMISFCG 17

DB 252 DGQTNLGLONEREMASFCG 271

RESULT 8

Q9M060 PRELIMINARY; PRT; 245 AA.

AC Q9M060;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Eukaryotic translation initiation factor 6 (EIF-6)-like protein

DE (A13955620).

GN Name=Flit6_30; Synonyms=At3g55520;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN (1)

SEQUENCE FROM N.A.

RA Benes V., Wurmbach E., Drzonek H., Ansoerge W., Mewes H.W., Rudd S.,

RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

SEQUENCE FROM N.A.

RA Arabidopsis sequencing project;

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

SEQUENCE FROM N.A.

RA Shin P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,

RA Dale J.M., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,

RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,

RA Nguyen-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,

RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,

RA Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

RN [4]

SEQUENCE FROM N.A.

RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,

RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinzaki K.,

RA Ecker J., Theologis A., Davis R.W.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL161667; CAB81587.1; -

DR EMBL; BT009656; AAP75806.1; -

DR EMBL; AY128351; AAM91554.1; -

DR PIR; T47701; T47701.

DR HSSP; Q12522; 1G62.

DR GO; GO:0003743; P:translation initiation factor activity; IEA.

DR GO; GO:0006413; P:translational initiation; IEA.

DR InterPro; IPR002769; eIF6.

DR Pfam; PF01912; eIF-6; 1.

DR ProDom; PD006880; eIF6; 1.

DR SMART; SM00654; eIF6; 1.

DR TIGRPFAM; TIGR00323; eIF-6; 1.

KW Initiation factor.

SEQUENCE 245 AA; 26482 MW; 73369A2A65F390D CRC64;

QY

Query Match 45.0%; Score 49; DB 2; Length 245;

Best Local Similarity 57.1%; Pred. No. 22;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 ADGPTLRWISFCG 17

DB 194 AAGMTVNDWTSFCG 207

RESULT 9

Q7V2B2 PRELIMINARY; PRT; 349 AA.

AC Q7V2B2;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Dihydroorotase (EC 3.5.2.3).

GN Name=pyrC; Ordered locus Names=PMW0569;

OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).

OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcales;

OC Prochlorococcus.

OX NCBI_TaxID=59919;

RN (1)

SEQUENCE FROM N.A.

RX MEDLINE=22825658; PubMed=12917642; DOI=10.1038/nature01947;

RA Roccap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
 RA Ailgren N.A., Ariellano A., Coleman M., Hauser L., Hees W.R.,
 RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
 RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
 RA Webb E.A., Zinser E.R., Chisholm S.W.;
 RT "genome divergence in two *Prochlorococcus* ecotypes reflects oceanic
 niche differentiation.";
 RT Nature 424:1042-1047(2003).
 RL EMBL; BX572091; CAB19028.1; -.
 DR HSSP; P05020; 1479.
 DR GO; GO:0004151; F:dihydroorotase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0019856; P:pyrimidine base biosynthesis; IEA.
 DR InterPro; IPR006680; Amidohydro_1.
 DR InterPro; IPR004721; DHodimr.
 DR InterPro; IPR002195; Dihydroorotase.
 DR Pfam; PF01979; Amidohydro_1; 1.
 DR TRGFAMs; TIGR00856; pyrc_dimer; 1.
 DR PROSITE; PS00482; DIHYDROOROTASE_1; UNKNOWN_1.
 DR PROSITE; PS00483; DIHYDROOROTASE_2; 1.
 KM Complete proteome; Hydrolase.
 SQ SEQUENCE 349 AA; 39958 MW; CC02P5AE02EC927 CRC64;

Query Match 45.0%; Score 49; DB 2; Length 349;
 Best Local Similarity 50.0%; Pred. No. 32;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GCADGPTLRWISFC 17
 Db 243 GTDSAPHLRWKARFCG 258

RESULT 10

Q9RKM5 PRELIMINARY; PRT; 319 AA.
 AC Q9RKM5; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Putative Merf family transcriptional regulator.
 GN OPRNames=SCD17.06c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=2196410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleiser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RT *coelicolor* A3(2).";
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: Contains 1 HTH merf-type DNA-binding domain.
 DR EMBL; AL939118; CAB56383.1; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000551; HTH_Merf.
 DR InterPro; IPR009061; Putativ_DNA_bind.
 DR Pfam; PF00376; Merf; 1.
 DR PRINTS; PR00040; HTMERF.
 DR SMART; SM00432; HTH_MERF; 1.
 DR PROSITE; PS50937; HTH_MERF_2; 1.
 KM Complete proteome; DNA-binding.

SQ SEQUENCE 319 AA; 34841 MW; 1F51905A8BA5365E CRC64;
 Query Match 44.0%; Score 48; DB 2; Length 319;
 Best Local Similarity 61.5%; Pred. No. 42;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCADGPTLRWIS 14
 Db 255 GRDGPRLRWLA 267

RESULT 11

Q6VNH4 PRELIMINARY; PRT; 342 AA.
 AC Q6VNH4; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Putative SARF family pathway specific regulatory protein.
 GN Name=alpu;
 OS Streptomyces ambofaciens.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1889;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23877;
 RX PubMed=14742212;
 RA Pang X., Aigle B., Girardet J.M., Mangenot S., Pernodet J.L.,
 RA Decaris B., Leblond P.;
 RT "Functional angucycline-like antibiotic gene cluster in the terminal
 RT inverted repeats of the *Streptomyces ambofaciens* linear chromosome.";
 RL Antimicrob. Agents Chemother. 48:575-588(2004).
 DR EMBL; AY338477; AAR30165.1; -.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0000156; F:two-component response regulator activity; IEA.
 DR GO; GO:0000160; P:two-component signal transduction system (p. . .); IEA.
 DR InterPro; IPR009059; bi_resp_regltr_C.
 DR InterPro; IPR005158; BTAD.
 DR Pfam; PF03704; BTAD; 1.
 DR Pfam; PF00486; Trans_reg_C; 1.
 SQ SEQUENCE 342 AA; 35639 MW; 945BC92E5AE3D CRC64;

Query Match 44.0%; Score 48; DB 2; Length 342;
 Best Local Similarity 46.7%; Pred. No. 45;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GCADGPTLRWISFC 16
 Db 112 GCGGPGSPRPWLESC 126

RESULT 12

Q73ZW7 PRELIMINARY; PRT; 461 AA.
 AC Q73ZW7; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=MAP184c;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=k10;
 RA Li L., Baumann J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017232; AAS03801.1; -.
 DR GO; GO:0005506; F:iron ion binding; IEA.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR005806; Rieseke, reg.
 DR InterPro: IPR001663; Ring_hydroxyl_A.
 DR Pfam: PF00355; Rieseke, 1.
 DR PRINTS: PR00090; RINGDIKXGNASE.
 DR Complete proteome.
 KW SEQUENCE 461 AA; 52010 MW; 208B39A89C121839 CRC64;

Query Match 44.0%; Score 48; DB 2; Length 461;
 Best Local Similarity 47.4%; Pred. No. 60;
 Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 1 GGCA-----DGPTLEWMI 13
 |||||
 156 GGCAMINLDDADPALDMM 174

RESULT 13

Q70C63 PRELIMINARY; PRT; 1123 AA.
 AC Q70C63;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE AgCP1221.
 GN Name=agCG53078; ORFNames=ENSANG00000018866;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST.
 RA Anopheles Genome Sequencing Consortium;
 RB Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

DR EMBL: AAB01008859; EAA08177.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0008898; F:homocysteine S-methyltransferase activity; IEA.
 DR GO; GO:0004672; F:protein kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011009; Kinase, like.
 DR InterPro: IPR000719; Prot. kinase.
 DR InterPro: IPR003725; S_methyl_trans.
 DR Pfam: PF00069; Kinase; 1.
 DR Pfam: PF02574; S-methyl_trans; 1.
 DR ProDom: PD000001; Prot. Kinase; 1.
 DR PROSITE: PSS0011; PROTEIN KINASE DOM; 1.
 SQ SEQUENCE 1123 AA; 12006 MW; D3CC001D8D4882AF CRC64;

Query Match 44.0%; Score 48; DB 2; Length 1123;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 ADGPTLEWMTSF 15
 |||||
 DB 969 ADHPTVAFWISF 980

RESULT 14

Q7ULR5 PRELIMINARY; PRT; 238 AA.
 AC Q7ULR5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Similar to phycoerythrin alpha phycoerythrin lyase CpeC (EC 4.-.-.-
).
 GN Name=cpeC; OrderedLocusNames=RB9340;

OS Rhodospirillum rubrum.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heltmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 strain 1.";
 RT Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).

DR EMBL: BX94149; CAD76204.1; -.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR InterPro: IPR008938; ARM.
 DR InterPro: IPR004155; PBS_lyase_HEAT.
 DR Pfam: PF03130; HEAT_PBS; 1.
 DR SMART: SM00567; EZ_HEAT; 3.
 DR Complete proteome; Lyase.
 KW SEQUENCE 238 AA; 26142 MW; B7CA7284593B0C72 CRC64;

Query Match 43.6%; Score 47.5; DB 2; Length 238;
 Best Local Similarity 39.1%; Pred. No. 37;
 Matches 9; Conservative 2; Mismatches 1; Indels 11; Gaps 1;

QY 1 GGCAADGP-----TLREW 12
 |||||
 DB 29 GGCHDPMVYALKHANYFTMRQW 51

RESULT 15

Q82CW2 PRELIMINARY; PRT; 283 AA.
 AC Q82CW2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative ICLR-family transcriptional regulator.
 DE OrderedLocusNames=SAV5226;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomyces; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=MA-4680;
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites.";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).

RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis.";
 RT Nat. Biotechnol. 21:526-531(2003).

DR EMBL: AP005042; BAC72938.1; -.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006555; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR005471; HTH_ICLR.
 DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
 DR Pfam: PF01614; ICLR; 1.
 DR Complete proteome.
 KW SEQUENCE 283 AA; 30503 MW; F63B1705578EEB67 CRC64;

Query Match	Similarity	Score	DB	Length
Best Local	50.0%	Pred. No. 44		
Matches	8; conservative	3; Mismatches	2; Indels	3; Gaps
QY	3 CADGPT---LRMISF	15		
	: : :			
DB	152 CAGGPTPAVHWVDF	167		

RESULT 16

ID	Q6MX73	PRELIMINARY;	PRT;	94 AA.
AC	Q6MX73;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Hypothetical protein.			
GN	ORFNames=C2B002;			
OS	Azoarcus sp. (strain EbN1).			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;			
OC	Rhodocyclaceae; Azoarcus.			
OX	NCBI_TaxID=76114;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=EbN1;			
RA	Kube M., Heider J., Amann J., Hufnagel P., Kuehner S., Beck A.,			
RL	Reinhardt R., Rabus R.;			
RL	submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=EbN1;			
RA	PROSCIENCE;			
RL	submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BX682953; CAF21985.1; -			
KW	Hypothetical protein.			
SQ	SEQUENCE 94 AA; 9829 MW; 91ACBCCAB8A7EDE CRC64;			
Query Match	43.1%;	Score 47;	DB 2;	Length 94;
Query Local Similarity	72.7%;	Pred. No. 18;		
Matches	8; Conservative	1; Mismatches	2; Indels	0;

RESULT 17

ID	Q8DHX7	PRELIMINARY;	PRT;	129 AA.
AC	Q8DHX7			
DT	01-MAR-2003 (TrEMBLrel. 23, Created)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE	Tll1816 protein.			
CN	OrderedLocusNames={tll1816;			
OS	Synechococcus elongatus (Thermosynechococcus elongatus).			
OC	Bacteria; Cyanobacteria; Chroococcales; Synechococcus.			
OX	NCBI_TaxID=32046;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BP-1;			
RX	MEDLINE=22225144; PubMed=12240834;			
RA	Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasaamoto S.,			
RA	Watanabe A., Iriyuchi M., Kawashima K., Kimura T., Kishida Y.,			
RA	Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,			
RA	Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;			
RT	"Complete genome structure of the thermophilic cyanobacterium			
RT	Thermosynechococcus elongatus BP-1."			
RL	DNA Res. 9:123-130(2002).			
DR	EMBL, AP005375, BAC09356.1; -.			
KM	Complete proteome.			
SO	SEQUENCE 129 AA; 1464 MW; EBB44691E7DD1E12 CRC64;			

RESULT 18

ID	PRELIMINARY:	PRT:	271 AA.
089PE8:			
DT 01-JUN-2003 (TEMBLrel. 24, Created)			
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)			
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)			
DE CutM protein.			
GN Name=cutM; OrderedLocusNames=dlr3534;			
OS Bradyrhizobium japonicum.			
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
OC Bradyrhizobiaceae; Bradyrhizobium.			
OX NCBI_TaxID=375;			
[1]			
SEQUENCE FROM N.A.			
RC STRAIN=USDA110.			
RX MEDLINE=22484998; PubMed=12597275;			
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiimi T.,			
RA Sasamoto S., Metanabe A., Ideasa K., Iriuguchi M., Kawashima K.,			
RA Kobara M., Matsumoto M., Shimpo S., Tsurutoka H., Wada T., Yamada			
RA Tabata S.;			
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium			
RT Bradyrhizobium japonicum USDA110. "			
RL DNA Res. 9:189-197 (2002).			
DR EMBL; AP005948; BAC4799.1. -			
DR HSSP; P19920; IN62.			
DR GO; GO:0016491; F:oxidoreductase activity; IEA.			
DR GO; GO:0006118; P:electron transport; IEA.			
DR InterPro; IPR005107; CO dehydrog. flav C.			
DR InterPro; IPR002346; CO dehydrog. molych.			
DR Pfam; PF00941; FAD_binding_5; 1.			
DR Complete proteome.			
QO SEQUENCE 271 AA; 29422 MW; 4995C9F9A814FDC6 CRC64;			

RESULT 19

ID	ORGANISM	PRELIMINARY	PRT	475 AA
AC	Ogunt5;			
DT	01-MAY-2000 (T-EMBLrel. 13, Created)			
DT	01-MAY-2000 (T-EMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (T-EMBLrel. 23, Last annotation update)			
DE	Hypothetical protein C01B4.7;			
GN	Name=C01B4.7; ORFNames=C01B4.7;			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea			
OC	Rhabditidae; Pelodierinae; Caenorhabditis.			
OX	NCBI_TaxId=6239;			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RC	MEDLINE=99069613; PubMed=9851916;			
RC	WormBase Consortium;			
RT	WormBase Consortium;			
RT	Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.;			

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RL Science 282:2012-2018(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Smith A., Mameley P., Fronick W.;
RT "The sequence of C. elegans cosmid C01B4.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN (4)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilsson R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN (5)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG Wormbase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: ARI25952; AAD14699.1; -.
DR PIR; T33943; T33943.
DR Wormbase; WBGene0015271; C01B4.7.
DR WormPep; C01B4.7; CE20476.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS50850; MFS; 1.
DR Hypothetical protein.
RW SEQUENCE 475 AA; 53094 MW; 79095D45572AF535 CRC64;
SQ
Query Match 43.1%; Score 47; DB 2; Length 475;
Best Local Similarity 50.0%; Pred. No. 89;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
Qy 3 CADGPTLRWISFCGG 18
Db 268 CTDRCVLSAWVSFLGG 283
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RA Waterston R.H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN (4)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN (5)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN (6)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN (7)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN (8)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG Wormbase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006722; AAK68417.1; -.
DR PDB; 1LUR; X-ray; A/B=483-821.
DR Wormbase; WBGene0021219; Y19D10A.4.
DR WormPep; Y19D10A.4; CE21450.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004034; F:aldose 1-epimerase activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006012; P:galactose metabolism; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR008183; Ald1 epimerase.
DR InterPro; IPR011013; Gal_mut1-like.
DR InterPro; IPR007114; MFS.
DR Pfam; PF01263; Aldose_epim; 1.
DR PROSITE; PS50850; MFS; 1.
DR Hypothetical protein.
RW SEQUENCE 821 AA; 91593 MW; 923A78BFC95D1A76 CRC64;
SQ
Query Match 43.1%; Score 47; DB 2; Length 821;
Best Local Similarity 50.0%; Pred. No. 1,5e+02;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
Qy 3 CADGPTLRWISFCGG 18
Db 268 CTDRCVLSAWVSFLGG 283
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RESULT 21
Q6CLJ9 PRELIMINARY; PRT; 956 AA.
ID Q6CLJ9
AC Q6CLJ9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P40825 Saccharomyces cerevisiae YOR333cc ALA1 alanyl-tRNA
DE synthetase.
GN ORFNames=KLA0F024319;
OS Kluyveromyces lactis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=284590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
LaMontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,

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RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barney S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
 RA Boisrame A., Boyer J., Caltolico L., Confanioli F., de Danovar A.,
 RA Despore L., Fabre B., Fairhead C., Ferry-Dumazet H., Giropi A.,
 RA Hantreay F., Henneguier C., Jaumais N., Joyet P., Kachouri R.,
 RA Kierret A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicard J.M., Nikolaki M., Oztas S., Ozler-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straud M.L., Suleau A.,
 RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissbach J.,
 RA Wincker P., Soulet J.L.,
 RT "Genome evolution in yeasts.",
 RL Nature 430:35-44 (2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RA Genoscope (JUL-2004) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382126; CAG97897.1; -
 DR GO; GO:0004813; F:alanine-tRNA ligase activity; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0006419; P:alanyl-tRNA aminoacylation; IEA.
 DR InterPro; IPR003156; Pesterase_DHHAL.
 DR InterPro; IPR02318; tRNA-synt_2c.
 DR InterPro; IPR06193; tRNA_synt_ALA.
 DR Pfam; PF02272; DHHAL; 1.
 DR Pfam; PF01411; tRNA-synt_2c; 1.
 DR PRINTS; PR00860; TRNA-SYNTALA.
 DR TIGRFAMs; TIGR00344; alas; 1.
 DR PROSITE; PS50860; AA-TRNA_LIGASE_II_ALA; 1.
 KM Aminoacyl-tRNA synthetase.
 SQ SEQUENCE 956 AA; 107100 MW; 4F5CE855880A3C CRC64;
 Query Match 43.1%; Score 47; DB 2; Length 956;
 Best Local Similarity 50.0%; Pred. NO. 1.8e+02;
 Matches 9; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
 Oy 5 DGPTLRW---ISFCG 18
 Db 704 ENPTSEKOKSIFFCG 721

RESULT 22
 Q9Y8B3 PRELIMINARY; PRT; 1926 AA.
 ID Q9Y8B3;
 AC Q9Y8B3;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Glucan synthase.
 GN Name=Fks;
 OS Paracoccidioides brasiliensis.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Oxygenales; mitosporic Oxygenales; Paracoccidioides.
 CX NCBI_TaxID=121759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Pb01;
 RX MEDLINE=20171859; PubMed=10705373;
 RX DOI=10.1002/SITC.1097-0061(200003)016:5<451::AID-YEAS40>3.0.CO;2-O;
 RA Pereira M., Felipe M.S.S., Brigido M.M., Soares C.M.A., Azevedo M.O.;
 RT "Molecular cloning and characterization of a glucan synthase gene from
 the human pathogenic fungus Paracoccidioides brasiliensis.";
 RL Yeast 16:451-462(2000).
 DR EMBL; AF148715; AAD37783.1; -
 DR GO; GO:0000148; C:1,3-beta-glucan synthase complex; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0003843; F:1,3-beta-glucan synthase activity; IEA.
 DR GO; GO:0006075; P:beta-1,3 glucan biosynthesis; IEA.
 DR InterPro; IPR003440; Glyco_trans_48.
 DR InterPro; IPR002114; HPT_Serp_S.

DR Pfam; PF02364; Glucan synthase; 1.
 DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN 1.
 SQ SEQUENCE 1926 AA; 220574 MW; BB0985050D2253DS CRC64;
 Query Match 43.1%; Score 47; DB 2; Length 1926;
 Best Local Similarity 46.7%; Pred. NO. 3.6e+02;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Oy 2 GCADGPTLRWISFC 16
 Db 1374 GCADTPTIDWVORC 1388

RESULT 23
 Q6KG99 PRELIMINARY; PRT; 166 AA.
 ID Q6KG99;
 AC Q6KG99;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Bacteriophage Felix 01.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales.
 CX NCBI_TaxID=77775;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stranganathan N., Whitchard J.M., Pierson F.W., Kapur V., Weigt L.A.;
 RT "Bacteriophage Felix 01: Genetic Characterization.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF320576; AAO14824.1; -
 KM Hypothetical protein.
 SQ SEQUENCE 166 AA; 19296 MW; 5AAB33B39DC3C989 CRC64;
 Query Match 42.7%; Score 46.5; DB 2; Length 166;
 Best Local Similarity 52.9%; Pred. NO. 37;
 Matches 9; Conservative 0; Mismatches 5; Indels 3; Gaps 1;
 Oy 1 GGCADGPTLRWISFC 17
 Db 8 GSC---PTYGHWISLCG 21

RESULT 24
 Q89HD8 PRELIMINARY; PRT; 426 AA.
 ID Q89HD8;
 AC Q89HD8;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE B1r6053 protein.
 GN OrderedLocustNames=b1r6053;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Bradyrhizobiaceae; Bradyrhizobium.
 CX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USD110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyumi T.,
 RA Sasano S., Watanabe A., Ideawa K., Iriuguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpo S., Tsunoda H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 Bradyrhizobium japonicum USD110.";
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005957; BAC51318.1; -
 DR HSSP; P27017; 1000.
 KM Complete proteome.
 SQ SEQUENCE 426 AA; 47042 MW; AE20A1BC6CBE038 CRC64;
 Query Match 42.7%; Score 46.5; DB 2; Length 426;
 Best Local Similarity 66.7%; Pred. NO. 95;

Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
 QY 1 GGCADGPTLRW 12
 ||||: ||: ||
 Db 416 GGCAG-PTREXW 426

RESULT 25
 O8FPC4 PRELIMINARY; PRT; 97 AA.

AC O8FPC4; 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN OrderedlocusNames=CEI185;
 OS Corynebacterium efficiens.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=152794;
 RX SRRAIN=VS-314;
 RC MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
 RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
 RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
 RA Gojohori T.;
 RT "Comparative complete genome sequence analysis of the amino acid
 RT replacements responsible for the thermostability of Corynebacterium
 RT efficiens."
 RL Genome Res. 13:1572-1579(2003).
 DR EMBL; AP005220; BAC18668.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 97 AA; 10632 MW; 6CF1DA566EB304C CRC64;

Query Match 42.2%; Score 46; DB 2; Length 97;
 *Best Local Similarity 58.3%; Pred. No. 26;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCADGPTLRW 12
 ||||: ||: ||
 Db 77 GGALDGRTRKRW 88

RESULT 26
 O7MW49 PRELIMINARY; PRT; 117 AA.
 AC O7MW49; 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN OrderedlocusNames=PG1251;
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RX STRAIN=837;
 RC STRAIN=837;
 RX MEDLINE=22829867; PubMed=12949112;
 DOI=10.1128/JB.185.18.5591-5601.2003;
 RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
 RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwin M.L.,
 RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
 RA Ganger D., Trevelin H., Dong H., Galvin J.L., Duncan M.J.,
 RA Dewhirst F.E., Fraser C.M.;
 RT "Complete genome sequence of the oral pathogenic bacterium
 RT Porphyromonas gingivalis strain W83."
 RL J. Bacteriol. 185:5591-5601(2003).
 DR EMBL; AF017176; AA066334.1; -;
 TIGR; PG1251; -;
 KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 117 AA; 12589 MW; B4421EB01D186859 CRC64;
 Query Match 42.2%; Score 46; DB 2; Length 117;
 *Best Local Similarity 52.9%; Pred. No. 32;
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 GGCADGPTLRWTSFCG 18
 ||||: ||: ||
 Db 17 GGCVCPTVAWITIGAG 33

RESULT 27
 O8N852 PRELIMINARY; PRT; 159 AA.

AC O8N852; 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DE 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ40008.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RX SRRAIN=VS-314;
 RC TISSUE=Stomach;
 PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoliti T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katetani N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Iehibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Iehida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotura T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara T., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terasawa Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsunaga K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs."
 RL Nat. Genet. 36:40-45(2004).
 DR EMBL; AK097327; BAC04499.1; -;
 SQ SEQUENCE 159 AA; 17782 MW; DF63A4A6D7129A8 CRC64;

Query Match 42.2%; Score 46; DB 2; Length 159;
 *Best Local Similarity 52.6%; Pred. No. 43;
 Matches 10; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

QY 1 GGCA-----DGPTRWISF 15
 ||||: ||||: ||||
 Db 17 GGCGLLVKGMITRNWASF 35

RESULT 28
 O63KH8 PRELIMINARY; PRT; 162 AA.

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AC 063K18;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BPSS1383;
OC Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Tilball R.W., Peacock S.J., Cerdano-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebailia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshaizer D.,
RA Felwell T., Fraser A., Hance Z., Hauser H., Holtroyd S., Jagsels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songstivai S., Stevens K., Tumapa S., Vesaratchavee M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,
RT "Genomic plasticity of the causative agent of melioidosis,"
RT Burkholderia pseudomallei."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL; BX571966; CAH38655.1; -.
SQ SEQUENCE 162 AA; 17186 MW; 27CDFP4999112A83 CRC64;
QY 2 GCADGPTLR 10
Db 93 GCADGPTLR 101

RESULT 29
Q7VWM5 PRELIMINARY; PRT; 196 AA.
ID Q7VWM5
AC Q7VWM5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative lipoprotein.
GN OrderedLocustNames=BP2072;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagsels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640417; CAF42350.1; -.
KM Complete proteome; Lipoprotein.
SQ SEQUENCE 196 AA; 21519 MW; FF6E2B86B5E9968 CRC64;

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Query Match 42.2%; Score 46; DB 2; Length 196;
Best Local Similarity 88.9%; Pred. No. 53;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCADGPTLR 10
Db 18 GCASGPTLR 26

RESULT 30
Q7W9K1 PRELIMINARY; PRT; 196 AA.
ID Q7W9K1
AC Q7W9K1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative lipoprotein.
GN OrderedLocustNames=BP1756;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagsels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640428; CAE37057.1; -.
KM Complete proteome; Lipoprotein.
SQ SEQUENCE 196 AA; 21562 MW; D082FBA6CA765 CRC64;

Query Match 42.2%; Score 46; DB 2; Length 196;
Best Local Similarity 88.9%; Pred. No. 53;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCADGPTLR 10
Db 18 GCASGPTLR 26

RESULT 31
Q8GVF5 PRELIMINARY; PRT; 245 AA.
ID Q8GVF5
AC Q8GVF5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 26, Last annotation update)
DE Putative eukaryotic translation initiation factor 6.
GN Name=OJ1340_C08.131;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=33947;
RN [1]
RP SEQUENCE FROM N.A.
RC Sasaki T., Matsumoto T., Katayose Y.;
RA "Oryza sativa nippohare (GA3) genomic DNA, chromosome 7, BAC
RT clone:OJ1340_C08."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF005292; BAC45212.1; -.
 DR HSSP; 012522; 1G62.
 DR Gramene; ORGV5; -.
 DR GO; GO:0003743; P:translation initiation factor activity; IEA.
 DR GO; GO:0006413; P:translational initiation; IEA.
 DR InterPro; IPR002769; eIF6.
 DR Pfam; PF01912; eIF-6; 1.
 DR ProDom; PD006880; eIF6; 1.
 DR SMART; SM00654; eIF6; 1.
 DR TIGRfams; TIGR00323; eIF-6; 1.
 DR TrEMBL; A00000; eIF6; 1.
 KW Initiation factor.
 SQ SEQUENCE 245 AA; 26388 MW; EB526A7DD103291B CRC64;

Query Match 42.2%; Score 46; DB 2; Length 245;
 Best Local Similarity 50.0%; Pred. No. 66;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 ADGPTLRWISFCG 17
 DB 194 AAGMTVNDWTAFCG 207

RESULT 32
 ID 013090 PRELIMINARY; PRT; 275 AA.

AC 013090;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 GN Nckx-3.2.
 GN Name=PvNckx-3.2;
 OS Pleurodeles waltlilii (Iberian ribbed newt).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae;
 OC Pleurodeles
 NCBI_TaxID=8319;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9255950; PubMed=1032640;
 RI DOI=10.1002/(SICI)1520-6408(1999)24:3/4<319::AID-DVG15>3.0.CO;2-#;
 RA Nicolas S., Caudin X., Massacrier A., Cau P., Le Parco Y.;
 RT "Two Nckx-3-related genes are expressed in the adult and regenerating
 central nervous system of the urodele *Pleurodeles waltlilii*."
 RL Dev. Genet. 24:319-328(1999).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; U88714; AAC08704.1; -.
 DR HSSP; P22808; 1NK3.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR009057; Homeobox.
 DR InterPro; IPR000047; HTH_1ambrerepres.
 DR Pfam; PF00046; Homeobox_1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOK; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR DNA-binding; Homeobox; Nuclear protein.
 KW SEQUENCE 275 AA; 30341 MW; 4519CD44E3348DE0 CRC64;

Query Match 42.2%; Score 46; DB 2; Length 275;
 Best Local Similarity 43.8%; Pred. No. 74;
 Matches 7; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFCG 18
 DB 32 CAEPGACGWRRLCAG 47

RESULT 33

Q7PP6
 ID Q7PP6 PRELIMINARY; PRT; 347 AA.
 AC Q7PP6;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ENSANGP0000020769 (Fragment).
 GN Name=ENSANGP0000020769 (Fragment).
 OS Anopheles gambiae str. PEST.
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 NCBI_TaxID=180454;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION. The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AAB01008944; EAA10075.2; -.
 DR GO; GO:0008898; F:homocysteine S-methyltransferase activity; IEA.
 DR InterPro; IPR003726; S_methyl_trans.
 DR Pfam; PF02574; S-methyl_trans; 1.
 FT NON_TER
 SQ SEQUENCE 347 AA; 38585 MW; 66FF58A1000CDA4F CRC64;

Query Match 42.2%; Score 46; DB 2; Length 347;
 Best Local Similarity 61.5%; Pred. No. 93;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 CADGPTLRWISF 15
 DB 201 CDEYPTVRWISF 213

RESULT 34
 ID Q88NU2 PRELIMINARY; PRT; 403 AA.
 AC Q88NU2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=Pp112;
 OS Pseudomonas putida (strain KT2440).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NCBI_TaxID=160488;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22423060; PubMed=12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Nelson K.E., Weinel C., Paulsen I.T., Gill S.R., Pop M., Holmes M.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Kollonay J.F.,
 RA Brinac L.M., Beaman M.C., White O., Peterson J.D., Khouri H.M.,
 RA Madupu R., Nelson W.C., Holtzapple E.K., Scanlan D., Tran K.,
 RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
 RA Moazzes A., Utechtback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
 RA Medler H., Lauber J., Stepanovic D., Hoheisel J., Straetz M., Helm S.,
 RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuenmler B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 metabolically versatile *Pseudomonas putida* KT2440.";
 RL Environ. Microbiol. 4:799-808(2002).
 DR EMBL; AE016778; AAN6737.1; -.
 DR TIGR; A01112; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 403 AA; 42380 MW; 4D71AA1F370C58A7 CRC64;

Query Match 42.2%; Score 46; DB 2; Length 403;
 Best Local Similarity 61.5%; Pred. No. 11e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GPTLREWISFCG 18
 |||||
 Db 149 GPTLREWLVDVG 161

RESULT 35

Q9P858 PRELIMINARY; PRT; 443 AA.
 AC Q9P858; TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein. (Septoria nodorum).
 OS Phaeosphaeria nodorum (Septoria nodorum).
 OG Plasmid deltal.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
 NCBI_TaxID=13684;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BS444;
 RA "Transposable elements in the phytopathogenic fungus Stagonospora
 nodorum".
 RT Thesis (2000), PhD thesis, University of Birmingham, UK.
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BS444;
 RA Rawson J.M., Cutler S.B., Caten C.B.;
 RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
 DE EMBL; AJ277966; CAB91876.1;
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 443 AA; 49466 MW; 367E0762EB839E68 CRC64;

Query Match 42.2%; Score 46; DB 2; Length 443;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CADGPTLREWISFCG 18
 |||||
 Db 170 CSENGTLREWITALQG 185

RESULT 36
 Q6AIT0 PRELIMINARY; PRT; 482 AA.
 ID Q6AIT0;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=DP3021;
 OS Desulfotalea psychrophila.
 CC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
 CC Desulfobulbaceae; Desulfotalea.
 NCBI_TaxID=84980;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LSY54; DSM 12343;
 RX PubMed=15305914;
 RA Rabe R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 from permanently cold Arctic sediments."
 RL Environ. Microbiol. 6:887-902(2004).
 DR EMBL; CR522870; CAG37750.1;
 DR InterPro; IPR003846; UPF0061.
 DR Pfam; PF02696; UPF0061; 1.
 KW Complete proteome.
 SQ SEQUENCE 482 AA; 54161 MW; 5F401BE2D89323D CRC64;

Query Match 42.2%; Score 46; DB 2; Length 482;
 Best Local Similarity 69.2%; Pred. No. 1.3e+02;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGCADGPTLREWT 13
 |||||
 Db 120 GRCVGPALREFI 132

RESULT 37

AAS HUMAN STANDARD; PRT; 926 AA.
 ID AAS HUMAN
 AC Q9UDR5; O95462;
 DT 05-JUN-2004 (Rel. 44, Created)
 DT 05-JUN-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-aminoadipic semialdehyde synthase, mitochondrial precursor
 (LKR/SDH) [includes: lysine ketoglutarate reductase (EC 1.5.1.8) (LOR)
 (LKR); Saccharopine dehydrogenase (EC 1.5.1.9) (SDH)].
 GN Name=AAS;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX PubMed=10775527;
 RA Sacksteder K.A., Biery B.J., Morrell J.C., Goodman B.K.,
 RA Geisbrecht B.V., Cox R.P., Gould S.J., Geraghty M.T.;
 RT "Identification of the alpha-aminoadipic semialdehyde synthase gene,
 which is defective in familial hyperlysinemia."
 RL Am. J. Hum. Genet. 66:1736-1743(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Papes F., Kemper E.L., Cord-Neto G., Langone F., Arruda P.;
 RT "Cloning and expression analysis of the LKR/SDH gene in human
 tissues."
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
 RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
 RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
 RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.B.,
 RA Fewell G.A., Delehaunty K.D., Miner T.B., Nash W.E., Cordes M., Du H.,
 RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
 RA Zehrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
 RA Overby P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
 RA Strong C.M., Hou S., Tomlinson C., Daughin-Kohlberg S.,
 RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
 RA Tin-Mollam A.-M., Abbott A., Minx P., Maupin R., Stromwater C.,
 RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
 RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieghel J.,
 RA Bieri T.A., Nelson J.O., Bertowicz N., Wohldmann P.E., Cook L.L.,
 RA Hickenbotham M.T., Eldred J., Williams D., Beckett J.A., Martin E.R.,
 RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,
 RA Simms E., Zhou Y., James R., Phelps K., Iadonco S., Bubb K.,
 RA Baertsch R.A., Brent M.R., Keibler E., Plicek P., Bork P., Suyama M.,
 RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
 RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
 RA Waterston R.H., Wilson R.K.;
 RT "The DNA sequence of human chromosome 7."
 RL Nature 424:157-164(2003).
 CC -1- FUNCTION: A bifunctional enzyme that catalyzes the first two steps
 in lysine degradation. The N-terminal and the C-terminal contain
 lysine-ketoglutarate reductase and saccharopine dehydrogenase
 activity, respectively.
 CC -1- CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine +
 NADP(+) + H(2)O = L-lysine + 2-oxoglutarate + NADPH.
 CC -1- CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine + NAD(+) +
 H(2)O = L-glutamate + 2-aminoadipate 6-semialdehyde + NADH.

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CC -1- PATHWAY: Lysine degradation; Saccharopine pathway; first step.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed in all 16 tissues examined with
CC highest expression in the liver.
CC -1- INDUCTION: Induced by starvation (By similarity).
CC -1- DISEASE: Defects in AASS are the cause of hyperlysinemia
CC [MIM:238700]. Hyperlysinemia is an autosomal recessive condition
CC characterized by hyperlysinemia, lysinuria and variable
CC saccharopururia.
CC -1- SIMILARITY: In the N-terminal section; belongs to the ALADH/PNT
CC family.
CC -1- SIMILARITY: In the C-terminal section; belongs to the saccharopine
CC dehydrogenase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF229180; AAF44328.1; -.
CC EMBL; AJ007714; CAA07619.2; -.
CC EMBL; AC006020; AAF03526.1; -.
CC Genew; HGNC:17366; AASS.
CC Reactome; Q9UDR5; -.
CC MIM; 605113; -.
CC MIM; 238700; -.
CC InterPro; IPR007698; Aladh_PNT_C.
CC InterPro; IPR007886; Aladh_PNT_N.
CC InterPro; IPR005097; Saccharop_dh.
CC Pfam; PF01262; Aladh_PNT_N; 1.
CC Pfam; PF05222; Aladh_PNT_N; 1.
CC Pfam; PF03435; Saccharop_dh; 1.
CC KEGG; K03435; Multifunctional enzyme; NAD; NADP; Oxidoreductase;
CC KM Transist peptide.
CC TRANSIT 1 32 Mitochondrion (By similarity).
CC FT CHAIN 33 926 Alpha-aminoacidic semialdehyde synthase.
CC FT DOMAIN 33 455 Lysine-ketoglutarate reductase.
CC FT DOMAIN 477 926 Saccharopine dehydrogenase.
CC FT CONFLICT 589 589 S -> C (in Ref. 2).
CC SQ SEQUENCE 926 AA; 102131 MW; CB4194014351A18D CRC64;

Query Match 42.2%; Score 46; DB 1; Length 926;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GPTLRWISFPCG 18
Db 623 GATIESIYICG 635

RESULT 38
Q9Y878 PRELIMINARY; PRT; 1902 AA.
ID 09Y878;
AC 09Y878;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Glucan synthase.
DE Name=FKSI;
OS Coccidioides posadasii.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Omygenales; mitosporic Omygenales; Coccidioides.
OX NCBI_TaxID=199306;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Silveira;
RA Siegel E.M., Ozborn K.I., Galgiani J.N.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF159533; AAD45326.2; -.
DR GO; GO:0000148; C:1,3-beta-glucan synthase complex; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003843; F:1,3-beta-glucan synthase activity; IEA.
DR GO; GO:0006075; P:beta-1,3 glucan biosynthesis; IEA.
DR InterPro; IPR003440; Glyco_trans_48.
DR Pfam; PF02364; Glucan_synthase; I.
DR SEQUENCE 1902 AA; 217552 MW; 66FC3C60E725F2F CRC64;

Query Match 42.2%; Score 46; DB 2; Length 1902;
Best Local Similarity 46.7%; Pred. No. 5.1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GCADGPTLRWISFC 16
Db 1381 GCADINPVADWVQRC 1395

RESULT 39
Q8XZNS PRELIMINARY; PRT; 309 AA.
ID 08XZNS;
AC 08XZNS;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE PROBABLE TRANSCRIPTION REGULATOR PROTEIN.
DE Name=RS04642; OrderedAccessionNames=RS01360;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RC MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arias M., Billault A., Brotier P., Camus J.C., Cartolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RA "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646064; CAD15062.1; -.
DR HSSP; Q9WXC7; IIXC.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PROSITE; PS50931; HTH_LYSR; 1.
KW Complete proteome.
SQ SEQUENCE 309 AA; 33774 MW; 733551741CE83182 CRC64;

Query Match 41.7%; Score 45.5; DB 2; Length 309;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy 1 GG---CADGPTLRW 12
Db 216 GGTMECTDGAIVREW 230

RESULT 40
Q7RUAS PRELIMINARY; PRT; 108 AA.
ID 07RUAS;
AC 07RUAS;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein B24B19.30.
DE Name=NCU03933.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

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OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0874a;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
 Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte D.,
 RA Koche G.O., Jedd G., Mewes W., Straben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kamal M., Kamyvaselis M., Mauceli E., Bielke C., Rudd S., Friseman D.,
 RA Kyrstova S., Rasmussen C., Metzendorf R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osman S.A.,
 RA Desouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Nectvig D.O., Alex L.A., Mannheim G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.",
 RL Nature 0.0-0(2003).
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data
 CC EMBL: AABX01000719; EAA28336.1; -.
 DR KM Hypothetical protein.
 SJ SEQUENCE 108 AA; 11994 MW; 093DC0D617A252E CRC64;
 QY Query Match 41.3%; Score 45; DB 2; Length 108;
 'Best Local Similarity 50.0%; Pred. No. 42;
 'Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Db 70 CQCCPILRNMLSMWC 83

RESULT 41
 ID 06ZTT4 PRELIMINARY; PRT; 146 AA.
 AC 06ZTT4;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein FLJ44235.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
 RA Tanai H., Matanabe S., Ishida S., Ono Y., Houta T., Watanabe M.,
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
 RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Wagauma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
 RA Suzuki Y., Sugano S., Nagahara K., Masuo Y., Nagai K., Isogai T.,
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK126223; BAC86495.1; -.
 SQ SEQUENCE 146 AA; 16475 MW; COB7BBE49151B89B CRC64;
 QY Query Match 41.3%; Score 45; DB 2; Length 146;
 'Best Local Similarity 69.2%; Pred. No. 56;
 'Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

08C4M6
 ID 08C4M6 PRELIMINARY; PRT; 173 AA.
 AC 08C4M6;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
 DE library, clone: C130070D15 product: unclassifiable, full insert
 DE sequence.
 GN Name=C130070B15Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Ikawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
 RA Furuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozawa T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono H., Okazaki N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa Y., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK081706; BAC38302.1; -;
 DR MGD; MG:2444974; C130070B1SRK.
 SQ SEQUENCE 173 AA; 19340 MW; 6227DD672552PCD CRC64;

Query Match 41.3%; Score 45; DB 2; Length 173;
 Best Local Similarity 63.6%; Pred. No. 67;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GPTLRWISFC 16
 DB 75 GVTREMASWC 85

RESULT 43
 ID 007291 PRELIMINARY; PRT; 180 AA.

AC 007291;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein orfs.
 GN Name-orfs;
 OS Natronomonas pharaonis (Natronobacterium pharaonis).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Natronomonas.
 OX NCBI_TaxID=2257;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SP1/28;
 RX MEDLINE=98088958; PubMed=9428682;
 RA Matar S., Engelhard M.;
 RT "Cytochrome b3 from Natronobacterium pharaonis: An archaeal four-subunit cytochrome-c-type oxidase.";
 RL Eur. J. Biochem. 250:332-341(1997).
 DR EMBL; Y10500; CAA71527.1; -;
 DR PIR; T44944; T44944.
 DR GO; GO:0003677; P:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR010985; Met_repress_like.
 KM Hypothetical protein.
 SQ SEQUENCE 180 AA; 20215 MW; A8C3739C8C11310 CRC64;

Query Match 41.3%; Score 45; DB 2; Length 180;
 Best Local Similarity 77.8%; Pred. No. 69;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 LREWISFCG 17
 DB 116 LLEWLSFCG 124

RESULT 44
 ID 06N1X5 PRELIMINARY; PRT; 209 AA.
 AC 06N1X5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedlocusNames=RP44277;
 OS Rhodopseudomonas palustris.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodopseudomonas.
 OX NCBI_TaxID=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres Y. Torres J.L., Perez C.,
 RA Harrison F.H., Gibson J., Harwood C.S.;

RT "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium Rhodopseudomonas palustris.";
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL; BX572606; CAE29718.1; -;
 DR InterPro; IPR008938; ARM.
 DR InterPro; IPR000357; HEAT.
 DR Pfam; PF02985; HEAT; 2.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 209 AA; 23238 MW; 6FE082A84DB040EE CRC64;

Query Match 41.3%; Score 45; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 81;
 Matches 9; Conservative 2; Mismatches 1; Indels 6; Gaps 1;

QY 3 CADG-----PTLRWIS 14
 DB 98 CADTGYEALPTLRWLS 115

RESULT 45

ID 089JUR5 PRELIMINARY; PRT; 290 AA.
 AC 089JUR5;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE B115207 protein.
 GN OrderedlocusNames=b115207;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 OX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyumi T.,
 RA Sasamoto S., Matanabe A., Iidesawa K., Iriguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpo S., Tsurunoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AF005954; BAC50472.1; -;
 DR Complete proteome.
 KW Complete proteome.
 SQ SEQUENCE 290 AA; 30111 MW; CAE33930D6CFC7FF CRC64;

Query Match 41.3%; Score 45; DB 2; Length 290;
 Best Local Similarity 61.5%; Pred. No. 1,1e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 DGPTLRWISFCG 17
 DB 269 DGAPLPFWIAFAG 281

Search completed: September 1, 2005, 16:20:56
 Job time : 72.9496 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:02 ; Search time 87.3453 Seconds
(without alignments)
84.131 Million cell updates/sec

Title: US-10-083-768-7

Perfect score: 108

Sequence: 1 GNADGPTLRQWLEGRRPKN 19

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004as:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	100.0	19	2	AAW09457 Thrombopo
2	108	100.0	19	2	AAW09492 Thrombopo
3	108	100.0	19	2	AAW36651 Thrombopo
4	108	100.0	19	2	AAW33024 Thrombopo
5	108	100.0	19	2	AAW36643 Thrombopo
6	108	100.0	19	3	AAW17021 TPO-mimet
7	108	100.0	19	4	AAW25862 Human thr
8	108	100.0	19	4	AAW25870 Human thr
9	108	100.0	19	4	AAW25821 Human thr
10	108	100.0	19	5	ABB72907 TPO mimet
11	108	100.0	19	7	ADJ73059 TPO mimet
12	108	100.0	19	8	ADJ52694 CHI delet
13	108	100.0	19	8	ADJ51655 CHI delet
14	62	57.4	18	5	ABP51687 TPO mimet
15	62	57.4	18	7	ADN59655 Thrombopo
16	62	57.4	18	8	ADQ16617 TPO mimet
17	62	57.4	22	7	ADN59822 TMP pepti
18	62	57.4	23	7	ADN59792 Peptide-v
19	62	57.4	23	7	ADN59774 Peptide-v
20	62	57.4	25	7	ADN59692 Thrombopo
21	62	57.4	36	7	ADN59762 Peptide-v
22	62	57.4	41	7	ADN59768 Peptide-v
23	62	57.4	43	7	ADN59761 Peptide-v
24	62	57.4	44	7	ADN59817 Peptide-v
25	62	57.4	46	7	ADN59780 Peptide-v

26	62	57.4	46	7	ADN59786 Peptide-v
27	60	55.6	18	7	ADN59667 Thrombopo
28	60	55.6	22	7	ADN59834 TMP pepti
29	60	55.6	25	7	ADN59716 Thrombopo
30	60	55.6	34	3	AAV96527 Thrombopo
31	60	55.6	42	7	ADN59818 Peptide-
32	59	54.6	15	5	ADP51670 Thrombopo
33	59	54.6	15	8	ADQ16585 TPO mimet
34	59	54.6	18	5	ADP51689 TPO mimet
35	59	54.6	18	5	ADP51688 TPO mimet
36	59	54.6	18	5	ADP51686 TPO mimet
37	59	54.6	18	5	ADP51693 TPO mimet
38	59	54.6	18	5	ADP51684 TPO mimet
39	59	54.6	18	5	ADP51691 TPO mimet
40	59	54.6	18	5	ADP51690 TPO mimet
41	59	54.6	18	5	ADP51675 TPO mimet
42	59	54.6	18	8	ADQ16611 TPO mimet
43	59	54.6	18	8	ADQ16619 TPO mimet
44	59	54.6	18	8	ADQ16621 TPO mimet
45	59	54.6	18	8	ADQ16646 TPO mimet
46	59	54.6	18	8	ADQ16615 TPO mimet
47	59	54.6	18	8	ADQ16625 TPO mimet
48	59	54.6	18	8	ADQ16629 TPO mimet
49	59	54.6	18	8	ADQ16623 TPO mimet
50	59	54.6	22	8	ADQ16710 TPO mimet
51	59	54.6	128	8	ADQ16705 Modified
52	59	54.6	225	8	ADQ16704 Modified
53	59	54.6	472	5	ADP51695 SGL.1-TPO
54	59	54.6	472	8	ADQ16647 Immunoglo
55	58	53.7	18	3	AAW16957 PEGylated
56	58	53.7	18	3	AAW16956 PEGylated
57	58	53.7	18	5	ADP51674 TPO mimet
58	58	53.7	18	5	ADP51683 TPO mimet
59	58	53.7	18	8	ADQ16607 TPO mimet
60	58	53.7	18	8	ADQ16609 TPO mimet
61	58	53.7	19	5	ADW73390 TPO-mimet
62	58	53.7	20	3	AAW18003 FC-TMP pe
63	58	53.7	20	5	ADW73403 TPO mimet
64	58	53.7	22	8	ADQ16709 Immunoglo
65	58	53.7	30	3	AAW17287 TPO-mimet
66	58	53.7	31	3	AAW17288 TPO-mimet
67	58	53.7	32	3	AAW17289 TPO-mimet
68	58	53.7	33	3	AAW17290 TPO-mimet
69	58	53.7	34	3	AAW17291 TPO-mimet
70	58	53.7	35	3	AAW17292 TPO-mimet
71	58	53.7	36	3	AAW17295 TPO-mimet
72	58	53.7	36	3	AAW17289 TPO-mimet
73	58	53.7	36	3	AAW17301 TPO-mimet
74	58	53.7	36	3	AAW17306 TPO-mimet
75	58	53.7	36	3	AAW17307 TPO-mimet
76	58	53.7	36	3	AAW17293 TPO-mimet
77	58	53.7	36	3	AAW17303 TPO-mimet
78	58	53.7	36	3	AAW16963 TPO-mimet
79	58	53.7	36	3	AAW17301 TPO-mimet
80	58	53.7	36	3	AAW17306 TPO-mimet
81	58	53.7	36	5	AAW172403 TPO-mimet
82	58	53.7	37	5	AAW17294 TPO-mimet
83	58	53.7	38	3	AAW17295 TPO-mimet
84	58	53.7	39	3	AAW17304 TPO-mimet
85	58	53.7	39	3	AAW17305 TPO-mimet
86	58	53.7	40	3	AAW17302 TPO-mimet
87	58	53.7	41	3	AAW17308 TPO-mimet
88	58	53.7	41	5	AAW17389 TPO-mimet
89	58	53.7	41	5	AAW17388 TPO-mimet
90	58	53.7	42	3	AAW17296 TPO-mimet
91	58	53.7	42	3	AAW17308 TPO-mimet
92	58	53.7	42	3	AAW17282 TPO-mimet
93	58	53.7	42	3	AAW17281 TPO-mimet
94	58	53.7	42	5	AAW173404 TPO-mimet
95	58	53.7	60	3	AAW17311 TPO-mimet
96	58	53.7	60	5	AAW173405 TPO-mimet
97	58	53.7	247	3	AAW16958 FC-TMP pr
98	58	53.7			

99 58 53.7 247 5 AAB73411 Abb73411 FC-TPO mi
100 58 53.7 268 3 AAB16959 Aab16959 FC-TWP-TM

ALIGNMENTS

RESULT 1

AAW09457
ID AAW09457 standard; protein; 19 AA.

AC AAW09457;
XX
XX

DT 10-SEP-1997 (first entry)
XX

DE Thrombopoietin receptor binding compound peptide.

XX Haematology; thrombocytopenia; TPO; TR; proliferation;
KW bone marrow transfusion; chemotherapy; radiation therapy.

XX Synthetic.

OS
XX

PH Key Location/Qualifiers

FT Misc-difference 1..19

FT /note= "Preferably linkages are selected from: -
CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -C(O)NR6
; -NHC(O)NH; where R is hydrogen or lower alkyl and R6 is
lower alkyl"

FT Modified-site 1

FT /note= "Preferably N-terminus is selected from: -NRR1;-
NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NR; succinimide;
benzyloxycarbonyl-NH; benzyloxycarbonyl-NH with 1-3
substitutions on the phenyl ring selected from lower
alkyl, lower alkoxy, chloro, bromo; where R and R1 are
independently selected from hydrogen and lower alkyl"

FT Modified-site 19

FT /note= "Preferably C-terminus is -C(O)R2 where R2 is
selected from hydroxy, lower alkoxy, and -NR3R4, where R3
and R4 are independently selected from hydrogen and lower
alkyl, and where the nitrogen atom of the -NR3R4 group
can optionally be the amine group of the N-terminus of
the peptide forming a cyclic peptide"

XX WO9640189-A1.

XX PD 19-DEC-1996.

XX PF 05-JUN-1996; 96WO-US008998.

XX PR 07-JUN-1995; 95US-00472371.

XX PR 07-JUN-1995; 95US-00473604.

XX PR 07-JUN-1995; 95US-00476168.

XX PR 07-JUN-1995; 95US-00478128.

XX PR 07-JUN-1995; 95US-00484900.

XX PR 07-JUN-1995; 95US-00485301.

XX (GLAXO) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX WPI; 1997-051883/05.

XX Thrombopoietin receptor-binding/activating peptide(s) and peptide
PT mimetic(s) - useful in treatment of haematological disorders, esp.
XX thrombocytopenia resulting from chemotherapy, etc.

XX Claim 18; Page 89; 106pp; English.

XX The present sequence is a compound which binds to thrombopoietin (TPO)
CC receptor (TR). It has a molecular weight of < 8000 Da, and a binding
CC affinity to TR as expressed by an IC50 of no more than about 100 nM. The
CC compound (especially if modified, see features table) can be used for

CC treating patients suffering from haematological disorders and
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC marrow transfusions. The peptide may also be used to maintain the
CC proliferation and growth of TPO-dependent cell lines and for use in
CC biological research, for detecting TPO receptors on living cells

XX Sequence 19 AA;

Query Match 100.0%; Score 108; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.1e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNADGPTLRQWLEGRAPKN 19
|||||

Db 1 GNADGPTLRQWLEGRAPKN 19

RESULT 2

AAW09492
ID AAW09492 standard; protein; 19 AA.

AC AAW09492;
XX
XX

DT 10-SEP-1997 (first entry)
XX

DE Thrombopoietin receptor binding peptide.

XX Haematology; thrombocytopenia; TPO; TR; proliferation;
KW bone marrow transfusion; chemotherapy; radiation therapy.

XX Synthetic.

XX WO9640189-A1.

XX PD 19-DEC-1996.

XX PF 05-JUN-1996; 96WO-US008998.

XX PR 07-JUN-1995; 95US-00472371.

XX PR 07-JUN-1995; 95US-00473604.

XX PR 07-JUN-1995; 95US-00476168.

XX PR 07-JUN-1995; 95US-00478128.

XX PR 07-JUN-1995; 95US-00484900.

XX PR 07-JUN-1995; 95US-00485301.

XX (GLAXO) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX WPI; 1997-051883/05.

XX Thrombopoietin receptor-binding/activating peptide(s) and peptide
PT mimetic(s) - useful in treatment of haematological disorders, esp.
XX thrombocytopenia resulting from chemotherapy, etc.

XX Disclosure; Page 26; 106pp; English.

XX The present sequence is a peptide which binds to thrombopoietin (TPO)
CC receptor (TR). The compound can be used for treating patients suffering
CC from haematological disorders and thrombocytopenia resulting from
CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide
CC may also be used to maintain the proliferation and growth of TPO-
CC dependent cell lines and for use in biological research, for detecting
CC TPO receptors on living cells

XX Sequence 19 AA;

Query Match 100.0%; Score 108; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.1e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNADGPTLRQWLEGRAPKN 19

Db 1 GNAAGPTLRQWLBSGRPRN 19

RESULT 3

AAW36651 ID AAW36651 standard; peptide; 19 AA.

AC AAW36651;

DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopaenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

XX Synthetic.

OS WO9640750-A1.

XX 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

PI Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;

PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

PT Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopaenia resulting from chemotherapy, etc.

PS Disclosure; Page 27; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be

CC used to treat disorders which are susceptible to treatment with a

CC thrombopoietin agonist, preferably haematological disorders and

CC thrombocytopaenia resulting from chemotherapy, radiation therapy or bone

CC marrow transfusions. It can also be used diagnostically, e.g. to

CC investigate the mechanism of thrombopoietin signal transduction and

CC receptor activation, or to maintain the proliferation and growth of

CC thrombopoietin dependent cell lines

XX

SO Sequence 19 AA;

Query Match 100.0%; Score 108; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNAAGPTLRQWLBSGRPRN 19

Db 1 GNAAGPTLRQWLBSGRPRN 19

RESULT 4

AAW33024 ID AAW33024 standard; peptide; 19 AA.

AC AAW33024;

DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

XX

Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopaenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

XX Synthetic.

OS WO9640750-A1.

XX 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

PI Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;

PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

PT Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopaenia resulting from chemotherapy, etc.

PS Claim 19; Page 89; 106pp; English.

XX The present peptide binds the thrombopoietin receptor (TR), has a

CC molecular weight of less than 8000 Da and a TR binding affinity as

CC expressed by an IC50 of no more than about 100 microm. It can be used to

CC treat disorders which are susceptible to treatment with a thrombopoietin

CC agonist, preferably haematological disorders and thrombocytopaenia

CC resulting from chemotherapy, radiation therapy or bone marrow

CC transfusions. It can also be used diagnostically, e.g. to investigate the

CC mechanism of thrombopoietin signal transduction and receptor activation,

CC or to maintain the proliferation and growth of thrombopoietin dependent

CC cell lines

XX

SO Sequence 19 AA;

Query Match 100.0%; Score 108; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNAAGPTLRQWLBSGRPRN 19

Db 1 GNAAGPTLRQWLBSGRPRN 19

RESULT 5

AAW36643 ID AAW36643 standard; peptide; 19 AA.

AC AAW36643;

DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

XX

Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopaenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

XX Synthetic.

OS WO9640750-A1.

XX 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

XX 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 PI Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX WPI; 1997-052226/05.
 DR
 PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Disclosure; Page 26; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 CC
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 108; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY
 1 GNADGPTLRQWLEGRRPKN 19
 1 GNADGPTLRQWLEGRRPKN 19
 Db
 RESULT 6
 AAB17021
 ID AAB17021 standard; peptide; 19 AA.
 XX
 XX AAB17021;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE TPO-mimetic peptide sequence SEQ ID NO:77.
 XX
 DE Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; Epo; TPO; CTAA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US025044.
 XX
 XX 23-OCT-1998; 98US-0105371P.
 PR 22-OCT-1999; 99US-00428082.
 XX
 PA (AMGEN-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 XX
 DR WPI; 2000-350702/30.
 XX
 PT Novel composition of matter comprising an Fc domain and pharmacologically

PT active peptides, useful for treating cancer and autoimmune diseases.
 XX
 XX Claim 19; Page 220; 608pp; English.
 XX
 PS The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)-C-P1, -(L1)-C-P1-(L2)-d-P2, -(L1)-C-P1-
 CC (L2)-d-P2-(L3)-e-P3, or -(L1)-C-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AA69443 to AA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 CC
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 108; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY
 1 GNADGPTLRQWLEGRRPKN 19
 1 GNADGPTLRQWLEGRRPKN 19
 Db
 RESULT 7
 AAU25862
 ID AAU25862 standard; peptide; 19 AA.
 XX
 XX AAU25862;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #48.
 XX
 XX Peptide mimetic; human; thrombopoietin receptor. TPO-R; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX
 XX 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US008623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RM, Dextrince RB, Poddaturi S;
 PI Yin Q;
 XX
 DR WPI; 2001-564142/63.
 XX
 PT Activating thrombopoietin receptors in cells, used to treat

PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 XX
 PS Disclosure; Col 20; 128pp; English.
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent hematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX
 XX Sequence 19 AA;
 SQ
 Query Match 100.0%; Score 108; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GNADGPTLRQWLEGRRPKN 19
 Db 1 GNADGPTLRQWLEGRRPKN 19
 RESULT 8
 AAU25870
 ID AAU25870 standard; peptide; 19 AA.
 XX
 AC AAU25870;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #56.
 XX
 KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; hematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RW, Cwirja SE, Gates CM, Schatz PJ,
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S,
 PI Yin Q;
 XX WPI; 2001-564142/63.
 XX

PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 XX
 PS Disclosure; Col 20; 128pp; English.
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent hematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX
 XX Sequence 19 AA;
 SQ
 Query Match 100.0%; Score 108; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GNADGPTLRQWLEGRRPKN 19
 Db 1 GNADGPTLRQWLEGRRPKN 19
 RESULT 9
 AAU25821
 ID AAU25821 standard; peptide; 19 AA.
 XX
 AC AAU25821;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #7.
 XX
 KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; hematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RW, Cwirja SE, Gates CM, Schatz PJ,
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S,
 PI Yin Q;
 XX WPI; 2001-564142/63.
 XX

XX Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 PS Disclosure; Col 65-66; 128pp; English.
 XX
 CC Sequences AAU25815-AAU26049 represent peptide and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent hematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX
 SQ Sequence 19 AA;
 XX
 QY
 Query Match 100.0%; Score 108; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Db 1 GNADGPTLRQWLEGRPRKN 19
 1 GNADGPTLRQWLEGRPRKN 19
 XX
 RESULT 10
 ABB72907
 ID ABB72907 standard; peptide; 19 AA.
 XX
 AC ABB72907;
 XX
 DT 05-APR-2002 (first entry)
 XX
 DE TPO mimetic peptide SEQ ID NO:77.
 XX
 KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNF;
 KW TPO mimetic peptide; EPO mimetic peptide; BMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antineoplastic; antiarthritic; antidiabetic; ophthalmological;
 KW antinaemic; anorectic; antifertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200183525-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US014310.
 XX
 PR 03-MAY-2000; 2000US-00563286.
 XX
 PA (AMGE-) AMGEN INC.
 XX

PI Feige U, Liu C, Cheetham JC, Boone TC, Gudae JW;
 XX WPI; 2002-130313/17.
 DR
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 XX
 PS Claim 39; Page 44; 176pp; English.
 XX
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antineoplastic, antiarthritic, antidiabetic, ophthalmological,
 CC antinaemic, anorectic, antifertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, EPO-
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB72426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 AA;
 XX
 QY
 Query Match 100.0%; Score 108; DB 5; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Db 1 GNADGPTLRQWLEGRPRKN 19
 1 GNADGPTLRQWLEGRPRKN 19
 XX
 RESULT 11
 ADJ73059
 ID ADJ73059 standard; peptide; 19 AA.
 XX
 AC ADJ73059;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE TPO mimetic peptide sequence SeqID 513.
 XX
 KW mimetic; CDR mimeticbody; gene therapy; transgenic; immune;
 KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
 KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
 KW TPO.
 XX
 OS Synthetic.
 OS
 PN WO2003084477-A2.
 XX
 PD 16-OCT-2003.
 XX
 PF 24-MAR-2003; 2003WO-US009139.
 XX
 PR 29-MAR-2002; 2002US-0368791P.
 XX
 PA (CENTO) CENTOCOR INC.
 XX
 PI Heavner GA, Knight DM, Scallion BJ, Ghayeb J;
 XX

XX	WPI, 2003-804237/75.
XX	
PT	New CDR mimetibody comprising a portion of a heavy or light chain
CC	variable region comprising human framework or ligand binding region,
PR	useful for preparing a composition for treating e.g., immune,
PT	cardiovascular or neurologic disease.
XX	
P8	Disclosure; SEQ ID NO 513; 97pp; English.
XX	
CC	This invention relates to novel mammalian CDR mimetibodies, specific
CC	portions or variants thereof. Specifically, it refers to an antibody
CC	fragment where a protein has been inserted into, or replaces a portion
CC	of, one or more CDR regions, such that each CDR mimetibody comprises at
CC	least one portion of a heavy chain or light chain variable region, which
CC	itself comprises at least one human framework region and at least one
CC	ligand binding region (LBR). The present invention describes human
CC	mimetibodies, including modified immunoglobulin and cleavage products
CC	that can be useful in gene therapy and the generation of transgenic
CC	plants and animals. Furthermore, the CDR mimetibody is useful for
CC	preparing compositions for modulating, treating or reducing the symptoms
CC	of immune, cardiovascular, infectious, malignant and/or neurological
CC	diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC	cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC	peptide sequence is a TPO mimetic peptide sequence used to make a
CC	mimetibody of the invention.
SQ	
	Sequence 19 AA;
	Query Match 100.0%; Score 108; DB 7; Length 19;
	Best Local Similarity 100.0%; Pred. No. 1.1e-09; Indels 0; Gaps 0;
	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY	
	1 GNADGPTLRQWLGGRRPKN 19
DB	1 GNADGPTLRQWLGGRRPKN 19
RESULT 12	
ID	ADJ52694
	ADJ52694 standard; peptide; 19 AA.
AC	ADJ52694;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	CH1 deleted mimetibody-related peptide SeqID513.
XX	
KM	CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
KM	hypotensive; neuroprotective; nootropic; antibacterial; virutide;
KM	fungalid; gene therapy; immune disorder; cardiovascular disease;
KM	arhythmia; hypertension; heart failure; neurodegenerative;
KM	multiple sclerosis; dementia; Alzheimer's disease; anemia;
KM	cancerous condition; infectious disease; bacterial infection;
KM	viral infection; fungal infection.
XX	
OS	Unidentified.
OS	Synthetic.
XX	
PN	WO2004002417-A2.
PD	08-JAN-2004.
XX	
PF	27-JUN-2003; 2003WO-US020347.
XX	
PR	28-JUN-2002; 2002US-0392431P.
XX	
PA	(GENZ) CENTOCOR INC.
XX	
PI	Heavner GA, Knight DM, Ghirayeb J, Scallon BJ, Nespor TC;
PI	Kuclooski KA;
XX	
DR	WPI, 2004-082870/08.
XX	

PT	New CHI deleted mimetibody polypeptides and nucleic acids, useful for
PT	modulating, treating, alleviating, preventing an immune, cardiovascular,
PT	or neurodegenerative disease or disorder, anemia, cancer, or infectious
PT	diseases.
PS	Claim 2; SEQ ID NO 513; 129pp; English.
XX	
CC	This invention relates to CHI deleted mimetibodies (and the DNA sequences
CC	which encode them), compositions, methods and uses. The invention may be
CC	useful for the development of compounds with an immunosuppressive,
CC	cardiovascular, cardiac, hypotensive, neuroprotective, nootropic,
CC	antibacterial, virocidic or fungicidal activity. In addition, the disclosed
CC	sequences may prove useful for gene therapy. The CHI-deleted mimetibody
CC	is useful for diagnosing or treating a disease condition in a cell,
CC	tissue, organ or animal, specifically for modulating, treating,
CC	alleviating, preventing the incidence or reducing the symptoms of an
CC	immune, cardiovascular (for example arrhythmia, hypertension or heart
CC	failure), or neurodegenerative (for example multiple sclerosis, dementia
CC	or Alzheimer's disease) diseases or disorders, anemia, cancerous
CC	conditions, or infectious diseases (for example bacterial, viral or
CC	fungal infection). The present sequence is that of a peptide which may be
CC	used during the creation of a mimetibody of the invention.
XX	
SEQ	Sequence 19 AA;
Query Match	100.0%; Score 108; DB 8; Length 19;
Best Local Similarity	100.0%; Pred. No. 1.1e-03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	
QY	1 GNADPTLQWL EGRPRKN 19
DB	1 GNADPTLQWL EGRPRKN 19
RESULT 13	
ADJ51655	
ID	ADJ51655 standard; peptide; 19 AA.
AC	
XX	ADJ51655;
DT	
XX	06-MAY-2004 (first entry)
DE	
CHI	deleted mimetibody-related peptide SeqID513.
XX	
KW	CHI deleted mimetibody; osteopathic; cardiovascular-Gen;
KW	dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
KW	gynaecological-Gen; hepatotropic; haemostatic; immunomodulatory;
KW	antiallergic; muscular-Gen; cytostatic; antinflammatory; neuroleptic;
KW	ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
KW	TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
KW	dental disorder; oral disorder; dermatological disorder; ear disorder;
KW	nose disorder; throat disorder; endocrine disorder; metabolic disorder;
KW	gastrointestinal disorder; gynaecological disorder; hepatic disorder;
KW	obstetric disorder; haematologic disorder; immunological disorder;
KW	allergic disorder; infectious disorder; musculoskeletal disorder;
KW	oncological disorder; neurological disorder; nutritional disorder;
KW	ophthalmologic disorder; pediatric disorder; psychiatric disorder;
KW	renal disorder; pulmonary disorder.
XX	
OS	Unidentified.
OS	Synthetic.
XX	
PN	WO2004002424-A2.
XX	
PD	08-JAN-2004.
XX	
PF	30-JUN-2003; 2003WO-US020495.
XX	
PR	28-JUN-2002; 2002US-0392431P.
PR	19-SEP-2002; 2002US-0412144P.
XX	
PA	(CENZ) CENTOCOR INC.
XX	

PI Heavener GA, Knight DM, Ghraeyeb J, Scallion BJ, Neespor TC;
 PI Kutolowski KA;
 XX
 DR WPI; 2004-082872/08.
 XX
 PT New CHI deleted mimetic polypeptide and nucleic acid, useful for
 PT diagnosing, preventing or treating cardiovascular, dermatologic,
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
 PT nutritional disorders.
 XX
 PS Claim 15; SEQ ID NO 513; 123pp; English.
 XX
 CC This invention relates to CHI deleted mimetic bodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an osteopathic,
 CC cardiovascular-gen, dermatological-gen, auditory, endocrine-gen,
 CC gastrointestinal-gen, gynaecological-gen, hepatotropic, haemostatic,
 CC immunomodulator, antiallergic, muscular-gen, cytostatic,
 CC antiinflammatory, neuroleptic, ophthalmological, nephrotropic or
 CC respiratory-gen activity acting as a tumour necrosis factor (TNF)-
 CC modulator or cytokine-agonist. The methods and compositions of the
 CC present invention are useful for the diagnosis, prevention and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the CHI deleted mimetic body, such as a bone or joint,
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
 CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
 CC obstructive, haematologic, immunological, allergic, infectious,
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
 CC pediatric, psychiatric, renal or pulmonary disorders. The present
 CC sequence is that of a peptide which may be used during the creation of a
 CC mimetic body of the invention.
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 108; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GNADGPTLRQWLEGRPPK 19
 1 GNADGPTLRQWLEGRPPK 19
 Db 1 GNADGPTLRQWLEGRPPK 19

RESULT 14
 ABP51687
 ID ABP51687 standard; peptide; 18 AA.
 XX
 AC ABP51687;
 XX
 DT 01-OCT-2002 (first entry)
 XX
 DE TPO mimetic peptide SEQ ID NO:37.
 XX
 KW TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 KW complementarity determining region; immunoglobulin; antianaemic;
 KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200246238-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 05-DEC-2001; 2001WO-US047656.
 XX
 PR 05-DEC-2000; 2000US-0251448P.
 PR 04-MAY-2001; 2001US-0288889P.
 PR 29-MAY-2001; 2001US-0294068P.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX
 DR WPI; 2002-566610/60.
 DR N-PSDB; ABQ73365.
 XX
 PT A novel immunogen molecule comprising a region in which amino acid
 PT residues corresponding to at least a portion of the complementary
 PT determining region are replaced or fused with an erythropoietin or
 PT thrombopoietin mimetic.
 XX
 PS Claim 20; Fig 5; 113pp; English.
 XX
 CC The present invention describes an immunoglobulin molecule or its fragment
 CC (I) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (I) has
 CC antianaemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, which results in increased platelet
 CC production. (I) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (I) is contacted with haematopoietic
 CC stem cells or their progenitors. (I) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 18 AA;
 Query Match 57.4%; Score 62; DB 5; Length 18;
 Best Local Similarity 64.7%; Pred. No. 0.016;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 GNADGPTLRQWLEGRPP 17
 1 GRIGGPTLRQWLARAP 17
 Db 1 GRIGGPTLRQWLARAP 17

RESULT 15
 ADN59655
 ID ADN59655 standard; peptide; 18 AA.
 XX
 AC ADN59655;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Thrombopoietin mimetic peptide (TMP4), seq id 4.
 XX
 KW Haemostatic; antianaemic; immunosuppressive; platelet;
 KW transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 KW TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 KW thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia;
 KW autoimmune haemolytic anaemia; Hughes' s syndrome;
 KW lupoid thrombocytopaenia.
 XX
 OS Homo sapiens.
 OS
 PN WO2003031589-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032552.
 XX
 PR 11-OCT-2001; 2001US-0328666P.
 PR 10-OCT-2002; 2002US-00269806.
 XX
 PI

PA (AMGE-) AMGEN INC.
 XX
 PI Min H, Sitney KC, Hartley C;
 XX
 DR WPI; 2003-403101/38.
 XX
 PT Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.
 XX
 PS Claim 6; SEQ ID NO 4; 126pp; English.
 XX
 CC The invention relates to a thrombopoietin mimetic peptide (TMP) (i) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (ii) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (ii) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,
 CC autoimmune haemolytic anaemia, Hughes' syndrome and lupoid
 CC thrombocytopenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a preferred TMP of the invention.
 CC
 XX
 SQ Sequence 18 AA;
 Query Match 57.4%; Score 62; DB 7; Length 18;
 Best Local Similarity 84.6%; Pred. No. 0.016;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 DGPTLRQWLEGRR 16
 |||||:|||||
 Db 4 DGPTLRQWLEYRR 16
 RESULT 16
 ADO16617
 ID ADO16617 standard; peptide; 18 AA.
 XX
 AC ADO16617;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 XX TPO mimetic peptide with random flanking residues SEQ ID NO:37.
 DE
 XX
 KW immunoglobulin; complementarity determining region; CDR; peptide mimetic;
 KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 KW immunotherapy; thrombocytopenia.
 XX
 OS Unidentified.
 OS
 PN WO2004050017-A2.
 PD 17-JUN-2004.
 XX
 PF 17-NOV-2003; 2003WO-US036894.
 XX
 PR 02-DEC-2002; 2002US-00307724.
 XX
 PA (ALEX-) ALEXION PHARM INC.

XX
 PI Bowdish KS, Frederickson S, Renshaw M;
 XX
 DR WPI; 2004-460973/43.
 DR N-PSDB; ADO16618.
 XX
 PT New immunoglobulin molecule comprising a region, where two
 PT complementarity determining regions (CDRs) are replaced with EPO mimetic
 PT or a TPO mimetic, useful for treating thrombocytopenia.
 XX
 PS Example 1; SEQ ID NO 37; 107pp; English.
 XX
 CC The invention relates to a novel immunoglobulin molecule or its fragment
 CC comprising a region where amino acid residues corresponding to at least a
 CC portion of a two complementarity determining regions (CDRs) are replaced
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 CC invention has immunosuppressive activity, and may have a use in
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow
 CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide with flanking
 CC residues.
 CC
 XX
 SQ Sequence 18 AA;
 Query Match 57.4%; Score 62; DB 8; Length 18;
 Best Local Similarity 64.7%; Pred. No. 0.016;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 GNDGPTLRQWLEGRRP 17
 :|||||:
 Db 1 GPLEGPTLRQWLARAP 17
 RESULT 17
 ADNS9822
 ID ADNS9822 standard; peptide; 22 AA.
 XX
 AC ADNS9822;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 XX TMP peptide TMP4.
 DE
 XX
 KW Haemostatic; antihaemic; immunosuppressive; platelet;
 KW transmembrane signalling; mpl receptor; thrombopoietin mimetic peptide;
 KW TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 KW thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
 KW autoimmune haemolytic anaemia; Hughes' syndrome;
 KW lupoid thrombocytopenia; linker.
 XX
 OS Homo sapiens.
 OS
 PN WO2003031589-A2.
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032552.
 XX
 PR 11-OCT-2001; 2001US-0328666P.
 PR 10-OCT-2002; 2002US-00269806.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Min H, Sitney KC, Hartley C;
 XX
 DR WPI; 2003-403101/38.
 XX
 PT Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.
 XX

PS Example 6; Page 83; 126pp; English.

XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune haemolytic anaemia, Hughes' syndrome and lupoid
 CC thrombocytopenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytopoietic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a TMP peptide of the invention to which a two amino acid "cap"
 CC has been added to the carboxy terminal to increase peptide affinity.

XX Sequence 22 AA;

SO

Query Match 57.4%; Score 62; DB 7; Length 22;
 Best Local Similarity 84.6%; Pred. No. 0.02;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DGEPTLRQMLEGRR 16
 |||||:|||||
 Db 6 DGEPTLRQMLEYRR 18

RESULT 18
 ADNS9792
 ID ADNS9792 standard; protein; 23 AA.
 XX
 AC ADNS9792;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Peptide-vehicle compound, seq id 144.
 XX
 XX Haemostatic; antihaemic; immunosuppressive; platelet;
 KM transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 KM TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 KM thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
 KM autoimmune haemolytic anaemia; Hughes' syndrome;
 KM lupoid thrombocytopenia.
 XX
 OS Unidentified.
 XX
 PN WO2003031589-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032552.
 XX
 PR 11-OCT-2001; 2001US-0328666P.
 PR 10-OCT-2002; 2002US-00269806.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Min H, Sitney KC, Hartley C;
 PI
 XX WPI; 2003-403101/38.
 DR
 XX

PT Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.

XX Disclosure; SEQ ID NO 144; 126pp; English.

PS

XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune haemolytic anaemia, Hughes' syndrome and lupoid
 CC thrombocytopenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytopoietic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a peptide-vehicle compound of the invention.

XX Sequence 23 AA;

SO

Query Match 57.4%; Score 62; DB 7; Length 23;
 Best Local Similarity 84.6%; Pred. No. 0.021;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DGEPTLRQMLEGRR 16
 |||||:|||||
 Db 4 DGEPTLRQMLEYRR 16

RESULT 19
 ADNS9774
 ID ADNS9774 standard; protein; 23 AA.
 XX
 AC ADNS9774;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Peptide-vehicle compound, seq id 126.
 XX
 XX Haemostatic; antihaemic; immunosuppressive; platelet;
 KM transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 KM TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 KM thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
 KM autoimmune haemolytic anaemia; Hughes' syndrome;
 KM lupoid thrombocytopenia.
 XX
 OS Unidentified.
 XX
 PN WO2003031589-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032552.
 XX
 PR 11-OCT-2001; 2001US-0328666P.
 PR 10-OCT-2002; 2002US-00269806.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Min H, Sitney KC, Hartley C;
 PI

XX WPI; 2003-403101/38.
 DR Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 XX PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.
 XX
 PS Disclosure; SEQ ID NO 126; 126pp; English.
 XX
 CC The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,
 CC autoimmune haemolytic anaemia, Hughes's syndrome and lupoid
 CC thrombocytopenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a peptide-vehicle compound of the invention.
 XX
 SQ Sequence 23 AA;
 Query Match 57.4%; Score 62; DB 7; Length 23;
 Best Local Similarity 84.6%; Pred. No. 0.021;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 4 DGPTLRQWLEGR 16
 |||||:|||||
 9 DGPTLRQWLEGR 21
 Db
 RESULT 20
 ADNS9692
 ID ADNS9692 standard; peptide; 25 AA.
 XX
 AC ADNS9692;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Thrombopoietin mimetic peptide TMP4, seq id 41.
 XX
 KW Haemostatic; antianaemic; immunosuppressive; platelet;
 KW transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 KW TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 KW thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
 KW autoimmune haemolytic anaemia; Hughes's syndrome;
 KW lupoid thrombocytopenia.
 XX
 OS Homo sapiens.
 XX
 PN WO2003031589-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032552.
 XX
 PR 11-OCT-2001; 2001US-032866P.
 XX
 PR 10-OCT-2002; 2002US-00269806.
 XX

PA (AMGE-) AMGEN INC.
 XX
 PI Min H, Sitney KC, Hartley C;
 XX
 DR WPI; 2003-403101/38.
 DR N-PSDB; ADNS9690.
 XX
 PT Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.
 XX
 PS Disclosure; SEQ ID NO 41; 126pp; English.
 XX
 CC The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,
 CC autoimmune haemolytic anaemia, Hughes's syndrome and lupoid
 CC thrombocytopenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a TMP fragment.
 XX
 SQ Sequence 25 AA;
 Query Match 57.4%; Score 62; DB 7; Length 25;
 Best Local Similarity 84.6%; Pred. No. 0.022;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 4 DGPTLRQWLEGR 16
 |||||:|||||
 7 DGPTLRQWLEGR 19
 Db
 RESULT 21
 ADNS9762
 ID ADNS9762 standard; protein; 36 AA.
 XX
 AC ADNS9762;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Peptide-vehicle compound, seq id 114.
 XX
 KW Haemostatic; antianaemic; immunosuppressive; platelet;
 KW transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 KW TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 KW thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
 KW autoimmune haemolytic anaemia; Hughes's syndrome;
 KW lupoid thrombocytopenia.
 XX
 OS unidentified.
 XX
 PN WO2003031589-A2.
 XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032552.
 XX

XX 11-OCT-2001; 2001US-0328666P.
 PR 10-OCT-2002; 2002US-00269806.
 XX
 PA (AMGE-) AMGEN INC.
 PI Min H, Sitney KC, Hartley C;
 DR WPI; 2003-403101/38.
 XX
 PT Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.
 PS
 PS Disclosure; SEQ ID NO 114; 126pp; English.
 XX
 CC The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.,
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune haemolytic anaemia, drug induced immune thrombocytopenia,
 CC thrombocytopenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytopenic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a peptide-vehicle compound of the invention.
 CC
 SQ Sequence 36 AA;
 XX
 Query Match 57.4%; Score 62; DB 7; Length 36;
 Best Local Similarity 84.6%; Pred. No. 0.033;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 DGPTLRQWLEGR 16
 Db 4 DGPTLRQWLEGR 16
 XX
 RESULT 22
 ID ADN59768 standard; protein; 41 AA.
 AC ADN59768;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Peptide-vehicle compound, seq id 120.
 XX
 XX Haemostatic; anti-anaemic; immunosuppressive; platelet;
 KM transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 KM TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 KM thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
 KM autoimmune haemolytic anaemia; Hughes' syndrome;
 KM lupoid thrombocytopenia.
 XX
 OS Unidentified.
 XX
 PN W02003031589-A2.
 XX

PD 17-APR-2003.
 XX
 XX 11-OCT-2002; 2002WO-US032552.
 PF
 XX
 PR 11-OCT-2001; 2001US-0328666P.
 PR 10-OCT-2002; 2002US-00269806.
 XX
 PA (AMGE-) AMGEN INC.
 PI Min H, Sitney KC, Hartley C;
 DR WPI; 2003-403101/38.
 XX
 PT Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.
 PS
 PS Disclosure; SEQ ID NO 120; 126pp; English.
 XX
 CC The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.,
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune haemolytic anaemia, drug induced immune thrombocytopenia,
 CC thrombocytopenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytopenic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a peptide-vehicle compound of the invention.
 CC
 SQ Sequence 41 AA;
 XX
 Query Match 57.4%; Score 62; DB 7; Length 41;
 Best Local Similarity 84.6%; Pred. No. 0.038;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 DGPTLRQWLEGR 16
 Db 4 DGPTLRQWLEGR 16
 XX
 RESULT 23
 ID ADN59761 standard; protein; 43 AA.
 AC ADN59761;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Peptide-vehicle compound, seq id 113.
 XX
 XX Haemostatic; anti-anaemic; immunosuppressive; platelet;
 KM transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 KM TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 KM thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
 KM autoimmune haemolytic anaemia; Hughes' syndrome;
 KM lupoid thrombocytopenia.
 XX
 OS Unidentified.
 XX

XX WO2003031589-A2.
 PN 17-APR-2003.
 PD 11-OCT-2002; 2002WO-US032552.
 PF 11-OCT-2001; 2001US-0328666P.
 PR 10-OCT-2002; 2002US-00269806.
 XX
 XX (AMGEN-) AMGEN INC.
 PA Min H, Sitney KC, Hartley C;
 PI WPI; 2003-403101/38.
 DR
 XX
 XX Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.
 XX
 XX Disclosure; SEQ ID NO 113; 126pp; English.
 PS
 XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.,
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,
 CC thrombocytopenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a peptide-vehicle compound of the invention.
 XX
 SQ Sequence 43 AA;
 Query Match 57.4%; Score 62; DB 7; Length 43;
 Best Local Similarity 84.6%; Pred. No. 0.041;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 DGPTLRQWLKGR 16
 DB 4 DGPTLRQWLKGR 16
 RESULT 24
 ID ADN59817 standard; peptide; 44 AA.
 AC ADN59817;
 DT 01-JUL-2004 (first entry)
 XX
 XX Peptide- linker compound, seq id 101.
 DB
 XX Haemostatic; anti-anaemic; immunosuppressive; platelet;
 KW transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 KW TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 KW thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
 KW autoimmune haemolytic anaemia; Hughes s syndrome;

KW lupoid thrombocytopenia; linker.
 XX
 OS unidentified.
 XX
 XX WO2003031589-A2.
 PN 17-APR-2003.
 PD 11-OCT-2002; 2002WO-US032552.
 PF 11-OCT-2001; 2001US-0328666P.
 PR 10-OCT-2002; 2002US-00269806.
 XX
 XX (AMGEN-) AMGEN INC.
 PA Min H, Sitney KC, Hartley C;
 PI WPI; 2003-403101/38.
 DR
 XX
 XX Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.
 XX
 XX Disclosure; SEQ ID NO 101; 126pp; English.
 PS
 XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.,
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,
 CC thrombocytopenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a peptide-linker compound.
 XX
 SQ Sequence 44 AA;
 Query Match 57.4%; Score 62; DB 7; Length 44;
 Best Local Similarity 84.6%; Pred. No. 0.042;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 DGPTLRQWLKGR 16
 DB 30 DGPTLRQWLKGR 42
 RESULT 25
 ID ADN59780 standard; protein; 46 AA.
 AC ADN59780;
 DT 01-JUL-2004 (first entry)
 XX
 XX Peptide-vehicle compound, seq id 132.
 DB
 XX Haemostatic; anti-anaemic; immunosuppressive; platelet;
 KW transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;

KW TWP; c-mpl receptor; platelet precursor; megakaryocyte;
 KW thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia;
 KW autoimmune haemolytic anaemia; Hughes' syndrome;
 KW lupoid thrombocytopaenia.
 XX
 OS Unidentified.
 PN WO2003031589-A2.
 PD 17-APR-2003.
 PF 11-OCT-2002; 2002WO-US032552.
 PR 11-OCT-2001; 2001US-0328666P.
 PR 10-OCT-2002; 2002US-00269806.
 PA (AMGE-) AMGEN INC.
 PI Min H, Sitney KC, Hartley C;
 PI WPI; 2003-403101/38.
 DR
 XX
 XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopaenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.,
 CC disease conditions involving thrombocytopaenia such as aplastic anaemia,
 CC autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia,
 CC autoimmune haemolytic anaemia, Hughes' syndrome and lupoid
 CC thrombocytopaenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytopoietic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a peptide-vehicle compound of the invention.
 XX
 SQ Sequence 46 AA;
 Query Match 57.4%; Score 62; DB 7; Length 46;
 Best Local Similarity 84.6%; Pred. No. 0.044;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DGPTLRQWLEGR 16
 ||||:||||||
 Db 9 DGPTLRQWLEGR 21

RESULT 26
 ADN59786
 ID ADN59786 standard; protein; 46 AA.
 XX
 AC ADN59786;
 DT 01-JUN-2004 (first entry)
 XX
 DE Peptide-vehicle compound, seq id 138.

XX
 KW Haemostatic; antihaemic; immunosuppressive; platelet;
 KW transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 KW TWP; c-mpl receptor; platelet precursor; megakaryocyte;
 KW thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia;
 KW autoimmune haemolytic anaemia; Hughes' syndrome;
 KW lupoid thrombocytopaenia.
 XX
 OS Unidentified.
 PN WO2003031589-A2.
 PD 17-APR-2003.
 PF 11-OCT-2002; 2002WO-US032552.
 PR 11-OCT-2001; 2001US-0328666P.
 PR 10-OCT-2002; 2002US-00269806.
 PA (AMGE-) AMGEN INC.
 PI Min H, Sitney KC, Hartley C;
 PI WPI; 2003-403101/38.
 DR
 XX
 XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopaenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.,
 CC disease conditions involving thrombocytopaenia such as aplastic anaemia,
 CC autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia,
 CC autoimmune haemolytic anaemia, Hughes' syndrome and lupoid
 CC thrombocytopaenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytopoietic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a peptide-vehicle compound of the invention.
 XX
 SQ Sequence 46 AA;
 Query Match 57.4%; Score 62; DB 7; Length 46;
 Best Local Similarity 84.6%; Pred. No. 0.044;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DGPTLRQWLEGR 16
 ||||:||||||
 Db 4 DGPTLRQWLEGR 16

RESULT 27
 ADN59667
 ID ADN59667 standard; peptide; 18 AA.
 XX
 AC ADN59667;
 XX

DT 01-JUL-2004 (first entry)
XX Thrombopoietin mimetic peptide (TMP16), seq id 16.
DE
XX Haemostatic; antianaemic; immunosuppressive; platelet;
KW transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
KW TMP; c-mpl receptor; platelet precursor; megakaryocyte;
KW thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
KW autoimmune haemolytic anaemia; Hughes's syndrome;
XX lupoid thrombocytopenia.
OS Homo sapiens.
XX
XX WO2003031589-A2.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032552.
XX
XX 11-OCT-2001; 2001US-0328666P.
XX 10-OCT-2002; 2002US-00269806.
XX
XX (AMGE-) AMGEN INC.
XX
XX Min H, Sitney KC, Hartley C;
XX
XX WPI; 2003-403101/38.
XX
XX Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
PT which stimulate the production of platelets and/or the production of
PT platelet precursors, useful for treating thrombocytopenia.
XX
XX Claim 6; SEQ ID NO 16; 126bp; English.
XX
XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
CC platelets and/or the production of platelet precursors, is new. Further
CC disclosed is a composition of matter (II) that binds to an mpl receptor,
CC and a pharmaceutical composition comprising (II) and a carrier. The
CC pharmaceutical composition of the invention is useful for treating
CC thrombocytopenia in an animal, and for increasing megakaryocytes or
CC platelets in a patient. The TMP of the invention is useful for treating
CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.
CC disease conditions involving thrombocytopenia such as aplastic anaemia,
CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,
CC autoimmune haemolytic anaemia, Hughes's syndrome and lupoid
CC thrombocytopenia. The TMP of the invention is also useful for
CC maintaining the viability or storage life of platelets and/or
CC megakaryocytes and its derived cells. The compounds demonstrate an
CC improved ability to bind to and/or trigger transmembrane signal through,
CC i.e. activating, the mpl receptor the compounds have superior
CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
CC vitro, the production of platelets and/or megakaryocytic activity,
CC i.e. the ability to stimulate, in vivo and in vitro, the production of
CC platelet precursors. Further, certain of the compounds also exhibit
CC superior therapeutic properties, such as improved plasma half-life,
CC biological activity and in vivo circulation time. The current sequence
XX represents a preferred TMP of the invention.
SQ Sequence 18 AA;
Query Match 55.6%; Score 60; DB 7; Length 18;
Best Local Similarity 71.4%; Pred. No. 0.032;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 ADGPTLRQMLEGRR 16
|:|||||:|:
Db 3 AEGPTLRMLEQRK 16
RESULT 28
ADNS9834
ID ADNS9834 standard; peptide; 22 AA.

XX
AC ADNS9834;
XX
DT 01-JUL-2004 (first entry)
XX
XX TMP peptide TMP16.
DE
XX Haemostatic; antianaemic; immunosuppressive; platelet;
KW transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
KW TMP; c-mpl receptor; platelet precursor; megakaryocyte;
KW thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
KW autoimmune haemolytic anaemia; Hughes's syndrome;
XX lupoid thrombocytopenia; linker.
XX
XX Homo sapiens.
XX
XX WO2003031589-A2.
XX
XX 17-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032552.
XX
XX 11-OCT-2001; 2001US-0328666P.
XX 10-OCT-2002; 2002US-00269806.
XX
XX (AMGE-) AMGEN INC.
XX
XX Min H, Sitney KC, Hartley C;
XX
XX WPI; 2003-403101/38.
XX
XX Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
PT which stimulate the production of platelets and/or the production of
PT platelet precursors, useful for treating thrombocytopenia.
XX
XX Example 6; Page 83; 126bp; English.
XX
XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
CC platelets and/or the production of platelet precursors, is new. Further
CC disclosed is a composition of matter (II) that binds to an mpl receptor,
CC and a pharmaceutical composition comprising (II) and a carrier. The
CC pharmaceutical composition of the invention is useful for treating
CC thrombocytopenia in an animal, and for increasing megakaryocytes or
CC platelets in a patient. The TMP of the invention is useful for treating
CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.
CC disease conditions involving thrombocytopenia such as aplastic anaemia,
CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,
CC autoimmune haemolytic anaemia, Hughes's syndrome and lupoid
CC thrombocytopenia. The TMP of the invention is also useful for
CC maintaining the viability or storage life of platelets and/or
CC megakaryocytes and its derived cells. The compounds demonstrate an
CC improved ability to bind to and/or trigger transmembrane signal through,
CC i.e. activating, the mpl receptor the compounds have superior
CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
CC vitro, the production of platelets and/or megakaryocytic activity,
CC i.e. the ability to stimulate, in vivo and in vitro, the production of
CC platelet precursors. Further, certain of the compounds also exhibit
CC superior therapeutic properties, such as improved plasma half-life,
CC biological activity and in vivo circulation time. The current sequence
XX represents a TMP peptide of the invention to which a two amino acid "cap"
XX has been added to the carboxy terminal to increase peptide affinity.
SQ Sequence 22 AA;
Query Match 55.6%; Score 60; DB 7; Length 22;
Best Local Similarity 71.4%; Pred. No. 0.04;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 3 ADGPTLRQMLEGRR 16
|:|||||:|:
Db 5 AEGPTLRMLEQRK 18

RESULT 29
ADN59716
ID ADN59716 standard; peptide; 25 AA.
XX
AC ADN59716;
XX
DT 01-JUL-2004 (first entry)
XX
DE Thrombopoietin mimetic peptide TMP16, seq id 65.
XX
KM Haemostatic; antihaemic; immunosuppressive; platelet;
KM transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
KM TMP; c-mpl receptor; platelet precursor; megakaryocyte;
KM thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia;
KM autoimmune haemolytic anaemia; Hughes's syndrome;
KM lupoid thrombocytopaenia.
XX
OS Homo sapiens.
XX
PN WO2003031589-A2.
XX
PD 17-APR-2003.
XX
PF 11-OCT-2002; 2002WO-US032552.
XX
XX 11-OCT-2001; 2001US-0328666P.
PR 10-OCT-2002; 2002US-00269806.
XX
PA (AMGE-) AMGEN INC.
XX
PI Min H, Sitney KC, Hartley C;
XX
DR WPI; 2003-403101/38.
XX
DR N-PSDB; ADN59715.
XX
PT Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
PT which stimulate the production of platelets and/or the production of
PT platelet precursors, useful for treating thrombocytopaenia.
XX
PS Disclosure; SEQ ID NO 65; 126pp; English.
XX
XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
XX binds to the c-mpl (mpl) receptor, and which stimulates the production of
XX platelets and/or the production of platelet precursors, is new. Further
XX disclosed is a composition of matter (II) that binds to an mpl receptor,
XX and a pharmaceutical composition comprising (II) and a carrier. The
XX pharmaceutical composition of the invention is useful for treating
XX thrombocytopaenia in an animal, and for increasing megakaryocytes or
XX platelets in a patient. The TMP of the invention is useful for treating
XX conditions involving a megakaryocyte and/or platelet deficiency, e.g.,
XX disease conditions involving thrombocytopaenia such as aplastic anaemia,
XX autoimmune thrombocytopaenia, drug induced immune thrombocytopaenia,
XX autoimmune haemolytic anaemia, Hughes's syndrome and lupoid
XX thrombocytopaenia. The TMP of the invention is also useful for
XX maintaining the viability or storage life of platelets and/or
XX megakaryocytes and its derived cells. The compounds demonstrate an
XX improved ability to bind to and/or trigger transmembrane signal through,
XX i.e. activating, the mpl receptor the compounds have superior
XX thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
XX vitro, the production of platelets and/or megakaryocytopoietic activity,
XX i.e. the ability to stimulate, in vivo and in vitro, the production of
XX platelet precursors. Further, certain of the compounds also exhibit
XX superior therapeutic properties, such as improved plasma half-life,
XX biological activity and in vivo circulation time. The current sequence
XX represents a TMP fragment.
XX
SQ Sequence 25 AA;

Query Match 55.6%; Score 60; DB 7; Length 25;
Best Local Similarity 71.4%; Pred. No. 0.046;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 ADGPTLRQWLEGR 16
|:|||||:|:|:
Db 6 AEGPTLRQWLEGRK 19

RESULT 30
AA96527
ID AA96527 standard; peptide; 34 AA.
XX
AC AA96527;
XX
DT 04-SEP-2000 (first entry)
XX
DE Thrombopoietin mimetic peptide compound 8.
XX
KM Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production;
KM anti-human immunodeficiency virus; anti-HIV; anti-aneimic; dermatological;
KM immunosuppressive; anti-inflammatory; linker.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX Peptide /note= "optionally linked to an Fc molecule"
XX Peptide 3..16
XX Peptide /label= TMP_1
XX Peptide 17..20
XX Peptide /label= linker
XX Peptide 21..34
XX Peptide /label= TMP_2
XX
PN WO200024770-A2.
XX
XX 04-MAY-2000.
XX
PF 22-OCT-1999; 99WO-US024834.
XX
PR 23-OCT-1998; 98US-0105348P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Liu C, Feige U, Cheetham J;
XX
DR WPI; 2000-365108/31.
XX
PT Thrombopoietic peptides which activate mpl receptors and increase the
PT production of platelets or platelet precursors, useful for treatment of
PT diseases which involve thrombocytopaenia.
XX
PS Claim 16; Page 64; 91pp; English.
XX
XX A compound which binds to an mpl receptor comprising a thrombopoietin
XX mimetic peptide (TMP) dimer joined by a linker (TMP_1-(L_1) nTMP_2), is
XX new. TMP_1 and TMP_2 are amino acid sequences varying from at least 10 to
XX 14 residues in length comprising X_2-X_1_0, X_2-X_1_1, X_2-X_1_2, X_2-
XX X_1_3, X_2-X_1_4, X_1-X_1_0, X_1-X_1_1, X_1-X_1_2, X_1-X_1_3 and X_1-
XX X_1_4. X_1 = I, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A; X_4 =
XX F; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N, or E;
XX X_9 = W, Y or F; X_1_0 = L, I, V, A, F, M, or K; X_1_1 = A, I, V, L, F,
XX S, T, K, H, or E; X_1_2 = A, I, V, L, F, G, S, or Q; X_1_3 = R, K, T, V,
XX N, Q or G; X_1_4 = A, I, V, L, F, T, R, E, or G; L_1 = linker comprising
XX 1 to 20 amino acids, and n = 0 or 1. The compounds bind to and activate
XX the c-Mpl receptor which mediates the activity of endogenous
XX thrombopoietin. The TWPs are useful for increasing the production of
XX platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which
XX is useful for treatment of diseases which involve thrombocytopaenia, e.g.
XX aplastic anaemia, immune thrombocytopaenia (ITP), human immunodeficiency
XX virus associated ITP, and systemic lupus erythematosus
XX
SQ Sequence 34 AA;

Query Match 55.6%; Score 60; DB 3; Length 34;
Best Local Similarity 57.9%; Pred. No. 0.065;

Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GNADGPTLRQWLEGGRRPN 19
 Db 1 GGIEGPTLRQWLAARAGPN 19

RESULT 31

ADNS9818
 ID ADNS9818 standard; peptide; 42 AA.

AC ADNS9818;

DT 01-JUN-2004 (first entry)

DE Peptide- linker compound, seq id 102.

XX Haemostatic; antihaemic; immunosuppressive; platelet;

KM transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;

KM TGF- β receptor; platelet precursor; megakaryocyte;

KM thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;

KM autoimmune haemolytic anaemia; Hughes' syndrome;

XX lupoid thrombocytopenia; linker.

XX Unidentified.

XX MO2003031589-A2.

XX 17-APR-2003.

XX 11-OCT-2002; 2002WO-US032552.

XX 11-OCT-2001; 2001US-032866P.

XX 10-OCT-2002; 2002US-00269806.

XX (AMGE-) AMGEN INC.

XX Min H, Stiney KC, Hartley C;

XX WPI; 2003-403101/38.

XX Novel thrombopoietin mimetic peptides which bind to mpl receptor, and

PT which stimulate the production of platelets and/or the production of

PT platelet precursors, useful for treating thrombocytopenia.

XX Disclosure; SEQ ID NO 102; 126pp; English.

XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that

CC binds to the c-mpl (mpl) receptor, and which stimulates the production of

CC platelets and/or the production of platelet precursors, is new. Further

CC disclosed is a composition of matter (II) that binds to an mpl receptor,

CC and a pharmaceutical composition comprising (II) and a carrier. The

CC pharmacological composition of the invention is useful for treating

CC thrombocytopenia in an animal, and for increasing megakaryocytes or

CC platelets in a patient. The TMP of the invention is useful for treating

CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.

CC disease conditions involving thrombocytopenia such as aplastic anaemia,

CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,

CC autoimmune haemolytic anaemia, Hughes' syndrome and lupoid

CC thrombocytopenia. The TMP of the invention is also useful for

CC maintaining the viability or storage life of platelets and/or

CC megakaryocytes and its derived cells. The compounds demonstrate an

CC improved ability to bind to and/or trigger transmembrane signal through,

CC i.e. activating, the mpl receptor the compounds have superior

CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in

CC vitro, the production of platelets and/or megakaryocytic activity,

CC i.e. the ability to stimulate, in vivo and in vitro, the production of

CC platelet precursors. Further, certain of the compounds also exhibit

CC superior therapeutic properties, such as improved plasma half-life,

CC biological activity and in vivo circulation time. The current sequence

CC represents a peptide-linker compound.

XX Sequence 42 AA;

Query Match 55.6%; Score 60; DB 7; Length 42;

Best Local Similarity 71.4%; Pred. No. 0.081; Indels 0; Gaps 0;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ADGPTLRQWLEGGRR 16
 Db 3 AEGPTLRQWLEGGRR 16

RESULT 32

ABP51670
 ID ABP51670 standard; peptide; 15 AA.

AC ABP51670;

DT 01-OCT-2002 (first entry)

XX Thrombopoietin (TPO) agonist mimetic peptide SEQ ID NO:2.

KM TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;

KM complementarity determining region; immunoglobulin; antihaemic;

KM haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX Homo sapiens.

XX Synthetic.

XX MO200246238-A2.

XX 13-JUN-2002.

XX 05-DEC-2001; 2001WO-US047656.

XX 05-DEC-2000; 2000US-0251448P.

XX 04-MAY-2001; 2001US-0288889P.

XX 29-MAY-2001; 2001US-0294068P.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Barbas-Frederickson S, Ranshaw M;

XX WPI; 2002-566610/60.

XX Claim 19; Page 6; 113pp; English.

XX The present invention describes an immunoglobulin molecule or its fragment

CC (I) comprising a region where amino acid residues corresponding to at

CC least a portion of the complementarity determining region (CDR) are

CC replaced or fused with biologically active peptides e.g. a peptide

CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,

CC that is flanked with proline at its carboxy terminus. (I) has

CC antihaemic, haemostatic and nephrotropic activities, and can be used as

CC a stimulator of proliferation, differentiation and maturation of

CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful

CC for stimulating proliferation, differentiation or growth of

CC promegakaryocytes or megakaryocytes, where (I) is contacted with

CC promegakaryocytes or megakaryocytes, which results in increased platelet

CC production. (I) with a region where amino acid residues corresponding to

CC a portion of CDR is replaced with an EPO mimetic, or which has one or

CC more of its CDRs fused to an EPO mimetic, is useful for increasing the

CC production of red blood cells, where (I) is contacted with haematopoietic

CC stem cells or their progenitors. (I) is useful for diagnosis or

CC therapeutics, in cell isolation strategies, and for treating patients

CC suffering from deficiency in cell populations caused by disease,

CC disorders or treatments related to the suppression of haematopoiesis.

CC AB073288 to AB073377 and ABP51669 to ABP51696 represent sequences used in

CC the exemplification of the present invention

XX

SQ Sequence 15 AA;

Query Match 54.6%; Score 59; DB 5; Length 15;
 Best Local Similarity 71.4%; Pred. No. 0.038;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 DGPTLRQWLEGRRP 17
 :|||||||
 Db 2 EGPTLRQWLAARAP 15

RESULT 33

ADQ16585 standard; peptide; 15 AA.

ADQ16585;

09-SEP-2004 (first entry)

TPO mimetic peptide SEQ ID NO:2.

immunoglobulin; complementarily determining region; CDR; peptide mimetic;

erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;

immunotherapy; thrombocytopenia.

Unidentified.

WO2004050017-A2.

17-JUN-2004.

17-NOV-2003; 2003WO-US036894.

02-DEC-2002; 2002US-00307724.

(ALEX-) ALEXION PHARM INC.

Bowdish KS, Frederickson S, Renshaw M;

WPI; 2004-460973/43.

New immunoglobulin molecule comprising a region, where two
 complementarily determining regions (CDRs) are replaced with EPO mimetic
 or a TPO mimetic, useful for treating thrombocytopenia.

Disclosure; SEQ ID NO 2; 107pp; English.

The invention relates to a novel immunoglobulin molecule or its fragment
 comprising a region where amino acid residues corresponding to at least a
 portion of a two complementarily determining regions (CDRs) are replaced
 with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 invention has immunosuppressive activity, and may have a use in
 immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 treating thrombocytopenia as a result of chemotherapy, bone marrow
 transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 The present sequence represents a TPO mimetic peptide.

Sequence 15 AA;

Query Match 54.6%; Score 59; DB 8; Length 15;
 Best Local Similarity 71.4%; Pred. No. 0.038;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 DGPTLRQWLEGRRP 17
 :|||||||
 Db 2 EGPTLRQWLAARAP 15

RESULT 34

ABP51689 standard; peptide; 18 AA.

ID ABP51689

XX

AC ABP51689;

01-OCT-2002 (first entry)

TPO mimetic peptide SEQ ID NO:41.

TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 complementarily determining region; immunoglobulin; antianemic;
 haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

Homo sapiens.

Synthetic.

WO200246238-A2.

13-JUN-2002.

05-DEC-2001; 2001WO-US047656.

05-DEC-2000; 2000US-0251448P.

04-MAY-2001; 2001US-0288899P.

29-MAY-2001; 2001US-0294068P.

(ALEX-) ALEXION PHARM INC.

Bowdish KS, Barbas-Frederickson S, Renshaw M;

WPI; 2002-566610/60.

N-PSDB; ABQ73367.

A novel immunogen molecule comprising a region in which amino acid

residues corresponding to at least a portion of the complementary

determining region are replaced or fused with an erythropoietin or

thrombopoietin mimetic.

Claim 20; Fig 5; 113pp; English.

The present invention describes an immunoglobulin molecule or its fragment
 (I) comprising a region where amino acid residues corresponding to at
 least a portion of the complementary determining region (CDR) are
 replaced or fused with biologically active peptides e.g. a peptide
 mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 that is flanked with proline at its carboxy terminus. (I) has
 antianemic, haemostatic and nephrotropic activities, and can be used as
 a stimulator of proliferation, differentiation and maturation of
 haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
 for stimulating proliferation, differentiation or growth of
 promegakaryocytes or megakaryocytes, where (I) is contacted with
 production. (I) with a region where amino acid residues corresponding to
 a portion of CDR is replaced with an EPO mimetic, or which has one or
 more of its CDRs fused to an EPO mimetic, is useful for increasing the
 production of red blood cells, where (I) is contacted with haematopoietic
 stem cells or their progenitors. (I) is useful for diagnostics or
 therapeutics, in cell isolation strategies, and for treating patients
 suffering from deficiency in cell populations caused by disease,
 disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP51689 to ABP51696 represent sequences used in
 the exemplification of the present invention

Sequence 18 AA;

Query Match 54.6%; Score 59; DB 5; Length 18;
 Best Local Similarity 71.4%; Pred. No. 0.046;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 DGPTLRQWLEGRRP 17
 :|||||||
 Db 4 EGPTLRQWLAARAP 17

RESULT 35

ABP51688

ID	ABP51688 standard; peptide; 18 AA.
XX	
AC	ABP51688;
XX	
DT	01-OCT-2002 (first entry)
XX	
DE	TPO mimetic peptide SEQ ID NO:39.
XX	
XX	TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
KW	complementarity determining region; immunoglobulin; antianemic;
KW	haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
XX	
OS	Homo sapiens.
OS	Synthetic.
PN	WO200246238-A2.
XX	
PD	13-JUN-2002.
XX	
PF	05-DEC-2001; 2001WO-US047656.
XX	
PR	05-DEC-2000; 2000US-0251448P.
PR	04-MAY-2001; 2001US-0288889P.
PR	29-MAY-2001; 2001US-0294068P.
XX	
PA	(ALEX-) ALEXION PHARM INC.
XX	
PI	Bowditch KS, Barbas-Frederickson S, Renshaw M;
DR	WPI; 2002-566610/60.
DR	N-PSDB; ABQ73366.
XX	
PT	A novel immunogen molecule comprising a region in which amino acid
PT	determining region are replaced or fused with an erythropoietin or
PT	thrombopoietin mimetic.
XX	
XX	
PS	Claim 20; Fig 5; 113bp; English.
XX	
CC	The present invention describes an immunoglobulin molecule or its fragment
CC	(I) comprising a region where amino acid residues corresponding to at
CC	least a portion of the complementary determining region (CDR) are
CC	replaced or fused with biologically active peptides e.g. a peptide
CC	mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC	that is flanked with proline at its carboxy terminus. (I) has
CC	antianemic, haemostatic and nephrotropic activities, and can be used as
CC	a stimulator of proliferation, differentiation and maturation of
CC	haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
CC	for stimulating proliferation, differentiation or growth of
CC	promegakaryocytes or megakaryocytes, where (I) is contacted with
CC	promegakaryocytes or megakaryocytes, which results in increased platelet
CC	production. (I) with a region where amino acid residues corresponding to
CC	a portion of CDR is replaced with an EPO mimetic, or which has one or
CC	more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC	production of red blood cells, where (I) is contacted with haematopoietic
CC	stem cells or their progenitors. (I) is useful for diagnostics or
CC	therapeutics, in cell isolation strategies, and for treating patients
CC	suffering from deficiency in cell populations caused by disease,
CC	disorders or treatments related to the suppression of haematopoiesis.
CC	ABQ73288 to ABQ73377 and ABP51695 to ABP51696 represent sequences used in
CC	the exemplification of the present invention
XX	
SEQ	Sequence 18 AA:

Query Match 54.6%; Score 59; DB 5; Length 18;

Best Local Similarity 71.4%; Pred. No. 0.046;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0

```

OY      4 DGETLROWLEGRP 17
        : ||||| |
DB      4 EGETLROWLAAP 17

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RESULT 36

ABP51686 standard; peptide; 18 AA.

AC ABP51686;

DT	01-OCT-2002 (first entry)
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TPO mimetic peptide SEQ ID NO:35.

TPQ; EPO; thrombopoietin; erythropoietin; antibody; CDR region;

haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

OS Homo sapiens.

XX

XX

XX 3

XX

PR 04-MAY-2001; 2001US-0288889P.

XX

XX	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	

XX

DR N-PSDB; ABQ73364.

PT A novel immunogen comprising a region in which amino acid

PT determining region ar

XX

PS Claim 20; Fig 5; 113pp; English.

xx The present invention describes an immunoglobulin molecule or its fragment
cc (I) comprising a region where amino acid residues corresponding to at
cc least a portion of the complementary determining region (CDR) are
cc replaced or fused with biologically active peptides e.g. a peptide
cc mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
cc that is flanked with proline at its carboxy terminus. (I) has
cc anti-anemic, haemostatic and nephrotoxic activities, and can be used as
cc a stimulator of proliferation, differentiation and maturation of
cc haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
cc for stimulating proliferation, differentiation or growth of
cc promegakaryocytes or megakaryocytes, where (I) is contacted with
cc promegakaryocytes or megakaryocytes, which results in increased platelet
cc production. (I) with a region where amino acid residues corresponding to
cc a portion of CDR is replaced with an EPO mimetic, or which has one or
cc more of its CDRs fused to an EPO mimetic, is useful for increasing the
cc production of red blood cells, where (I) is contacted with haematopoietic
cc stem cells or their progenitors. (I) is useful for diagnostics or
cc therapeutics, in cell isolation strategies, and for treating patients
cc suffering from deficiency in cell populations caused by disease,
cc disorders or treatments related to the suppression of haematopoiesis.
cc ABQ73288 to ABQ73377 and ABP5169 to ABP51696 represent sequences used in
cc the exemplification of the present invention

SQ Sequence 18 AA;

Query Match 54.6%; Score 59; DB 5; Length 18;

Matches 10; Conservative
QY 4 DGPLRQWLEGRP 17

Db 4 EGPTLRQWLAARAP 17

RESULT 37

ABP51693
ID ABP51693 standard; peptide; 18 AA.

XX
AC ABP51693;

XX
DT 01-OCT-2002 (first entry)

XX
DE TPO mimetic peptide SEQ ID NO:49.

XX
KW TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
complementarity determining region; immunoglobulin; antianaemic;
KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX
OS Homo sapiens.
OS Synthetic.

XX
PN WO200246238-A2.

XX
PD 13-JUN-2002.

XX
PF 05-DEC-2001; 2001WO-US047656.

XX
PR 05-DEC-2000; 2000US-0251448P.

XX
PR 04-MAY-2001; 2001US-028889P.

XX
PR 29-MAY-2001; 2001US-0294068P.

XX
PA (ALEX-) ALEXION PHARM INC.

XX
PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX
DR WPI: 2002-566610/60.

XX
DR N-PSDB; ABQ73371.

XX
PT A novel immunogen molecule comprising a region in which amino acid
PT residues corresponding to at least a portion of the complementary
PT determining region are replaced or fused with an erythropoietin or
PT thrombopoietin mimetic.

XX
PS Claim 20; Fig 5; 113pp; English.

XX
CC The present invention describes an immunoglobulin molecule or its fragment
CC (1) comprising a region where amino acid residues corresponding to at
CC least a portion of the complementary determining region (CDR) are
CC replaced or fused with biologically active peptides e.g. a peptide
CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC that is flanked with proline at its carboxy terminus. (1) has
CC antianaemic, haemostatic and nephrotropic activities, and can be used as
CC a stimulator of proliferation, differentiation and maturation of
CC haematopoietic cells, and a stimulator of haematopoiesis. (1) is useful
CC for stimulating proliferation, differentiation or growth of
CC promegakaryocytes or megakaryocytes, where (1) is contacted with
CC promegakaryocytes or megakaryocytes, which results in increased platelet
CC production. (1) with a region where amino acid residues corresponding to
CC a portion of CDR is replaced with an EPO mimetic, or which has one or
CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC production of red blood cells, where (1) is contacted with haematopoietic
CC stem cells or their progenitors. (1) is useful for diagnostics or
CC therapeutics, in cell isolation strategies, and for treating patients
CC suffering from deficiency in cell populations caused by disease,
CC disorders or treatments related to the suppression of haematopoiesis.
CC ABQ73288 to ABQ73377 and ABP51693 to ABP51696 represent sequences used in
CC the exemplification of the present invention

XX
SQ Sequence 18 AA;

Query Match 54.6%; Score 59; DB 5; Length 18;

Best Local Similarity 71.4%; Pred. No. 0.046;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 DGPLTQWLEGRAP 17

DB 4 EGPLTQWLEGRAP 17

RESULT 38

ABP51684
ID ABP51684 standard; peptide; 18 AA.

XX
AC ABP51684;

XX
DT 01-OCT-2002 (first entry)

XX
DE TPO mimetic peptide SEQ ID NO:31.

XX
KW TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
complementarity determining region; immunoglobulin; antianaemic;
KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX
OS Homo sapiens.
OS Synthetic.

XX
PN WO200246238-A2.

XX
PD 13-JUN-2002.

XX
PF 05-DEC-2001; 2001WO-US047656.

XX
PR 05-DEC-2000; 2000US-0251448P.

XX
PR 04-MAY-2001; 2001US-028889P.

XX
PR 29-MAY-2001; 2001US-0294068P.

XX
PA (ALEX-) ALEXION PHARM INC.

XX
PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX
DR WPI: 2002-566610/60.

XX
DR N-PSDB; ABQ73362.

XX
PT A novel immunogen molecule comprising a region in which amino acid
PT residues corresponding to at least a portion of the complementary
PT determining region are replaced or fused with an erythropoietin or
PT thrombopoietin mimetic.

XX
PS Claim 20; Fig 5; 113pp; English.

XX
CC The present invention describes an immunoglobulin molecule or its fragment
CC (1) comprising a region where amino acid residues corresponding to at
CC least a portion of the complementary determining region (CDR) are
CC replaced or fused with biologically active peptides e.g. a peptide
CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC that is flanked with proline at its carboxy terminus. (1) has
CC antianaemic, haemostatic and nephrotropic activities, and can be used as
CC a stimulator of proliferation, differentiation and maturation of
CC haematopoietic cells, and a stimulator of haematopoiesis. (1) is useful
CC for stimulating proliferation, differentiation or growth of
CC promegakaryocytes or megakaryocytes, where (1) is contacted with
CC promegakaryocytes or megakaryocytes, which results in increased platelet
CC production. (1) with a region where amino acid residues corresponding to
CC a portion of CDR is replaced with an EPO mimetic, or which has one or
CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC production of red blood cells, where (1) is contacted with haematopoietic
CC stem cells or their progenitors. (1) is useful for diagnostics or
CC therapeutics, in cell isolation strategies, and for treating patients
CC suffering from deficiency in cell populations caused by disease,
CC disorders or treatments related to the suppression of haematopoiesis.
CC ABQ73288 to ABQ73377 and ABP51693 to ABP51696 represent sequences used in
CC the exemplification of the present invention

XX
SQ Sequence 18 AA;

Query Match 54.6%; Score 59; DB 5; Length 18;

Best Local Similarity 71.4%; Pred. No. 0.046;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 DGPTLRQWLGRRP 17
:|||||
Db 4 EGPTLRQWLARAP 17

RESULT 39

ABP51691
ID ABP51691 standard; peptide; 18 AA.

AC ABP51691;

DT 01-OCT-2002 (first entry)

DE TPO mimetic peptide SEQ ID NO:45.

XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
KM complementarity determining region; immunoglobulin; antianaemic;
KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX Homo sapiens.

OS Synthetic.

PN WO200246238-A2.

PD 13-JUN-2002.

PF 05-DEC-2001; 2001WO-US047656.

PR 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

XX (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

DR WPI; 2002-566610/60.

DR N-PSDB; ABQ73369.

PT A novel immunogen molecule comprising a region in which amino acid
PT residues corresponding to at least a portion of the complementary
PT determining region are replaced or fused with an erythropoietin or
PT thrombopoietin mimetic.

PS Claim 20; Fig 5; 113pp; English.

XX The present invention describes an immunoglobulin molecule or its fragment
CC (I) comprising a region where amino acid residues corresponding to at
CC least a portion of the complementary determining region (CDR) are
CC replaced or fused with biologically active peptides e.g. a peptide
CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC that is flanked with proline at its carboxy terminus. (I) has
CC antianaemic, haemostatic and nephrotropic activities, and can be used as
CC a stimulator of proliferation, differentiation and maturation of
CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
CC for stimulating proliferation, differentiation or growth of
CC promegakaryocytes or megakaryocytes, where (I) is contacted with
CC promegakaryocytes or megakaryocytes, which results in increased platelet
CC production. (I) with a region where amino acid residues corresponding to
CC a portion of CDR is replaced with an EPO mimetic, or which has one or
CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC production of red blood cells, where (I) is contacted with haematopoietic
CC stem cells or their progenitors. (I) is useful for diagnostics or
CC therapeutics, in cell isolation strategies, and for treating patients
CC suffering from deficiency in cell populations caused by disease,
CC disorders or treatments related to the suppression of haematopoiesis.
CC ABQ73288 to ABQ73377 and ABP51691 to ABP51696 represent sequences used in
CC the exemplification of the present invention
SQ Sequence 18 AA;

Query Match

54.6%; Score 59; DB 5; Length 18;

Best Local Similarity 71.4%; Pred. No. 0.046;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 DGPTLRQWLGRRP 17
:|||||
Db 4 EGPTLRQWLARAP 17

RESULT 40

ABP51690
ID ABP51690 standard; peptide; 18 AA.

AC ABP51690;

DT 01-OCT-2002 (first entry)

DE TPO mimetic peptide SEQ ID NO:43.

XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
KM complementarity determining region; immunoglobulin; antianaemic;
KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX Homo sapiens.

OS Synthetic.

PN WO200246238-A2.

PD 13-JUN-2002.

PF 05-DEC-2001; 2001WO-US047656.

PR 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

XX (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

DR WPI; 2002-566610/60.

DR N-PSDB; ABQ73368.

PT A novel immunogen molecule comprising a region in which amino acid
PT residues corresponding to at least a portion of the complementary
PT determining region are replaced or fused with an erythropoietin or
PT thrombopoietin mimetic.

PS Claim 20; Fig 5; 113pp; English.

XX The present invention describes an immunoglobulin molecule or its fragment
CC (I) comprising a region where amino acid residues corresponding to at
CC least a portion of the complementary determining region (CDR) are
CC replaced or fused with biologically active peptides e.g. a peptide
CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC that is flanked with proline at its carboxy terminus. (I) has
CC antianaemic, haemostatic and nephrotropic activities, and can be used as
CC a stimulator of proliferation, differentiation and maturation of
CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
CC for stimulating proliferation, differentiation or growth of
CC promegakaryocytes or megakaryocytes, where (I) is contacted with
CC promegakaryocytes or megakaryocytes, which results in increased platelet
CC production. (I) with a region where amino acid residues corresponding to
CC a portion of CDR is replaced with an EPO mimetic, or which has one or
CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC production of red blood cells, where (I) is contacted with haematopoietic
CC stem cells or their progenitors. (I) is useful for diagnostics or
CC therapeutics, in cell isolation strategies, and for treating patients
CC suffering from deficiency in cell populations caused by disease,
CC disorders or treatments related to the suppression of haematopoiesis.
CC ABQ73288 to ABQ73377 and ABP51691 to ABP51696 represent sequences used in
CC the exemplification of the present invention
SQ Sequence 18 AA;

Query Match 54.6%; Score 59; DB 5; Length 18;
 Best Local Similarity 71.4%; Pred. No. 0.046;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 DGPTLRQWLEGRRP 17
 :|||||||
 Db 4 EGPTLRQWLAARAP 17

RESULT 41

ABP51675
 ID ABP51675 standard; peptide; 18 AA.

XX ABP51675;
 AC
 XX

DT 01-OCT-2002 (first entry)

DE TPO mimetic antibody related peptide graft SEQ ID NO:66.

XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 KM complementarity determining region; immunoglobulin; antihaemic;
 KM haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX Homo sapiens.
 OS Synthetic.

XX WO200246238-A2.

XX 13-JUN-2002.

XX 05-DEC-2001; 2001WO-US047656.

XX 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

PA (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX WPI; 2002-566610/60.

PT A novel immunogen molecule comprising a region in which amino acid
 PT residues corresponding to at least a portion of the complementary
 PT determining region are replaced or fused with an erythropoietin or
 PT thrombopoietin mimetic.

PS Example 4; Page 55; 113pp; English.

XX The present invention describes an immunoglobulin molecule or its fragment
 CC (1) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (1) has
 CC antihaemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (1) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (1) is contacted with
 CC promegakaryocytes or megakaryocytes, which results in increased platelet
 CC production. (1) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (1) is contacted with haematopoietic
 CC stem cells or their progenitors. (1) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in
 CC the exemplification of the present invention
 XX

SQ Sequence 18 AA.

Query Match 54.6%; Score 59; DB 5; Length 18;
 Best Local Similarity 71.4%; Pred. No. 0.046;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 DGPTLRQWLEGRRP 17
 :|||||||
 Db 4 EGPTLRQWLAARAP 17

RESULT 42

ADQ16611
 ID ADQ16611 standard; peptide; 18 AA.

XX ADQ16611;
 AC
 XX

DT 09-SEP-2004 (first entry)

DE TPO mimetic peptide with random flanking residues SEQ ID NO:31.

XX immunoglobulin; complementarity determining region; CDR; peptide mimetic;
 KM erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 KM immunotherapy; thrombocytopenia.

XX Unidentified.

XX WO2004050017-A2.

XX 17-JUN-2004.

XX 17-NOV-2003; 2003WO-US036894.

XX 02-DEC-2002; 2002US-00307724.

XX (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Frederickson S, Renshaw M;

XX WPI; 2004-460973/43.

DR N-PSDB; ADQ16612.

PT New immunoglobulin molecule comprising a region, where two
 PT complementarity determining regions (CDRs) are replaced with EPO mimetic
 PT or a TPO mimetic, useful for treating thrombocytopenia.

PS Example 1; SEQ ID NO 31; 107pp; English.

XX The invention relates to a novel immunoglobulin molecule or its fragment
 CC comprising a region where amino acid residues corresponding to at least a
 CC portion of a two complementarity determining regions (CDRs) are replaced
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 CC invention has immunosuppressive activity, and may have a use in
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow
 CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide with flanking
 CC residues.
 XX

SQ Sequence 18 AA:

Query Match 54.6%; Score 59; DB 8; Length 18;
 Best Local Similarity 71.4%; Pred. No. 0.046;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 DGPTLRQWLEGRRP 17
 :|||||||
 Db 4 EGPTLRQWLAARAP 17

RESULT 43

ADQ16619

ID	ADQ16619	standard; peptide; 18 AA.
XX		
AC	ADQ16619;	
XX		
DT	09-SEP-2004	(first entry)
XX		
DE	TPO mimetic peptide with random flanking residues SEQ ID NO:39.	
XX		
KW	immunoglobulin; complementarity determining region; CDR; peptide mimetic;	
KW	erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;	
XX	immunotherapy; thrombocytopenia.	
OS	Unidentified.	
XX		
FN	WO2004050017-A2.	
XX		
PD	17-JUN-2004.	
XX		
PE	17-NOV-2003; 2003WO-US036894.	
XX		
PR	02-DEC-2002; 2002US-00307724.	
XX		
PA	(ALEX-) ALEXION PHARM INC.	
XX		
PI	Bowditch KS, Frederickson S, Renshaw M;	
XX		
DR	WPI; 2004-460973/43.	
XX		
DR	N-PSDB; ADQ16620.	
XX		
PT	New immunoglobulin molecule comprising a region, where two	
FT	complementarity determining regions (CDRs) are replaced with EPO mimetic	
XX	or a TPO mimetic, useful for treating thrombocytopenia.	
PS	Example 1; SEQ ID NO 39; 107pp; English.	
XX		
CC	The invention relates to a novel immunoglobulin molecule or its fragment	
CC	comprising a region where amino acid residues corresponding to at least a	
CC	portion of a two complementarity determining regions (CDRs) are replaced	
CC	with a peptide mimetic selected from an erythropoietin (EPO) mimetic and	
CC	a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the	
CC	invention has immunosuppressive activity, and may have a use in	
CC	immunotherapy. The immunoglobulin molecule is useful for diagnosing or	
CC	treating thrombocytopenia as a result of chemotherapy, bone marrow	
CC	transplantation, or chronic diseases such as idiopathic thrombocytopenia.	
CC	The present sequence represents a TPO mimetic peptide with flanking	
CC	residues.	
XX		
XX		
SO	Sequence 18 AA;	
	Query Match	54.6%; Score 59; DB 8; Length 18;
	Best Local Similarity	71.4%; Pred. No. 0.046;
	Matches 10; Conservative	1; Mismatches 3; Indels 0; Gaps 0;
Oy	4 DGPTRQWLEGRRP 17	
	:	
	:	
	:	
Db	4 EGPTRQWLAARAP 17	
	RESULT 44	
	ADQ16621	
ID	ADQ16621	standard; peptide; 18 AA.
XX		
AC	ADQ16621;	
XX		
DT	09-SEP-2004	(first entry)
XX		
DE	TPO mimetic peptide with random flanking residues SEQ ID NO:41.	
XX		
KW	immunoglobulin; complementarity determining region; CDR; peptide mimetic;	
KW	erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;	
XX	immunotherapy; thrombocytopenia.	
OS	Unidentified.	

[illegible]

DR WPI; 2004-460973/43.
DR N-PSDB; ADQ16645.
XX
XX New immunoglobulin molecule comprising a region, where two
PT complementarity determining regions (CDRs) are replaced with EPO mimetic
PT or a TPO mimetic, useful for treating thrombocytopenia.
XX
XX
PS Example 4; SEQ ID NO 66; 107pp; English.
XX
CC The invention relates to a novel immunoglobulin molecule or its fragment
CC comprising a region where amino acid residues corresponding to at least a
CC portion of a two complementarity determining regions (CDRs) are replaced
CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC invention has immunosuppressive activity, and may have a use in
CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC treating thrombocytopenia as a result of chemotherapy, bone marrow
CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC The present sequence represents a TPO mimetic peptide of the invention.
XX
SQ Sequence 18 AA;

Query Match 54.6%; Score 59; DB 8; Length 18;
Best Local Similarity 71.4%; Pred. No. 0.046;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 DGPTLRQWLEGRRP 17
:|||||||
Db 4 EGPTLRQWLAARAP 17

Search completed: September 1, 2005, 16:12:10
Job time : 89.3453 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:37 ; Search time 70.6691 Seconds

(without alignments)
137.677 Million cell updates/sec

Title: US-10-083-768-7

Perfect score: 108

Sequence: 1 GNADPTLRQWLEGRRPKN 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database: UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	59.5	55.1	297	2	Q7UGB4	Q7UGB4 rhodopirell
2	59	54.6	319	2	Q9RKM5	Q9RKM5 streptomyc
3	59	49.1	191	2	Q7PRF0	Q7PRF0 anopheles g
4	52	48.1	252	2	Q8XPO9	Q8XPO9 ralsiconia s
5	51	47.2	655	2	Q7XVQ9	Q7XVQ9 oryza sativ
6	50.5	46.8	168	2	Q9V492	Q9V492 drosophila
7	50.5	46.8	256	2	Q6LEMS	Q6LEMS bochrops ja
8	50	46.3	228	2	Q75LM1	Q75LM1 oryza sativ
9	50	46.3	391	2	Q8T511	Q8T511 anopheles g
10	50	46.3	391	2	Q7PUW8	Q7PUW8 anopheles g
11	49	45.4	242	2	Q82AV3	Q82AV3 streptomyc
12	49	45.4	271	2	Q8EUN8	Q8EUN8 mycoplasma
13	49	45.4	387	2	Q872W6	Q872W6 neurospora
14	49	45.4	531	2	Q92281	Q92281 rhizobium m
15	48.5	44.9	531	2	Q61G99	Q61G99 photobacter
16	48	44.4	81	2	Q8DHX7	Q8DHX7 hydra magni
17	48	44.4	129	2	Q8DHX7	Q8DHX7 synchococc
18	48	44.4	139	2	Q9GSP9	Q9GSP9 hydra atren
19	48	44.4	161	2	Q6A743	Q6A743 propionibac
20	48	44.4	282	1	Y356_MYCEN	Y356_MYCEN mycoplasma
21	48	44.4	364	2	Q7XUX8	Q7XUX8 oryza sativ
22	48	44.4	1023	2	Q65WR1	Q65WR1 oryza sativ
23	48	44.4	1189	2	Q7X5Z1	Q7X5Z1 oryza sativ
24	47.5	44.0	264	2	Q7UR10	Q7UR10 rhodopirell
25	47	43.5	81	2	Q9NDJ5	Q9NDJ5 tima formos
26	47	43.5	81	2	Q9NDL8	Q9NDL8 hydractinia
27	47	43.5	81	2	Q9NDL9	Q9NDL9 extreme sp.
28	47	43.5	133	2	Q87645	Q87645 methylococc
29	47	43.5	181	2	Q93KY0	Q93KY0 streptomyc
30	47	43.5	352	1	IP12_PYRAE	IP12_PYRAE pyrobaculum
31	47	43.5	452	2	Q6FXT5	Q6FXT5 candida gla

32	47	43.5	571	2	Q9P729	Q9P729 neurospora
33	47	43.5	986	1	Z445_MOUSE	Z445_MOUSE mus musculus
34	47	43.5	1005	2	Q8MTJ3	Q8MTJ3 drosophila
35	47	43.5	1005	2	Q9VSI2	Q9VSI2 drosophila
36	47	43.5	1171	2	Q9P3E2	Q9P3E2 neurospora
37	46.5	43.1	522	2	Q9LIW0	Q9LIW0 oryza sativ
38	46.5	43.1	690	1	EP42_HUMAN	EP42_HUMAN homo sapien
39	46.5	43.1	103	2	Q95OV6	Q95OV6 caenorhabdi
40	46	42.6	157	2	Q9NMG3	Q9NMG3 homo sapien
41	46	42.6	243	2	Q9RKP9	Q9RKP9 streptomyc
42	46	42.6	249	2	Q8W2V0	Q8W2V0 oryza sativ
43	46	42.6	249	2	Q7G7J1	Q7G7J1 oryza sativ
44	46	42.6	357	2	Q9SIQ2	Q9SIQ2 streptomyc
45	46	42.6	362	2	Q82ON3	Q82ON3 streptomyc
46	46	42.6	377	2	Q82PX5	Q82PX5 streptomyc
47	46	42.6	479	1	RPCL_AERPE	RPCL_AERPE aeropyrum p
48	46	42.6	656	2	Q6AF49	Q6AF49 leifsonia x
49	46	42.6	1049	2	Q9XBP6	Q9XBP6 myxococcus
50	46	42.6	1183	2	Q8H044	Q8H044 oryza sativ
51	46	42.6	1546	2	Q73UP3	Q73UP3 mycobacteri
52	45.5	42.1	88	2	Q6YS15	Q6YS15 oryza sativ
53	45.5	42.1	236	2	Q69TG4	Q69TG4 oryza sativ
54	45.5	42.1	446	2	Q828C4	Q828C4 streptomyc
55	45	41.7	147	2	Q825A6	Q825A6 streptomyc
56	45	41.7	147	2	Q82FW7	Q82FW7 streptomyc
57	45	41.7	151	2	Q826F1	Q826F1 streptomyc
58	45	41.7	272	2	Q7N6R2	Q7N6R2 photorhabdu
59	45	41.7	280	1	Y356_MYCCE	Y356_MYCCE mycoplasma
60	45	41.7	290	2	Q8K417	Q8K417 sigmodon hi
61	45	41.7	325	2	Q85MB2	Q85MB2 monoblephar
62	45	41.7	326	2	P95613	P95613 rhizobium g
63	45	41.7	340	2	Q95Y14	Q95Y14 acartaris bui
64	45	41.7	344	2	Q9HN36	Q9HN36 halobacteri
65	45	41.7	345	2	Q6DAE7	Q6DAE7 erwina car
66	45	41.7	542	2	Q6N2A1	Q6N2A1 rhodopseudo
67	45	41.7	559	2	Q66DB0	Q66DB0 yersinia ps
68	45	41.7	559	2	Q8ZH10	Q8ZH10 yersinia pe
69	45	41.7	589	2	Q8CZ27	Q8CZ27 yersinia pe
70	45	41.7	609	2	Q856X8	Q856X8 mycobacteri
71	45	41.7	636	2	Q656W4	Q656W4 oryza sativ
72	45	41.7	863	2	Q9ST50	Q9ST50 zea mays (m
73	45	41.7	1247	2	Q9SDJ4	Q9SDJ4 arabidopsis
74	45	41.7	1413	2	Q9NBD3	Q9NBD3 caenorhabdi
75	45	41.7	1493	2	Q9NED3	Q9NED3 nitrosomona
76	44.5	41.2	152	2	Q82X11	Q82X11 xanthomonas
77	44.5	41.2	173	2	Q8PLV3	Q8PLV3 streptomyc
78	44.5	41.2	446	2	Q88053	Q88053 streptomyc
79	44.5	41.2	600	2	Q93IU2	Q93IU2 streptomyc
80	44.5	41.2	602	2	P72407	P72407 streptomyc
81	44.5	41.2	1061	2	Q9W699	Q9W699 fugu rubrip
82	44.5	41.2	1456	2	Q8NUS1	Q8NUS1 leptosphaer
83	44	40.7	125	2	Q84HM5	Q84HM5 rhizobium s
84	44	40.7	127	2	Q86MB0	Q86MB0 lytechinus
85	44	40.7	189	2	Q9HS88	Q9HS88 halobacteri
86	44	40.7	192	2	Q7U7Q3	Q7U7Q3 synchococc
87	44	40.7	210	1	MDCG_PSEAE	MDCG_PSEAE pseudomonas
88	44	40.7	259	2	Q837Y4	Q837Y4 enterococcu
89	44	40.7	260	2	Q8DVQ5	Q8DVQ5 streptococc
90	44	40.7	263	2	Q9PT52	Q9PT52 agkistrodon
91	44	40.7	270	2	Q8EP23	Q8EP23 oceanobacil
92	44	40.7	273	2	Q66D70	Q66D70 yersinia ps
93	44	40.7	273	2	Q8ZGK5	Q8ZGK5 yersinia pe
94	44	40.7	302	2	Q742B3	Q742B3 mycobacteri
95	44	40.7	303	2	Q8FSC5	Q8FSC5 corynebacte
96	44	40.7	310	2	Q9MB12	Q9MB12 bacterioph
97	44	40.7	320	2	Q8VKZ7	Q8VKZ7 mycobacteri
98	44	40.7	324	1	G3P1_GLOBO	G3P1_GLOBO globodera r
99	44	40.7	330	1	G3PC_LETME	G3PC_LETME leishmania
100	44	40.7	330	2	Q82MF0	Q82MF0 streptomyc

ALIGNMENTS

```

RESULT 1
Q7UBA4 PRELIMINARY; PRT; 297 AA.
AC Q7UBA4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB6375;
OS Rhodopirella baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schlesner H., Aumann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; EX294144; CAD74759.1; -.
DR InterPro; IPR000194; ATPase_a/bcentre.
DR InterPro; IPR003169; GYP.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
DR PROSITE; PS00829; GYP. 1
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 297 AA; 31805 MW; 475f6f02c78b9b CRC64;

Query Match 55.1%; Score 59.5; DB 2; Length 297;
Best Local Similarity 68.8%; Pred. No. 0.77;
Matches 11; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 GNADPTLRQWL-BGR 15
Db 173 GPADGPTMKQWISGR 188

RESULT 2
Q9RKM5 PRELIMINARY; PRT; 319 AA.
AC Q9RKM5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative MerR family transcriptional regulator.
GN ORFNames=SCD17.06c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AA3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornbly T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabbilowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -|- STIMILARITY: Contains 1 HTM merr-type DNA-binding domain.
DR EMBL; AL339118; CAB56383.1; -.
DR GO; GO:0005622; C:intracellular; IEA.

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DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000551; HTM_Merr.
DR InterPro; IPR009061; Putativ_DNA_bind.
DR Pfam; PF00376; Merr; 1.
DR PRINTS; PR00040; HTHMERR.
DR SMART; SM00422; HTM_MERR. 1.
DR PROSITE; PS00937; HTM_MERR. 2; 1.
KM Complete proteome; DNA-binding.
SQ SEQUENCE 319 AA; 34841 MW; 1f51905a8ba5365e CRC64;

Query Match 54.6%; Score 59; DB 2; Length 319;
Best Local Similarity 66.7%; Pred. No. 0.99;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GNADPTLRQWLEGR 15
Db 255 GRPDGPELREWLGR 269

RESULT 3
Q7RPF0 PRELIMINARY; PRT; 191 AA.
AC Q7RPF0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000014364 (Fragment).
GN Name=ENSANG0000011875;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
CC -|- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008851; EAA07337.2; -.
FT NON TER 1
SQ SEQUENCE 191 AA; 21826 MW; 3DE9B8C839FAFCB CRC64;

Query Match 49.1%; Score 53; DB 2; Length 191;
Best Local Similarity 58.8%; Pred. No. 4.8;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 NADGPTLRQWLEGRPK 18
Db 74 HAAGPTERRRWLEKESPK 90

RESULT 4
Q8XPQ9 PRELIMINARY; PRT; 252 AA.
AC Q8XPQ9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.
GN Name=RS02135; OrderedLocusNames=RSp1579;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM1100;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

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RA Arlat M., Billault A., Brothier P., Camus J.C., Catolico L.,
 RA Chandler M., Christine N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Sigulier P., Thebaud P., Whalen M., Winkler P., Levy M.,
 RA Weisenbach J., Boucher C.A.,
 RT "genome sequence of the plant pathogen *Ralstonia solanacearum*.";
 RL Nature 415:497-502(2002).
 CC -1- STIMILARITY: Contains 1 HTH LuxR-type DNA-binding domain.
 DR EMBL; AL646085; CAD18730.1; -.
 DR HSSP; P11470; 1PSE.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR Pfam; PF00156; Gels; 1.
 DR PRINTS; PRO1590; HTHLUX.
 DR PRODOM; PD000307; HTH LuxR; 1.
 DR SMART; SM00421; HTH_LUXR; 1.
 KM Complete proteome; DNA-binding; Plasmid; Transcription;
 KW Transcription regulation.
 SQ SEQUENCE 252 AA; 2766 MW; 483403EE326F7C2E CRC64;

Query Match 48.1%; Score 52; DB 2; Length 252;
 Best Local Similarity 52.9%; Pred. No. 9.3;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GNADPTIRQWLEGRPP 17
 DB 74 GGDITPIMRWLWLRPP 90

RESULT 5
 ID Q7XVU9 PRELIMINARY; PRT; 655 AA.
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
 DE OSJNB0035B13.2 protein.
 GN Name=OSJNB0035B13.2;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihatoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN RN
 RP SEQUENCE FROM N.A.
 RX PubMed=12447439; DOI=10.1038/nature01183;
 RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 RA Wang Q., Zhang L., Lu Y., Mu Y., Lu Y., Zhang L.S., Yu Z., Fan D.,
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
 RA Chen J., Kang H., Chen C., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 RA Han B.;
 RT "Sequence and analysis of rice chromosome 4.";
 RL Nature 420:316-320(2002).
 DR EMBL; AL662966; CAD0429.1; -.
 DR Gramene; Q7XVU9; -.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
 DR InterPro; IPR000477; RYase.
 DR Pfam; PF00078; RVT_1; 2.
 KM RNA-directed DNA polymerase; Transferase.
 SQ SEQUENCE 655 AA; 74463 MW; 4F15BC16D1BC776 CRC64;

Query Match 47.2%; Score 51; DB 2; Length 655;
 Best Local Similarity 50.0%; Pred. No. 37;

Matches 10; Conservative 4; Mismatches 2; Indels 4; Gaps 1;
 Qy 4 DGPFLR---QWLEGRPPK 19
 DB 483 DGNTIRFWSAMWDGGRPK 502

RESULT 6
 ID Q9V492 PRELIMINARY; PRT; 168 AA.
 AC Q9V492;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE CG11077-PA (RE5125P).
 GN ORENames=CG11077;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer V.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Doeson K., Doup L.E., Downes W., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertier S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Hariri N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kemison U.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodaght, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA Geoghe R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Paclib J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 melanogaster euchromatic genome sequence.";

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RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Stirekas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celisner S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
RA Smith C.D., Tuzy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
RA Beuten-court B.R., Celisner S.E., de Grey A.D., Dysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkley.;
RA Chapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Fafan D., Frise E.,
RA Miranda A., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celisner S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AEO03846; AAF59393.1; -.
DR EMBL; AY071482; AAL49104.1; -.
DR FlyBase; FBgn003930; CG11077.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005778; C:peroxisomal membrane; IEA.
DR InterPro; IPR007248; Mpv17_PMP22.
DR Pfam; PF04117; Mpv17_PMP22; 1.
SQ SEQUENCE 168 AA; 19521 MW; 48E216A954E3D359 CRC64;

Query Match 46.8%; Score 50.5; DB 2; Length 168;
Best Local Similarity 64.7%; Pred. No. 10;
Matches 11; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 5 GPTLRQW---LEGRRP 18
Db 54 GPTLRWYHFLSRVPK 70

RESULT 7
Q6LEMS PRELIMINARY; PRT; 256 AA.
ID Q6LEMS
AC O6LEMS;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE Bradykinin-potentiating peptides and C-type natriuretic peptide.
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Venom gland;
RX MEDLINE=97188443; PubMed=9037028; DOI=10.1073/pnas.94.4.1189;
RA Murayama N., Hayashi M., Ohi H., Ferreira L., Hermann V., Saito H.,
RA Fujita Y., Higuchi S., Fernandes B., Yamane T., de Camargo A.;
RT "Cloning and sequence analysis of a Bothrops jararaca cDNA encoding a
precursor of seven bradykinin-potentiating peptides and a C-type
natriuretic peptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:1189-1193(1997).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the natriuretic peptide family.
DR EMBL; D85843; BAA12879.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00710; NATPEPTIDES.
DR Prodom; PD005617; Natr_peptide; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
SQ SEQUENCE 256 AA; 26814 MW; 85BDBA0A9520A45 CRC64;

Query Match 46.8%; Score 50.5; DB 2; Length 256;
Best Local Similarity 45.5%; Pred. No. 16;
Matches 10; Conservative 3; Mismatches 4; Indels 5; Gaps 1;

QY 1 GNADGP-----TLRWLEGRPP 17
Db 86 GRAPGPPIPLTVQQAQGRAP 107

RESULT 8
Q7SLMI PRELIMINARY; PRT; 228 AA.
ID Q7SLMI
AC Q7SLMI;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE Hypothetical protein OSUNBA0047E24.16.
GN Name=OSUNBA0047E24.16;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Taitlin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadriash D.W., Tallon U.J., Koo H., Ziemann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Uteirback T.T., Feldlyum T.V.,
RA Yang Q.O., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092556; AAR87260.1; -.
SQ SEQUENCE 228 AA; 25966 MW; 8B9E7D088D49F5F2 CRC64;

Query Match 46.3%; Score 50; DB 2; Length 228;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 10; Conservative 3; Mismatches 3; Indels 4; Gaps 1;

QY 4 DGPTLR---QMLEGRPPK 19
Db 99 DGNTARFWSAWIDGRPPK 118

RESULT 9

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08T511
ID 08T511      PRELIMINARY;      PRT;      391 AA.
AC 08T511;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Transcription factor.
GN Name=30E5.9;
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=7165;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RX MEDLINE=22056115; PubMed=12060762; DOI=10.1073/pnas.082235599;
RA Thomasova D., Ton L.Q., Copley R.R., Zdobnov E.M., Wang X., Hong Y.S.,
RA Sim C., Bork P., Kafatos F.C., Collins F.H.;
RT "Comparative genomic analysis in the region of a major Plasmodium-
RT reticorin locus of Anopheles gambiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:8179-8184(2002).
DR EMBL; AJ439353; CAD27931.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR008895; Y1L.
DR Pfam; PF05764; Y1L; 1.
SQ SEQUENCE 391 AA; 45110 MW; E3F5D6D396460A37 CRC64;

Query Match      46.3%; Score 50; DB 2; Length 391;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GNADGPTLRWLGR 16
DB 337 GNTDNPVAVRLWWRX 352

RESULT 10
Q7PUW8      PRELIMINARY;      PRT;      391 AA.
ID Q7PUW8;
AC Q7PUW8;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE ENSANGP0000018140.
GN Name=ENSANG00000015651;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008987; EAA00898.2; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR008895; Y1L.
DR Pfam; PF05764; Y1L; 1.
SQ SEQUENCE 391 AA; 45110 MW; E3F5D6D396460A37 CRC64;

Query Match      46.3%; Score 50; DB 2; Length 391;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GNADGPTLRWLGR 16
DB 337 GNTDNPVAVRLWWRX 352

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DB 337 GNTDNPVAVRLWWRX 352

RESULT 11
Q82AY3      PRELIMINARY;      PRT;      242 AA.
ID Q82AY3;
AC Q82AY3;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=SAV5922;
OS Streptomyces avermitilis.
OC Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa U., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa U., Hanamoto A., Takahashi C.,
RA Kikuchi H., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kituchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
DR EMBL; AP005044; BAC73634.1; -.
DR KW Complete proteome.
SQ SEQUENCE 242 AA; 26447 MW; 9D435A8C94401C1C CRC64;

Query Match      45.4%; Score 49; DB 2; Length 242;
Best Local Similarity 72.7%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 LRQWLGRPRK 18
DB 15 ISQWLGRPRK 25

RESULT 12
Q8EUN8      PRELIMINARY;      PRT;      271 AA.
ID Q8EUN8;
AC Q8EUN8;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Predicted choline kinase.
GN OrderedLocustNames=KYP9480;
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HF-2;
RX MEDLINE=22354719; PubMed=1246555; DOI=10.1093/nar/gkf667;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenti T., Furuya K.,
RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
RT "The complete genomic sequence of Mycoplasma penetrans, an
RT intracellular bacterial pathogen in humans.";
RL Nucleic Acids Res. 30:5293-5300(2002).
DR EMBL; AP004174; BAC44735.1; -.
DR HSSP; Q22942; INW1.
DR GO; GO:0016301; F:kinase activity; IEA.

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DR InterPro: IPR002573; Choline_kinase.
 DR InterPro: IPR011009; Kinase_like.
 DR Pfam: PF01633; Choline_kinase; 1.
 KW Complete proteome; Kinase.
 SQ SEQUENCE 271 AA; 33289 MW; CFPADCC9C24247D CRC64;

Query Match 45.4%; Score 49; DB 2; Length 271;
 Best Local Similarity 46.7%; Pred. No. 29;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 DEPTLRQWLEGRRP 18
 DB 81 DGNVIRKRWLEGNPK 95

RESULT 13

ID Q872W6 PRELIMINARY; PRT; 387 AA.

AC Q872W6; 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

GN Hypothetical protein B2G14.020.

OS Name=B2G14.020;

OC Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;

RP SEQUENCE FROM N.A.

RA Schulte U., Algen V., Hehseisel J., Brandt P., Fartmann B., Holland R.,

RA Nyakatura G., Mewes H.W., Mannhaupt G.;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

KW Hypothetical protein.

SQ SEQUENCE 387 AA; 42885 MW; 8C6PE22F50D7599 CRC64;

Query Match 45.4%; Score 49; DB 2; Length 387;
 Best Local Similarity 44.4%; Pred. No. 43;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GNADGPTLRQWLEGRRP 18
 DB 355 GNANGSRVHRWATGROR 372

RESULT 14

ID Q92281 PRELIMINARY; PRT; 531 AA.

AC Q92281; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

GN Hypothetical protein.

OR Names=Smal131;

OS Rhizobium meliloti (Sinorhizobium meliloti).

OG Plasmid pSymA.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.

NCBI_TaxID=382;

RP SEQUENCE FROM N.A.

RC STRAIN=1021;

RA MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;

RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

RA Barlov-Hubler F., Bowser L., Capela L., Galibert F., Gouzy J.,

RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,

RA Kaiman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;

RT "Nucleotide sequence and predicted functions of the entire

RT Sinorhizobium meliloti pSymA megaplasmid.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).

DR EMBL: AE007250; AAK65269.1; -.

DR PIR: C95338; C95338.

DR InterPro: IPR001279; Blactamase-like.

DR InterPro: IPR011108; RMBL.

DR Pfam: PF00753; Lactamase_B; 1.

DR Pfam: PF07521; RMBL; 1.

KW Complete proteome; Hypothetical protein; Plasmid.

SQ SEQUENCE 531 AA; 58948 MW; 93BECTPB167752E1 CRC64;

Query Match 45.4%; Score 49; DB 2; Length 531;
 Best Local Similarity 47.1%; Pred. No. 60;
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 GNADGPTLRQWLEGRRP 17
 DB 407 GNADGSELADWVRARQP 423

RESULT 15

ID O61G99 PRELIMINARY; PRT; 551 AA.

AC O61G99; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

GN Putative 2,3-dihydroxybenzoate-AMP ligase.

OS Name=S0514; Orderedlocustamenes-PBRP1823;

OS Photobacterium profundum (Photobacterium sp. (strain SS9)).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Photobacterium.

NCBI_TaxID=74109;

RP SEQUENCE FROM N.A.

RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,

RA Cestaro A., Malacrida G., Simonati B., Camata N., Bartlett D.,

RA Valle G.;

RT "Genome analysis of Photobacterium profundum reveals the complexity of

RT high pressure adaptations.";

CC Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme

CC family.

DR EMBL: CR378680; CAG23681.1; -.

DR GO: GO:0003824; F: catalytic activity; IEA.

DR GO: GO:0008152; P: metabolism; IEA.

DR InterPro: IPR000873; AMP-bind.

DR Pfam: PF00501; AMP-binding; 1.

DR PROSITE: PS00455; AMP_BINDING; UNKNOWN_1.

KW Complete proteome.

SQ SEQUENCE 551 AA; 60767 MW; B38B9F7A4F4B4BAD CRC64;

Query Match 44.9%; Score 48.5; DB 2; Length 551;
 Best Local Similarity 71.4%; Pred. No. 75;
 Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 2 NADGPTLRQWLEGR 14
 DB 147 NADPTLRHMLVVG 160

RESULT 16

ID Q9NDL7 PRELIMINARY; PRT; 81 AA.

AC Q9NDL7; 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

GN Glyceralddehyde-3-phosphate dehydrogenase (Fragment).

OS Name=GAPDH;

OS Hydra magnipapillata (Hydra).

OC Eukaryota; Metazoa; Chordata; Hydrozoa; Hydrozoa; Anthomedusae;

	OC	Hydriidae; Hydra.
	OX	NCHI_TaxID=6085;
RN	[1]	SEQUENCE FROM N.A.
RP	Mochizuki K.,	
RL	Submitted (JUN-2000) to the EMBL/genbank/DBJ databases.	
CC	-I CATALYTIC ACTIVITY:	D-glycerate dehydrogenase + phosphate + NADH.
CC	-I NA(+) = 3-phospho-D-glyceroyl phosphate + NADH.	
CC	-I PATHWAY:	Second phase of glycolysis, first step.
CC	-I SUBUNIT:	Homoctramer (by similarity).
CC	-I SUBCELLULAR LOCATION:	Cytoplasmic (by similarity).
CC	-I SIMILARITY:	Belongs to the glyceraldehyde-3-phosphate dehydrogenase family.
DR	EMBL:	AB044096 ; BA96506.1 ; - .
DR	HSP,	P06977, IDC3.
DR	GO:	GO:0004365; F:glycerate dehydrogenase (p...); IEA.
DR	GO:	GO:0016491; F:oxalodihydroxyacetate activity; IEA.
DR	InterPro:	IPIR00173; GAP_dhdrogenase.
DR	pfam:	PF02800; Gp_ch_C_1.
DR	pfam:	PF00044; Gp_ch_N_1.
DR	PRINTS:	PR00078; G3PDHDGNASE.
KM	PROSITE:	PS00071; GAPDH, 1.
FT	Glycolysis; NAD;	Oxidoreductase.
PT	NON TER	1
FT	NON TER	81
SQ	SEQUENCE	81 AA; 8577 MW; D3733493PDIJC5OD3 CRC64;
	Query Match	44.4%; Score 48; DB 2; Length 81;
	Best Local Similarity	50.0%; Pred. No. 11;
	Matches	6; Conservative
		5; Mismatches
		1; Indels
		0; Gaps
		0;
OY	4 DEPTROWLEGR 15	::
Db	57 DGFSWKWRDGR 68	
	RESULT 17	
ID	QBHX7	PRELIMINARY; PRT; 129 AA.
AC	QBHX7;	
DT	01-MAR-2003 (TREMREL. 23, Created)	
DT	01-MAR-2003 (TREMREL. 23, Last sequence update)	
DT	01-MAR-2003 (TREMREL. 23, Last annotation update)	
DE	T11816 protein.	
GN	Ordered accession names=T11816;	
OS	Synchococcus elongatus (Thermosynechococcus elongatus).	
OC	Bacteria; Cyanobacteriota; Chroococcales; Synchococcaceae.	
OX	NCHI_TaxID=32046;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BP-1;	
RX	MEDLINE=22225144; PubMed=12240834;	
RA	Nakamura Y., Kaneko T., Sato S., Ikeuchi H., Sasamoto S., Watanabe A., Iriuguchi M., Kawashina K., Kimura T., Kishida Y., Kitayama C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpou S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;	
RT	"Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1."	
RL	DNA Res. 9:123-130 (2002).	
RM	EMBL: AP005375; BAC9368.1; -. Complete proteome.	
SQ	SEQUENCE	129 AA; 14644 MW; EBB4469IE7DDIE12 CRC64;

Query Match	44.4%	Score 48;	DB 2;	Length 129;
Best Local Similarity	75.0%	Pred. NO. 19;		
Matches 9; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

```

QY      1 GNADGPTLRQWL 12
          | | | | |
Db      38 GRAGGATLRQWL 49

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RESULT 18	
09GSF9	
ID	PRELIMINARY; PRF; 139 AA.
AC	09GSF9;
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, last annotation update)
DE	Glyceralddehyde-3-phosphate dehydrogenase (Fragment).
OS	Hydra attenuata (Hydra) (Hydra vulgaris).
OC	Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC	Hydrilia; Hydra.
OX	NCBI_TaxID=6087;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Soderstrom K., De Petrocellis L., Di Marzo V.;
RL	Submitted (SEP-2000) to the EMBL/Genbank/DBS databases.
CC	-1- CATALYTIC ACTIVITY: D-glyceralddehyde 3-phosphate + phosphate +
CC	NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC	-1- PATHWAY: Second phase of glycolysis; first step.
CC	-1- SUBUNIT: Homotetramer (By similarity).
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC	-1- SIMILARITY: Belongs to the glyceralddehyde-3-phosphate
CC	dehydrogenase family.
DR	EMBL; AF307863; AAC29828.1; -.
DR	HSSP; P46406; 110X.
DR	GO; GO:0004365; F:glyceralddehyde-3-phosphate dehydrogenase (p. . .; IEA.
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.
DR	GO; GO:0006096; P:glycolysis; IEA.
DR	InterPro; IPR00173; GAP_dhdrogenase.
DR	Pfam; PF02800; GP_dh_C; 1.
DR	Pfam; PF00044; GP_dh_N; 1.
DR	PRINTS; PR00078; G3PDHDKGNASE.
DR	PROSITE; PS00071; GAPDH; 1.
KW	Glycolysis; NAD; Oxidoreductase.
FT	NON TER 1
FT	NON TER 139
SEQUENCE	139 AA; 14689 MW; 55D8B0F533C1E32A CRC64;

Query Match	44.4%	Score 48;	DB 2;	Length 139;
Best Local Similarity	50.0%	Pred. No. 20;		
Matches	6;	Conservative	5;	Mismatches 1;
				Indels 0;
				Gaps 0
QY	4	DGPTKQWLEGR	15	
Db	62	DGPTKQWLEGR	73	

RESULT 19	
Q6A743	
ID Q6A743	PRELIMINARY; PRT; 161 AA

DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Conserved protein.
GN OrderedLocustNames-PPA1691;
OS Propionibacterium acnes.
OC Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
OC Propionibacteriineae; Propionibacteriaceae; Propionibacterium
OX NCBI_Taxid=1747;

RP SEQUENCE FROM N.A.
RC STRAIN=KPA171202 / DSM 16379;
RX PubMed=15286373; DOI=10.1126/science.1100330;
RA Brueggemann H., Henne A., Hoester F., Liesegang H., Wierer A.,
RT Strittmatter A., Hujer S., Duerre P., Gottschalk G.,
"The complete genome sequence of *Propionibacterium acnes*, a commensal

DR EMBL; AE017283; AAT83422.1; -.
 KW Complete proteome.
 SQ SEQUENCE 161 AA; 17762 MW; 52D0DF0CE1330F0E CRC64;

Query Match 44.4%; Score 48; DB 2; Length 161;
Best Local Similarity 52.9%; Pred. No. 24;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 GNADPTLAWLEGRPP 17
DB 84 GAEDVPTMDPTGRVP 100

RESULT 20

ID Y356_MYCPN STANDARD; PRT; 282 AA.

AC P75246;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein MG356 homolog (G12orf282b).
GN OrderedLocNames=MPN532; ORFNames=MP310;
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
RA Himmelreich R., Hilbert H., Plagens H., Pirkil E., Li B.-C.,
RA Hermann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC
CC EMBL: AEO00028; AAB5958.1; -.
DR PIR; S73636; S73636.
DR InterPro; IPR011009; Kinase like.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 282 AA; 33295 MW; 5662F03B9E06A89A CRC64;

Query Match 44.4%; Score 48; DB 1; Length 282;
Best Local Similarity 42.9%; Pred. No. 43;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 5 GPTLRQWLEGRPP 18
DB 85 GNAIKKWEKOPK 98

RESULT 21

ID Q7XUX8 PRELIMINARY; PRT; 364 AA.

AC Q7XUX8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE OSJNBa0027G07.11 protein.
GN Name=OSJNBa0027G07.11;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,

RA Meng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL; AL662937; CAD40947.1; -.
DR Gramene; Q7XUX8; -.
SQ SEQUENCE 364 AA; 41484 MW; 734879D485FFD13 CRC64;

Query Match 44.4%; Score 48; DB 2; Length 364;
Best Local Similarity 50.0%; Pred. No. 57;
Matches 10; Conservative 3; Mismatches 3; Indels 4; Gaps 1;

QY 4 DGPTLR----QWLEGRPPK 19
DB 166 DGNTVFWESAWIGRRPKD 185

RESULT 22

ID Q6SWR1 PRELIMINARY; PRT; 1023 AA.

AC Q6SWR1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative polypeptide.
GN Name=P0009H09.8;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chang C.-I., Han S.-Y., Hsiao S.-H.,
RA Heiting J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RT "Oryza sativa PAC P0009H09 genomic sequence.";
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC144743; AAU44186.1; -.
KW Polypeptide.
SQ SEQUENCE 1023 AA; 117011 MW; B2D7844463910046 CRC64;

Query Match 44.4%; Score 48; DB 2; Length 1023;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 10; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY 4 DGPTLR----QWLEGRPPK 19
DB 747 DGNTVFWESAWIGRRPKD 766

RESULT 23

ID Q7X5Z1 PRELIMINARY; PRT; 1189 AA.

AC Q7X5Z1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE OSJNBa0006A01.14 protein.
GN Name=OSJNBa0006A01.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.


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OX NCBI_TaxID=39947;
RN
RP SEQUENCE FROM N.A.
RX PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL; AL715179; CAD41559.2; -.
DR Gramene; 07X521; -.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003664; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR005135; Exo_endo_phos.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF03372; Exo_endo_phos; 1.
DR Pfam; PF00078; RVT_1; 1.
DR KMA-directed DNA polymerase; Transferase.
SQ SEQUENCE 1189 AA; 135959 MW; 441C5E4B0BDF2643 CRC64;

Query Match 44.4%; Score 48; DB 2; Length 1189;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 10; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

Qy 4 DGPTLR----QMLEGRPRPKN 19
|||
913 DGNTRFWDMSAMINGRRPKD 932

RESULT 24
Q7UR10 PRELIMINARY; PRT; 264 AA.
ID 07UR10
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=RB5963;
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schleuter H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
RW EMBL; BX294143; CAD74532.1; -.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 264 AA; 29816 MW; 932AF9B90DC59C19 CRC64;

Query Match 44.0%; Score 47.5; DB 2; Length 264;
Best Local Similarity 43.5%; Pred. No. 48;
Matches 10; Conservative 2; Mismatches 6; Indels 5; Gaps 1;

Qy 2 NADGP-----TLRQMLEGRPRPKN 19
|||
205 NLDSPKTKAKRIKRTMLEBHRPN 227

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RESULT 25
Q9NDL8 PRELIMINARY; PRT; 81 AA.
ID Q9NDL8
AC Q9NDL8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
GN Name=GAPDH;
OS Tima formosa.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
OC Eumimidae; Tima.
OX NCBI_TaxID=128134;
RN
RP SEQUENCE FROM N.A.
RA Mochizuki K.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC -1- PATHWAY: Second phase of glycolysis; first step.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the glyceraldehyde-3-phosphate
CC dehydrogenase family.
DR EMBL; AB044098; BA96508.1; -.
DR HSSP; P06977; IDC3.
DR GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. .; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR001073; GAP_dhdrogenase.
DR Pfam; PF02800; Gp_dh_C1.
DR Pfam; PF00044; Gp_dh_N1.
DR PRINTS; PR00078; G3PDHGNASE.
DR PROSITE; PS00071; GAPDH_1.
KW Glycolysis; NAD; Oxidoreductase.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 81 AA; 8499 MW; 32D2FFCA3C6D1C23 CRC64;

Query Match 43.5%; Score 47; DB 2; Length 81;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 4 DGPTLRQMLEGR 15
|||
57 DGPSMKKKRDRGR 68

RESULT 26
Q9NDL8 PRELIMINARY; PRT; 81 AA.
ID Q9NDL8
AC Q9NDL8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
GN Name=GAPDH;
OS Hydractinia echinata (Snail fur).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydractiniidae; Hydractinia.
OX NCBI_TaxID=35630;
RN
RP SEQUENCE FROM N.A.
RA Mochizuki K.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC -1- PATHWAY: Second phase of glycolysis; first step.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the glyceraldehyde-3-phosphate
CC dehydrogenase family.

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DR EMBL; AB044095; BAA96505.1; -.
DR HSSP; P46406; 1J0X.
DR GO; GO:0004365; F:glyceralddehyde-3-phosphate dehydrogenase (p. . .; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR001173; GAP_dhhdhogenase.
DR Pfam; PF02800; GP_dh_C1.
DR Pfam; PF00044; GP_dh_N1.
DR PRINTS; PR00078; G3PDHGRGNASE.
DR PROSITE; PS00071; GAPDH; 1.
KM Glycolysis; NAD; Oxidoreductase.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 8553 MW; AB14ED2546DCFPAB2 CRC64;

Query Match 43.5%; Score 47; DB 2; Length 81;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 DGPTLRQWLEGR 15
Db 57 DGPSMKKWRDGR 68
||||:|:|:|

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RESULT 27
Q9NDL9 PRELIMINARY; PRT; 81 AA.
ID Q9NDL9
AC Q9NDL9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Glyceralddehyde-3-phosphate dehydrogenase (Fragment).
GN Name=GAPDH;
OS Eirene sp. EML1.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Leptomedusae;
OC Campanuliniidae; Eirene.
OX NCBI_TaxID=128129;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EM11;
RC Mochizuki K.;
RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
CC NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
CC -1- PATHWAY: Second phase of glycolysis; first step.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the glyceralddehyde-3-phosphate
CC dehydrogenase family.
DR EMBL; AB044094; BAA96504.1; -.
DR HSSP; P06977; 1DC3.
DR GO; GO:0004365; F:glyceralddehyde-3-phosphate dehydrogenase (p. . .; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR001173; GAP_dhhdhogenase.
DR Pfam; PF02800; GP_dh_C1.
DR Pfam; PF00044; GP_dh_N1.
DR PRINTS; PR00078; G3PDHGRGNASE.
DR PROSITE; PS00071; GAPDH; 1.
KM Glycolysis; NAD; Oxidoreductase.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 8521 MW; D88CCF28614DBF5D CRC64;

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Query Match 43.5%; Score 47; DB 2; Length 81;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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QY 4 DGPTLRQWLEGR 15
Db 57 DGPSMKKWRDGR 68
||||:|:|:|

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RESULT 28
O87645 PRELIMINARY; PRT; 133 AA.
ID O87645
AC O87645;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Putative periplasmic protein.
OS Methylococcus capsulatus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
OC Methylococcaceae; Methylococcus.
OX NCBI_TaxID=414;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bath;
RC MEDLINE=99069315; PubMed=9851984;
RA Bergmann D.J., Zahn J.A., Hooper A.B., Dispirito A.A.;
RT "Cycochrome P460 genes from the methanotroph Methylococcus capsulatus
RT bath.";
RL J. Bacteriol. 180:6440-6445(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bath;
RA Bergmann D.B., Zahn J.A., Hooper A.B., Dispirito A.A.;
RA Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF091435; AAD03547.1; -. 89F6ED27D82959BA CRC64;
SQ SEQUENCE 133 AA; 14319 MW; 89F6ED27D82959BA CRC64;

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Query Match 43.5%; Score 47; DB 2; Length 133;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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QY 2 NADGPTLRQWLEGR 15
Db 63 NTDGATIKIWDGK 76
||||:|:|:|

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RESULT 29
Q93KY0 PRELIMINARY; PRT; 181 AA.
ID Q93KY0
AC Q93KY0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE AVIX5.
GN Name=avix5;
OS Streptomyces viridochromogenes.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1938;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Thes7;
RC MEDLINE=21303144; PubMed=11410376; DOI=10.1016/S1074-5521(01)00040-0;
RA Weitauer G., Muhlenweg A., Treffer A., Hoffmeister D., Susmuth R.D.,
RA Jung G., Weizel K., Vente A., Girsner U., Bechthold A.;
RT "Biosynthesis of the orthosomycin antibiotic avilamycin A: deductions
RT from the molecular analysis of the avl biosynthetic gene cluster of
RT Streptomyces viridochromogenes Tu57 and production of new
RT antibiotics.";
RL Chem. Biol. 8:569-581(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Thes7;
RA Mosbacher T., Weitauer G., Bechthold A., Schulz G.B.;
RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF33038; AAK83165.1; -. 6255D67625EAE6E CRC64;
SQ SEQUENCE 181 AA; 19999 MW; 6255D67625EAE6E CRC64;

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Query Match 43.5%; Score 47; DB 2; Length 181;
Best Local Similarity 45.0%; Pred. No. 39;
Matches 9; Conservative 4; Mismatches 3; Indels 4; Gaps 1;

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OY 2 NADGPTLRQWEG-----RRP 17
 DB 147 DADDPVSEWARGDPRTTRP 166

RESULT 30

ID12_PYPRAE STANDARD; PRT; 352 AA.
 AC Q82YF6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE (Isopentenyl)-diphosphate delta-isomerase (EC 5.3.3.2) (IPP isomerase)
 DE (Isopentenyl) pyrophosphate isomerase.
 GN Name=Enl; OrderedLocustNames=PAE0801;
 OS Pyrobaculum aerophilum.
 OC Archaeae; Crenarchaeota; Thermoprotei; Thermoproteales;
 CC Thermoproteaceae; Pyrobaculum.
 CX NCBI_TaxID=13773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
 RA Miller J.H.;
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 aerophilum.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
 CC -1- FUNCTION: Catalyzes the 1,3-allylic rearrangement of the
 homomallylic substrate isopentenyl (IPP) to its allylic isomer,
 dimethylallyl diphosphate (DMAPP) (By similarity).
 CC -1- CATALYTIC ACTIVITY: Isopentenyl diphosphate = dimethylallyl
 diphosphate.
 CC -1- COFACTOR: FMN and NADPH (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the IPP isomerase type 2 family.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AE009786; AAL63037.1; -
 DR HSSP; P50740; 1POK. -
 DR HAMAP; MF_00354; -; 1.
 DR InterPro; IPR003009; FMN_enzyme.
 DR InterPro; IPR011179; IPDP_isomerase.
 DR PIRSF; PIRSF003314; IPP_isomerase; 1.
 KW Complete proteome; Flavoprotein; FMN; Isomerase;
 KW Isoprene biosynthesis; NADP;
 SQ SEQUENCE 352 AA; 37966 MW; 684253886324C04 CRC64;

Query Match 43.5%; Score 47; DB 1; Length 352;
 Best Local Similarity 66.7%; Pred. No. 79;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 GPTLRQWEGRR 16
 DB 338 GPRLNWTEORR 349

RESULT 31

ID Q6FXT5 PRELIMINARY; PRT; 452 AA.
 AC Q6FXT5;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Similar to gp134221 Saccharomyces cerevisiae YBL056w PTC3.
 GN ORFNames=CAGLOA043019;

OS Candida glabrata CBS138.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; microsporid Saccharomycetales; Candida.
 CX NCBI_TaxID=284593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casarogla S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangul I., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissarie A., Boyer J., Cartolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Gropi A.,
 RA Hantre F., Hemequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerret A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicoud J.M., Nikolaki M., Oztas S., Ozer-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straud M.L., Suleau A.,
 RA Swenne D., Tekala F., Wesolowski-Louvel M., Weathof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 DR EMBL; CR380947; CAG57847.1; -
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR InterPro; IPR002222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS01032; PP2C; UNKNOWN 1.
 SQ SEQUENCE 452 AA; 48881 MW; EBF9E25621E3315D CRC64;

Query Match 43.5%; Score 47; DB 2; Length 452;
 Best Local Similarity 56.2%; Pred. No. 1e+02;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4 DGPTLRQWEGRRPKN 19
 DB 296 DSFTLEQWFERMRAXN 311

RESULT 32

ID Q9P729 PRELIMINARY; PRT; 571 AA.
 AC Q9P729;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Probable histone acetyltransferase.
 GN Name=BD4.110;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetiales; Sordariales; Sordariaceae; Neurospora.
 CX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hehseisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Manhaupt G.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL353819; CAB88553.1; -
 DR PIR; T48737; T48737.
 DR GO; GO:0016459; C:proton-transporting two-sector ATPase complex; IEA.
 DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.
 DR GO; GO:0046961; F:hydrogen-transporting ATP synthase activity, rota. . .; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.

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DR InterPro: IPR000793; ATPase_a/b_C.
DR InterPro: IPR006638; ELP3/MAB/NiFB.
DR InterPro: IPR005910; ELP3_Ac_trans.
DR InterPro: IPR000182; GCN5acetyl_trans.
DR InterPro: IPR007197; Radical_SAM.
DR Pfam: PF00583; Acetyltransferase_1.
DR Pfam: PF04055; Radical_SAM; 1.
DR SMART: SM00729; ELP3; 1.
DR TIGRFAMs: TIGR01211; ELP3; 1.
DR Transferrase.
SQ SEQUENCE 571 AA; 64684 MW; 3A36C5900C2BCAD6 CRC64;

Query Match 43.5%; Score 47; DB 2; Length 571;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DGPFTROWLEGR 15
Db 555 DGPFTSKMDGR 566

RESULT 33
2445 MOUSE
ID _2445_MOUSE STANDARD; PRT; 986 AA.
AC QGR2Y3; QGR216;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Zinc finger protein 445.
GN Name=Znf445;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J;
RA Zhou G., Wang J., Zhang Y.;
RT "Cloning of mouse zinc finger protein 445.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 345-986 FROM N.A.
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulysk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson W.C.;
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: May be involved in transcriptional regulation.
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- SIMILARITY: Belongs to the Krueppel C2H2-type zinc-finger protein
CC family.
CC -1- SIMILARITY: Contains 12 C2H2-type zinc fingers.
CC -1- SIMILARITY: Contains 1 KRAB domain.
CC -1- SIMILARITY: Contains 1 SCAN box domain.
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CC -----
DR EMBL: AY341877; AA024161.1; -.
DR EMBL: BC027167; AAH27167.1; -.
DR EMBL: BC034572; AAH34572.1; ALT_INIT.
DR MGD: MGI:2143340; AW610627.
DR InterPro: IPR001909; KRAB.
DR InterPro: IPR003309; Treg_SCAN.
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF01352; KRAB; 1.
DR Pfam: PF02023; SCAN; 1.
DR Pfam: PF00096; zf-C2H2; 12.
DR ProDom: PD000003; Znf_C2H2; 6.
DR SMART: SM00431; LER; 1.
DR SMART: SM00355; ZNF_C2H2; 12.
DR PROSITE: PS50805; KRAB; 1.
DR PROSITE: PS50804; SCAN_BOX; 1.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 12.
DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 12.
KW DNA-binding; Metal-binding; Nuclear protein; Repeat;
KW Transcription regulation; Zinc-finger.
FT DOMAIN 52 134
FT ZN_FING 219 289
FT ZN_FING 470 492
FT ZN_FING 498 520
FT ZN_FING 553 575
FT ZN_FING 581 604
FT ZN_FING 634 656
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FT ZN_FING 6903 6925
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RA Miranda A., Mungall C.J., Munoz J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY118408; AAA48437.1; -.
DR FlyBase: FBgn0035879; CG7112.
DR InterPro: IPR011036; PH related.
DR InterPro: IPR00195; RabGAP_TBC.
DR Pfam: PF00566; TBC; 1.
DR SMART: SM00164; TBC; 1.
DR PROSITE: PSS0086; TBC_RABGAP; 1.
SQ SEQUENCE 1005 AA; 113317 MW; 58C70A8326D2073A CRC64;

Query Match 43.5%; Score 47; DB 2; Length 1005;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 PTLRWLEGRPPK 19
Db 496 PILEWDESKRPKN 509

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Q9VSI2 PRELIMINARY; PRT; 1005 AA.
ID Q9VSI2
AC Q9VSI2
DT 01-MAY-2000 (TREMBLrel. 13; Created)
DT 01-OCT-2002 (TREMBLrel. 22; Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)
DE CG7112-PA
GN ORFNames=CG7112;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
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RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaratunga P.G., Scherer S.E., Li P.W., Hoekli R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blaise J.R.G., Champe M., Pfeiffer B.D.,
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RA Abell J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
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RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
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RA Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

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RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537572;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svrtkask R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.B., Myers R.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537572;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svrtkask R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003555; AAF50437.2; -.
DR FlyBase: FBgn0035879; CG7112.
DR InterPro: IPR011036; PH related.
DR InterPro: IPR00195; RabGAP_TBC.
DR Pfam: PF00566; TBC; 1.
DR SMART: SM00164; TBC; 1.
DR PROSITE: PSS0086; TBC_RABGAP; 1.
SQ SEQUENCE 1005 AA; 113287 MW; 59DF5B4F840E2A55 CRC64;

Query Match 43.5%; Score 47; DB 2; Length 1005;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 PTLRWLEGRPPK 19
Db 496 PILEWDESKRPKN 509

RESULT 36
Q9P3E2 PRELIMINARY; PRT; 1171 AA.
ID Q9P3E2
AC Q9P3E2
DT 01-OCT-2000 (TREMBLrel. 15; Created)
DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)
DE Related to transport protein USO1.
GN Name=B13118.10;

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OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Algen V., Hehseisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390189; CAB99171.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006866; P:intracellular protein transport; IEA.
DR GO; GO:0006938; ARM.
DR InterPro; IPR006955; Usol_p115_C.
DR InterPro; IPR006953; Usol_p115_head.
DR Pfam; PF04871; Usol_p115_C; 1.
DR Pfam; PF04869; Usol_p115_head; 1.
SQ SEQUENCE 1171 AA; 131632 MW; 33DF50E5931ED060 CRC64;

Query Match 43.5%; Score 47; DB 2; Length 1171;
Best Local Similarity 42.1%; Pred. No. 2.9e+02;
Matches 8; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 GNADGPTLRWLERRRKN 19
DB 259 GSTDGEVAAQWAEORNRN 277

RESULT 37
Q9LIW0 PRELIMINARY; PRT; 522 AA.
AC Q9LIW0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Similar to an Arabidopsis thaliana chromosome BAC genomic
DE sequence.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Hsing Y.C., Chow T., Chen C., Wu H., Chu M., Chao Y., Liu S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001111; BAA90509.1; -.
DR Q9LIW0; -.
SQ SEQUENCE 522 AA; 54697 MW; 21C6BAD2441B56BF CRC64;

Query Match 43.1%; Score 46.5; DB 2; Length 522;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 5; Gaps 3;

QY 1 GNADG---PTLRWL-EGRR 17
DB 452 GVADGCIWPA-RQWLREGRRP 471

RESULT 38
EP42 HUMAN STANDARD; PRT; 690 AA.
AC P16452;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Erythrocyte membrane protein band 4.2 (Erythrocyte protein 4.2)

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```

DE (P4.2).
GN Name=EP42; Synonyms=E42P;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC TISSUE=Reticulocytes;
RA MEDLINE=91271288; PubMed=2052563;
RX Korsgren C., Cohen C.M.;
RT "Organization of the gene for human erythrocyte membrane protein 4.2: structural similarities with the gene for the a subunit of factor XIII."
RL Proc. Natl. Acad. Sci. U.S.A. 88:4840-4844(1991).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM SHORT).
RC TISSUE=Reticulocytes;
RA MEDLINE=90138079; PubMed=2300550;
RX Korsgren C., Lawler J., Lambert S., Speicher D., Cohen C.M.;
RT "Complete amino acid sequence and homologues of human erythrocyte membrane protein band 4.2."
RL Proc. Natl. Acad. Sci. U.S.A. 87:613-617(1990).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC TISSUE=Reticulocytes;
RA MEDLINE=90138995; PubMed=1689063;
RX Sung L.A., Chien S., Chang L.-S., Lambert K., Bliss S.A.,
RA Buhassasira E.E., Nagel R.L., Schwartz R.S., Rydicki A.C.;
RT "Molecular cloning of human protein 4.2: a major component of the erythrocyte membrane."
RL Proc. Natl. Acad. Sci. U.S.A. 87:955-959(1990).
RN [4]
RP MYRISTOYLATION.
RX MEDLINE=92184834; PubMed=1544941;
RA Risinger M.A., Docimas E.M., Cohen C.M.;
RT "Human erythrocyte protein 4.2, a high copy number membrane protein, is N-myristylated."
RL J. Biol. Chem. 267:5680-5685(1992).
RN [5]
RP PHOSPHORYLATION SITE SER-247.
RX MEDLINE=93271204; PubMed=8499466; DOI=10.1016/0005-2736(93)90156-T;
RA Docimas E., Speicher D.W., Guptaroy B., Cohen C.M.;
RT "Structural domain mapping and phosphorylation of human erythrocyte pallidin (band 4.2)."
RL Biochim. Biophys. Acta 1148:19-29(1993).
RN [6]
RP VARIANT HS THR-111.
RX MEDLINE=92216098; PubMed=1558976;
RA Buhassasira E.E., Schwartz R.S., Yawata Y., Ata K., Kanazaki A.,
RA Qiu J.J.-H., Nagel R.L., Rydicki A.C.;
RT "An alanine-to-threonine substitution in protein 4.2 cDNA is associated with a Japanese form of hereditary hemolytic anemia (protein 4.2 Nippon)."
RL Blood 79:1846-1854(1992).
RN [7]
RP VARIANT HS THR-111.
RX MEDLINE=95118828; PubMed=7819064;
RA Takeaka Y., Ideguchi H., Matsuda M., Sakamoto N., Takeuchi T.,
RA Fukunaki Y.;
RT "A novel mutation in the erythrocyte protein 4.2 gene of Japanese patients with hereditary spherocytosis (protein 4.2 Fukuoka)."
RL Br. J. Haematol. 88:527-533(1994).
RN [8]
RP VARIANT HS GLN-279.
RX MEDLINE=95290393; PubMed=7772513;
RA Hayette S., Morle L., Bozon M., Ghanem A., Risinger M., Korsgren C.,
RA Tanner M.J.A., Fatoum S., Cohen C.M., Delaunay J.;
RT "A point mutation in the protein 4.2 gene (allele 4.2 Tozeur) associated with hereditary haemolytic anaemia."
RL Br. J. Haematol. 89:762-770(1995).
CC -!- FUNCTION: Probably plays an important role in the regulation of erythrocyte shape and mechanical properties.

```

CC -1- SUBUNIT: Oligomer. Interacts with the cytoplasmic domain of
 CC SLC4A1/band 3 anion transport protein.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated (cytoplasmic surface of
 CC erythrocyte membranes) and cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name-Short;
 CC IsoId=P16452-1; Sequence=Displayed;
 CC Note=Major isoform;
 CC Name=Long;
 CC IsoId=P16452-2; Sequence=VSP_006416;
 CC -1- PFM: Both cAMP-dependent kinase (CAK) and another kinase present
 CC in the red blood cells seem to be able to phosphorylate EPR42.
 CC -1- DISEASE: Defects in EPR42 are a cause of hereditary spherocytosis
 CC (HS) [MIM:177070], a hematologic disorder leading to chronic
 CC hemolytic anemia and characterized by numerous abnormally shaped
 CC erythrocytes which are generally spheroidal. Absence of band 4.2
 CC associated with spur or target erythrocytes has also been
 CC reported.
 CC -1- MISCELLANEOUS: The substitution of an Ala for a Cys in the active
 CC site may be responsible for the lack of transglutaminase activity
 CC of band 4.2.
 CC -1- SIMILARITY: Belongs to the transglutaminase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; M60298; AAA74589.1; -;
 DR EMBL; L06519; AAA52385.1; -;
 DR EMBL; L06447; AAA52385.1; JOINED.
 DR EMBL; L06448; AAA52385.1; JOINED.
 DR EMBL; L06449; AAA52385.1; JOINED.
 DR EMBL; L06450; AAA52385.1; JOINED.
 DR EMBL; L06512; AAA52385.1; JOINED.
 DR EMBL; L06511; AAA52385.1; JOINED.
 DR EMBL; L06513; AAA52385.1; JOINED.
 DR EMBL; L06515; AAA52385.1; JOINED.
 DR EMBL; L06516; AAA52385.1; JOINED.
 DR EMBL; L06517; AAA52385.1; JOINED.
 DR EMBL; L06518; AAA52385.1; JOINED.
 DR EMBL; M29399; AAA5798.1; -;
 DR EMBL; M30646; AAA56402.1; -;
 DR EMBL; M30647; AAA56401.1; -;
 DR PIR; A39707; A39707.
 DR HSSP; P52181; 1GOD.
 DR Genew; HGNC:3381; EPR42.
 DR MIM; 177070; -;
 DR GO; GO:0005856; C:cytoskeleton; TAS.
 DR GO; GO:0005866; C:plasma membrane; TAS.
 DR GO; GO:0005524; F:ATP binding; TAS.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; TAS.
 DR InterPro; IPR001102; Glutansf.
 DR InterPro; IPR008958; Transglut C.
 DR InterPro; IPR002931; Transglutase_1like.
 DR Pfam; PF00927; Transglut C_2.
 DR Pfam; PF01841; Transglut_core; 1.
 DR Pfam; PF00868; Transglut_N; 1.
 DR PROSITE; PS00547; TRANSGLUTAMINASES; 1.
 KW Alternative splicing; Cell shape; Cytoskeleton;
 KW Direct protein sequencing; Disease mutation; Erythrocyte maturation;
 KW Hereditary hemolytic anemia; Lipoprotein; Myristate; Phosphorylation;
 KW Structural protein.
 KM INIT_MET 0
 FT SITE 30 38 By similarity. (By similarity).
 FT LIPID 1 1 N-myristoyl glycine.
 FT MOD_RES 247 247 Phosphoserine (by PKA) (probable).
 FT VARSPLIC 2 2 Q->QGRPSQSTGLAGLYAAPAASPVFKSGMD (in
 FT isoform Long).

FT VARIANT 111 111 /FTId=VSP_006416.
 FT FT A->T (in HS; Nippon/FukuoKa).
 FT VARIANT 279 279 /FTId=VAR_007482.
 FT FT R->Q (in HS; Tozeur).
 FT CONFLICT 334 339 /FTId=VAR_012268.
 FT CONFLICT 349 349 TRPALP->KRGIPC (in Ref. 3).
 FT CONFLICT 375 375 D->H (in Ref. 3).
 FT CONFLICT 375 375 V->L (in Ref. 3).
 SQ SEQUENCE 690 AA; 76841 MW; C6E605E59A0A7A8B CRC64;
 Query Match 43.1%; Score 46.5; DB 1; Length 690;
 Best Local Similarity 76.9%; Pred. No. 1.9e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 6 PTLRQMLEGR-RP 17
 Db 249 PILRQWLTRGRP 261
 PTLRQMLEGR-RP 17
 PILRQWLTRGRP 261
 RESULT 39
 Q95QV6 PRELIMINARY; PRT; 103 AA.
 ID Q95QV6
 AC Q95QV6; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hypothetical protein C18A3.5.
 GN Name=C18A3.5; ORFNames=C18A3.5;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditidae;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 CX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG Wormbase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Hallsworth K.;
 RT "The sequence of C. elegans cosmid C18A3.";
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG Wormbase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U28944; AK68193.1; -;
 DR Wormbase; WbGene00015943; C18A3.5.
 DR WormPep; C18A3.5c; CE27710.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF00076; RRM_1; 1.
 DR PROSITE; PS0102; RRM; 1.
 KW Hypothetical protein.

SQ SEQUENCE 103 AA; 11420 MW; 6D3A1877857E5E64 CRC64;

Query Match 42.6%; Score 46; DB 2; Length 103;

Best Local Similarity 72.7%; Pred. No. 30;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GNADGPTLRQW 11
|||
92 GNQSTPTLRQW 102

RESULT 40

Q9NMW3 PRELIMINARY; PRT; 157 AA.

AC Q9NMW3; (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, last sequence update)
DE 01-OCT-2002 (T-EMBLrel. 22, last annotation update)
DE Hypothetical protein FLJ10043.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NC NCBL_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obaraishi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimura M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano Y.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musahiro K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunaga H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaishi T., Oyama N., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Maeno H., Yamashita R.,
RA Nakai K., Tada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RA RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL: AK009095; BAA91418.1; --
SQ SEQUENCE 157 AA; 17352 MW; 2B1C9C747758C2D23 CRC64;

Query Match 42.6%; Score 46; DB 2; Length 157;
Best Local Similarity 61.5%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 PTLRQWLEGRPK 18
|||||
Db 15 PTLRQWVTRRRP 27

RESULT 41
Q9RKRP9 PRELIMINARY; PRT; 243 AA.

AC Q9RKRP9; (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, last annotation update)
DE Hypothetical protein SCO2279.
GN ORFNames=SCC75A.25c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
NC NCBL_Taxid=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=1200953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.B., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrrell B.G., Parkhill J.,
RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)";
RL Nature 417:141-147(2002).
DR EMBL; AL939112; CAB61725.1; --
RX PIR; T50588; T50588.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 243 AA; 26559 MW; 13584D7A81A0EF90 CRC64;

Query Match 42.6%; Score 46; DB 2; Length 243;
Best Local Similarity 72.7%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 LKQWLEGRPK 18
|||||
Db 15 LSSWLEGRPK 25

RESULT 42
Q8W2V0 PRELIMINARY; PRT; 249 AA.

AC Q8W2V0; Q7XFP3; (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 27, last annotation update)
DE 05-JUL-2004 (T-EMBLrel. 27, last annotation update)
DE Hypothetical protein OSJNB0076H04.22 (Putative reverse
DE transcriptase).
GN Name=OSJNB0076H04.22; ORFNames=OSJNB0022D10.9;
OS Oryza sativa (japanese cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriarthridae; Oryzaceae; Oryza.
NC NCBL_Taxid=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC Buell C.R., Yuan Q., Cuyang S., Liu J., Moffet K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shwartsbeyn M.,
RA Teitlin T., Riggs F., Hsiao J., Ziemann V., Blunt S., Pai G.,
RA Vanaken S.E., Utterback T.R., Feldlyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.,
RN Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC Buell R.;

RP Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA "The Rice Chromosome 10 Sequencing Consortium;
RT In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569(2003).


```

RN (4)
RP SEQUENCE FROM N.A.
RA Buehl C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC093093; AL58152.1; -
DR EMBL; AB01082; AAP53273.1; -
DR Gramene; O7XFE3; -
DR Gramene; O8W2V0; -
DR GO; GO:0003964; P:RNA-directed DNA polymerase activity; IEA.
KM Hypothetical protein; RNA-directed DNA polymerase.
SQ SEQUENCE 249 AA; 28243 MW; 05E3D2406DFAB7CF CRC64;

Query Match 42.6%; Score 46; DB 2; Length 249;
Best Local Similarity 45.0%; Pred. NO. 77;
Matches 9; Conservative 4; Mismatches 3; Indels 4; Gaps 1;

Cy 4 DGPTLR---QWLGRRPRXN 19
Db 120 DGNTRFWDSAMIDGRRPKD 139

RESULT 43
07G731 PRELIMINARY; PRT; 249 AA.
AC 07G731;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)
DE Putative reverse transcriptase.
GN Name=OSJNB0022D10.9;
OS Oryza sativa (Rice)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriocarotaceae; Oryzae; Oryza.
OC NCB1_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
RA Saeki C., Henry D., Oates R., Simmons J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC093402; AAL79345.1; -
DR GO; GO:0003964; P:RNA-directed DNA polymerase activity; IEA.
KM RNA-directed DNA polymerase.
SQ SEQUENCE 249 AA; 28243 MW; 05E3D2406DFAB7CF CRC64;

Query Match 42.6%; Score 46; DB 2; Length 249;
Best Local Similarity 45.0%; Pred. NO. 77;
Matches 9; Conservative 4; Mismatches 3; Indels 4; Gaps 1;

Cy 4 DGPTLR---QWLGRRPRXN 19
Db 120 DGNTRFWDSAMIDGRRPKD 139

RESULT 44
09S1Q2 PRELIMINARY; PRT; 357 AA.
AC 09S1Q2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein SC00239.
GN ORFNames=SCJ9A.18c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OC NCB1_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=A3(12) / M145;
RC MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bertley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
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RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Gobie A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajadream M.A., Rutherford K.M., Ruter S., Taylor K.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wetzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)." (2002).
RL Nature 417:141-147(2002).
DR EMBL; AL939104; CAB53279.1; -
DR PIR; T37154; T37154.
DR InterPro; IPR011009; Kinase like.
DR Complete proteome; Hypothetical protein.
KM SEQUENCE 357 AA; 39139 MW; 731696F25D03B4AF CRC64;

Query Match 42.6%; Score 46; DB 2; Length 357;
Best Local Similarity 41.2%; Pred. NO. 1.1e+02;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Cy 1 GNADGPTLRQWLGRRP 17
Db 290 GTERGARLRWDGHP 306

RESULT 45
082Q03 PRELIMINARY; PRT; 362 AA.
AC 082Q03;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative regulatory protein.
GN OrderedLocNames=SAV472;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OC NCB1_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=MA-4680;
RC MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=MA-4680;
RC MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005023; BAC68182.1; -
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000005; HTHArac.
DR Pfam; PF00165; HTH_Arac; 1.
DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
KM Complete proteome; DNA-binding; Transcription;
KM Transcription regulation.
SQ SEQUENCE 362 AA; 39245 MW; 4D3162C6E6A56CA0 CRC64;

Query Match 42.6%; Score 46; DB 2; Length 362;
Best Local Similarity 50.0%; Pred. NO. 1.1e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

Qy	3	ADGPTLRQWLEGRPK	18
	:	:	:
Db	117	AEGETVNGWIRGRRLK	132

Search completed: September 1, 2005, 16:21:01
Job time : 75.6691 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:02 ; Search time 87.3453 Seconds
(without alignments)
84.131 Million cell updates/sec

Title: US-10-083-768-8

Perfect score: 114

Sequence: 1 GGCAADGPTLRKRWISFCGK 19

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: A_Geneseq_16Dec04:*
2: geneeqp19808:*
3: geneeqp19908:*
4: geneeqp20008:*
5: geneeqp20018:*
6: geneeqp20028:*
7: geneeqp20038:*
8: geneeqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	19	2	AAW09458 Thrombopo
2	114	100.0	19	2	AAW33025 Thrombopo
3	114	100.0	19	4	AAU25822 Human thr
4	109	95.6	18	2	AAW09456 Thrombopo
5	109	95.6	18	2	AAW33023 Thrombopo
6	109	95.6	18	3	AAU25820 Human thr
7	109	95.6	18	4	AAU25820 Human thr
8	109	95.6	18	5	ABW72906 TPO mimet
9	109	95.6	18	5	ABW72906 TPO mimet
10	109	95.6	18	8	ADJ52693 CHI delet
11	109	95.6	18	8	ADJ52693 CHI delet
12	109	95.6	18	8	ADJ52693 CHI delet
13	109	95.6	18	8	ADJ52693 CHI delet
14	109	95.6	18	8	ADJ52693 CHI delet
15	109	95.6	18	8	ADJ52693 CHI delet
16	109	95.6	18	8	ADJ52693 CHI delet
17	109	95.6	18	8	ADJ52693 CHI delet
18	109	95.6	18	8	ADJ52693 CHI delet
19	109	95.6	18	8	ADJ52693 CHI delet
20	109	95.6	18	8	ADJ52693 CHI delet
21	109	95.6	18	8	ADJ52693 CHI delet
22	109	95.6	18	8	ADJ52693 CHI delet
23	109	95.6	18	8	ADJ52693 CHI delet
24	109	95.6	18	8	ADJ52693 CHI delet
25	109	95.6	18	8	ADJ52693 CHI delet

26	85	74.6	14	4	AAU25866
27	85	74.6	14	5	ABW72900
28	85	74.6	14	7	ADJ73051
29	85	74.6	14	8	ADJ52686
30	85	74.6	14	8	ADJ51647
31	76	66.7	13	2	AAW09467
32	76	66.7	13	2	AAW35399
33	76	66.7	13	2	AAW35417
34	76	66.7	13	2	AAW33033
35	76	66.7	13	2	AAW35413
36	76	66.7	13	2	AAW35406
37	76	66.7	13	2	AAW35422
38	76	66.7	13	2	AAW35397
39	76	66.7	13	4	AAU25997
40	76	66.7	13	4	AAU25984
41	76	66.7	13	4	AAW35398
42	76	66.7	14	2	AAW35396
43	76	66.7	14	2	AAW35402
44	76	66.7	14	4	AAU25987
45	76	66.7	14	4	AAU25983
46	76	66.7	14	4	AAU25985
47	72	63.2	12	2	AAW35423
48	72	63.2	12	2	AAU26000
49	67	58.8	13	2	AAW35404
50	67	58.8	13	2	AAW35405
51	67	58.8	13	4	AAU25994
52	67	58.8	13	4	AAU25991
53	67	58.8	13	4	AAU25990
54	67	58.8	14	2	AAW35412
55	67	58.8	14	2	AAW35407
56	67	58.8	14	2	AAW35408
57	67	58.8	14	2	AAW35403
58	67	58.8	14	2	AAU25993
59	67	58.8	14	4	AAU25989
60	67	58.8	14	4	AAU25995
61	67	58.8	14	4	AAU25992
62	67	58.8	14	4	AAU25986
63	67	58.8	14	4	AAU25988
64	67	58.8	25	4	AAU26042
65	67	58.8	25	8	ADW72531
66	66	57.9	11	2	AAW35425
67	66	57.9	11	4	AAU26001
68	66	57.9	25	7	ADN59740
69	65	57.0	13	4	AAU26041
70	64	56.1	14	3	AAU26041
71	64	56.1	14	5	ABW72903
72	64	56.1	14	8	ADJ52689
73	64	56.1	14	8	ADJ51650
74	60	52.6	10	2	AAW35427
75	60	52.6	10	4	AAU26002
76	60	52.6	18	7	ADN59680
77	59	51.8	22	7	ADN59839
78	59	51.8	25	7	ADN59744
79	57	50.0	12	8	ADW72530
80	57	50.0	13	8	ADW72529
81	57	50.0	13	8	ADW72528
82	57	50.0	13	8	ADW72528
83	57	50.0	14	4	AAW6732
84	57	50.0	14	4	AAU26040
85	57	50.0	16	2	AAW09464
86	57	50.0	16	2	AAW33329
87	57	50.0	16	3	AAU26041
88	57	50.0	16	3	AAU26041
89	57	50.0	16	4	AAU25829
90	57	50.0	16	4	AAU25829
91	57	50.0	16	8	ADJ73057
92	57	50.0	16	8	ADJ52692
93	57	50.0	16	8	ADJ51653
94	56.5	49.6	23	7	ADN59778
95	56.5	49.6	41	7	ADN59816
96	56.5	49.6	41	7	ADN59772
97	56.5	49.6	46	7	ADN59790
98	56	49.1	13	3	AAU26041

AAU25866	Human thr
ABW72900	TPO mimet
ADJ73051	TPO mimet
ADJ52686	CHI delet
ADJ51647	CHI delet
AAW09467	Thrombopo
AAW35399	Thrombopo
AAW35417	Thrombopo
AAW33033	Thrombopo
AAW35413	Thrombopo
AAW35406	Thrombopo
AAW35422	Thrombopo
AAW35397	Thrombopo
AAU25997	Human thr
AAU25984	Human thr
AAW35398	Thrombopo
AAW35396	Thrombopo
AAW35402	Thrombopo
AAU25987	Human thr
AAU25983	Human thr
AAU25985	Human thr
AAU26000	Human thr
AAW35404	Thrombopo
AAW35405	Thrombopo
AAU25994	Human thr
AAU25991	Human thr
AAU25990	Human thr
AAW35412	Thrombopo
AAW35407	Thrombopo
AAW35408	Thrombopo
AAW35403	Thrombopo
AAU25993	Human thr
AAU25989	Human thr
AAU25995	Human thr
AAU25992	Human thr
AAU25986	Human thr
AAU25988	Human thr
AAU26042	Human thr
ADW72531	TPO mimet
AAW35425	Thrombopo
AAU26001	Human thr
ADN59740	Thrombopo
AAU26041	Human thr
AAU26041	Human thr
ABW72903	TPO mimet
ADJ52689	CHI delet
ADJ51650	CHI delet
AAW35427	Thrombopo
AAU26002	Human thr
ADN59680	Thrombopo
ADN59839	TMP Pepti
ADN59744	Thrombopo
ADW72530	TPO mimet
ADW72529	TPO mimet
ADW72528	TPO mimet
AAW6732	Peptide c
AAU26040	Human thr
AAW09464	Thrombopo
AAW33329	Thrombopo
AAU26041	TPO-mimet
AAU25829	Human thr
AAU25829	TPO mimet
ADJ73057	TPO mimet
ADJ52692	CHI delet
ADJ51653	CHI delet
ADN59778	Peptide-v
ADN59816	Peptide-v
ADN59790	Peptide-v
ADN59784	Peptide-v
AAU26041	TPO-mimet

99 56 49.1 13 5 ABB72901 TPO mimet
100 56 49.1 13 7 ADJ73054 TPO mimet

ALIGNMENTS

RESULT 1

AAW09458 standard; protein; 19 AA.

AAW09458;

10-SEP-1997 (first entry)

Thrombopoietin receptor binding compound peptide.

Haematology; thrombocytopenia; TPO; TR; proliferation;

bone marrow transfusion; chemotherapy; radiation therapy.

Synthetic.

Location/Qualifiers

Key

Misc-difference 1..19

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

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Modified-site

CC treating patients suffering from haematological disorders and
CC thrombocytopenia resulting from chemotherapy; radiation therapy or bone
CC marrow transfusions. The peptide may also be used to maintain the
CC proliferation and growth of TPO-dependent cell lines and for use in
CC biological research, for detecting TPO receptors on living cells

SQ Sequence 19 AA;

Query Match 100.0%; Score 114; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.3e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFGCGK 19

DB 1 GGCADGPTLRWISFGCGK 19

RESULT 2

AAW33025 standard; peptide; 19 AA.

AAW33025;

11-MAR-1998 (first entry)

Thrombopoietin receptor binding peptide.

Thrombopoietin receptor; binding peptide; treatment; agonist;

haematological disorder; thrombocytopenia; chemotherapy;

radiation therapy; bone marrow transfusion; diagnosis;

signal transduction; receptor activation; cell culture.

Synthetic.

WO9640750-A1.

19-DEC-1996.

07-JUN-1996; 96WO-US009623.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00485301.

(GLAX) GLAXO GROUP LTD.

Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

WPI; 1997-052226/05.

Claim 19; Page 89; 106pp; English.

The present peptide binds the thrombopoietin receptor (TR), has a

molecular weight of less than 8000 Da and a TR binding affinity as

expressed by an IC50 of no more than about 100 microm. It can be used to

treat disorders which are susceptible to treatment with a thrombopoietin

agonist, preferably haematological disorders and thrombocytopenia

resulting from chemotherapy, radiation therapy or bone marrow

transfusions. It can also be used diagnostically, e.g. to investigate the

mechanism of thrombopoietin signal transduction and receptor activation,

or to maintain the proliferation and growth of thrombopoietin dependent

cell lines

SQ Sequence 19 AA;

Query Match 100.0%; Score 114; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.3e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGCADGPTLRWISFCGK 19
 |||||
 Db 1 GGCADGPTLRWISFCGK 19

RESULT 3

AAU25822
 ID AAU25822 standard; peptide; 19 AA.

AAU25822;
 AC

DT 17-DEC-2001 (first entry)

DE Human thrombopoietin receptor (TPO-R) activator peptide #8.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 XX haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; Iacti gene.

OS Homo sapiens.

XX US6251864-B1.

PN 26-JUN-2001.

XX 01-MAR-2000; 2000US-00516704.

XX 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PR 07-JUN-1996; 96WO-00009623.

PR 15-AUG-1996; 96US-00699027.

XX (GLAX) GLAXO GROUP LTD.

PI Dower WJ, Barrett RM, Cwiria SE, Gates CM, Schatz PJ,
 PI Balasubramanian P, Wagstrom CR, Hendren RM, Deprince RB, Podduturi S;
 PI Yin Q;

DR WPI; 2001-564142/63.

PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.

PS Disclosure; Col 67-68; 128pp; English.

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines

XX Sequence 19 AA;

Query Match 100.0%; Score 114; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1,3e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGCADGPTLRWISFCGK 19
 |||||
 Db 1 GGCADGPTLRWISFCGK 19

RESULT 4

AAW09456
 ID AAW09456 standard; protein; 18 AA.

AAW09456;
 AC

DT 10-SEP-1997 (first entry)

DE Thrombopoietin receptor binding compound peptide.

XX Haematology; thrombocytopenia; TPO; TR; proliferation;
 KW bone marrow transfusion; chemotherapy; radiation therapy.

XX Synthetic.

OS Key

XX Misc-difference

FT 1.18

FT /note= "Preferably linkages are selected from: -CH2OC(O)NR-; -C(O)NR6

FT ; -NHC(O)NH; where R is hydrogen or lower alkyl and R6 is

FT lower alkyl"

FT Modified-site

FT /note= "Preferably N-terminus is selected from: -NR1; -

FT NRC(O)R; -NRC(O)OR; -NRC(O)2R; -NRC(O)NRH; succinimide;

FT benzylloxycarbonyl-NH; benzylloxycarbonyl-NH with 1-3

FT substitutions on the phenyl ring selected from lower

FT alkyl, lower alkoxy, chloro, bromo; where R and R1 are

FT independently selected from hydrogen and lower alkyl"

FT Modified-site

FT /note= "Preferably C-terminus is -C(O)R2 where R2 is

FT selected from hydroxy, lower alkoxy, and -NR3R4, where R3

FT and R4 are independently selected from hydrogen and lower

FT alkyl, and where the nitrogen atom of the -NR3R4 group

FT can optionally be the amine group of the N-terminus of

FT the peptide forming a cyclic peptide"

XX (GLAX) GLAXO GROUP LTD.

PI Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

DR WPI; 1997-051883/05.

XX Thrombopoietin receptor-binding/activating peptide(s) and peptide

XX mimetic(s) - useful in treatment of haematological disorders, esp.

XX thrombocytopenia resulting from chemotherapy, etc.

PS Claim 18; Page 89; 106pp; English.

XX The present sequence is a compound which binds to thrombopoietin (TPO)

XX receptor (TR). It has a molecular weight of < 8000 Da, and a binding

XX affinity to TR as expressed by an IC50 of no more than about 100 nm. The

XX compound (especially if modified, see features table) can be used for

XX treating patients suffering from haematological disorders and

CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. The peptide may also be used to maintain the
 CC proliferation and growth of TPO-dependent cell lines and for use in
 CC biological research, for detecting TPO receptors on living cells
 XX

SQ Sequence 18 AA;

Query Match 95.6%; Score 109; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFCGG 18
 |||||
 DB 1 GGCADGPTLRWISFCGG 18

RESULT 5
 ID AAW33023 standard; peptide; 18 AA.

XX AAW33023;

DT 11-MAR-1998 (first entry)

XX Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

OS Synthetic.

XX MO640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;

PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

PT Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX Claim 19; Page 89; 106pp; English.

XX The present peptide binds the thrombopoietin receptor (TR), has a

XX molecular weight of less than 8000 Da and a TR binding affinity as

XX expressed by an IC50 of no more than about 100 microm. It can be used to

XX treat disorders which are susceptible to treatment with a thrombopoietin

XX agonist, preferably haematological disorders and thrombocytopenia

XX resulting from chemotherapy, radiation therapy or bone marrow

XX transfusions. It can also be used diagnostically, e.g. to investigate the

XX mechanism of thrombopoietin signal transduction and receptor activation,

XX or to maintain the proliferation and growth of thrombopoietin dependent

XX cell lines

SQ Sequence 18 AA;

Query Match 95.6%; Score 109; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.6e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFCGG 18

DB |||||
 1 GGCADGPTLRWISFCGG 18

RESULT 6
 ID AAB17020 standard; peptide; 18 AA.

XX AAB17020;

DT 31-OCT-2000 (first entry)

XX TPO-mimetic peptide sequence SEQ ID NO:76.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;

KW autoimmune disease; cytostatic; antineoplastic; thrombolytic; VEGF;

KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;

KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;

KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;

KW vascular endothelial growth factor; matrix metalloproteinase; asthma;

XX thrombosis; pharmaceutical.

OS Synthetic.

XX WO200024782-A2.

PD 04-MAY-2000.

PF 25-OCT-1999; 99WO-US025044.

PR 23-OCT-1998; 98US-0105371P.

PR 22-OCT-1999; 99US-00428082.

XX (AMGEN) AMGEN INC.

PI Feige U, Liu C, Cheatham J, Boone TC;

PI WPI; 2000-350702/30.

PT Novel composition of matter comprising an Fc domain and pharmacologically

PT active peptides, useful for treating cancer and autoimmune diseases.

XX Claim 19; Page 220; 608pp; English.

XX The present invention describes composition of matter (I) comprising an

XX Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

XX (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

XX independently selected from -(L1)-c-P1, -(L1)-c-P1-(L2)-d-P2, -(L1)-c-P1-

XX (L2)-d-P2-(L3)-e-P3, or -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,

XX P3, and P4 = are each independently sequences of pharmacologically active

XX peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,

XX c, d, e, and f = are each independently 0 or 1, provided that at least 1

XX of a and b is 1. The composition can have cytostatic, antineoplastic,

XX thrombolytic and immunosuppressive activities. DNAs, vectors and host

XX cells from the present invention can be used for producing pharmaceutical

XX compositions. The compositions are useful for treating cancer, asthma,

XX thrombosis, or autoimmune diseases. The use of an Fc domain (rather than

XX a Fab domain) can provide a longer half-life or incorporate functions, and

XX such as Fc receptor binding, protein A binding, complement fixation, and

XX possibly placental transfer. AAB69443 to AAB69526 and AAB16955 to

XX AAB18003 represent nucleotide and amino acid sequences used in the

XX exemplification of the present invention

SQ Sequence 18 AA;

Query Match 95.6%; Score 109; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.6e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFCGG 18

DB 1 GGCADGPTLRWISFCGG 18

RESULT 7
AAU25820 standard; peptide, 18 AA.
XX
AC AAU25820;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human thrombopoietin receptor (TPO-R) activator peptide #6.
XX
KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
KW bone marrow transplantation; haematological disorder; platelet disorder;
KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lact gene.
XX
OS Homo sapiens.
XX
PN US6251864-B1.
XX
PD 26-JUN-2001.
XX
PF 01-MAR-2000; 2000US-00516704.
XX
PR 07-JUN-1995; 95US-00478128.
PR 07-JUN-1995; 95US-00485301.
PR 07-JUN-1996; 96WO-US0009623.
PR 15-AUG-1996; 96US-00699027.
XX
PA (GLAXO) GLAXO GROUP LTD.
XX
PI Dower WJ, Barrett RM, Cwiria SE, Gates CM, Schatz PJ,
PI Balasubramanian P, Magstrom CR, Hendren RM, Deprince RB, Poddururt S;
PI Yin Q;
XX
DR WPI; 2001-564142/63.
XX
PT Activating thrombopoietin receptors in cells, used to treat
PT thrombocytopenia and hematological disorders, comprises contacting cells
PT with peptides and peptide mimetics attached to hydrophilic polymers.
XX
PS Disclosure; Col 65-66; 128pp; English.
XX
CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
CC of activating thrombopoietin receptors in cells comprise contacting the
CC cells with effective amounts of peptides and peptide mimetics attached to
CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
CC as that due to chemotherapy, radiation therapy or bone-marrow
CC transplantation and to prevent thrombocytopenia in patients at risk. The
CC sequences are used to treat and prevent haematological disorders
CC including thrombocytopenia and platelet disorders. They are used in vitro
CC as unique tools for understanding the biological role of thrombopoietin
CC (TPO) and to develop other compounds that bind to and activate the TPO
CC receptor. The peptides can be used to detect TPO receptors on living
CC cells and fixed cells, in biological fluids, in tissue homogenates, and
CC in purified or natural biological materials. They may also be used for in
CC situ staining, fluorescence-activated cell sorting, Western blotting and
CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
CC be used for in vitro expansion of megakaryocytes and their committed
CC progenitors alone or in conjunction with additional cytokines
XX
SQ Sequence 18 AA;
Query Match 95.6%; Score 109; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
ABB72906 standard; peptide, 18 AA.
XX
AC ABB72906;
XX
DT 05-APR-2002 (first entry)
XX
DE TPO mimetic peptide SEQ ID NO:76.
XX
KW Modified peptide; mimetic; FC domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; Interleukin 1 antagonist; IL-1 antagonist; TNF;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antifertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
XX
PN Synthetic.
XX
PD WO200183525-A2.
XX
PF 08-NOV-2001.
XX
PR 02-MAY-2001; 2001WO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGEN-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
PI WPI; 2002-130313/17.
XX
DR Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Claim 39; Page 44; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cyostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antifertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABB75655 to ABB75777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 18 AA;

07 1 GGCAAGPTLRMISFCGG 18
Db 1 GGCAAGPTLRMISFCGG 18

Query Match 95.6%; Score 109; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFCGG 18
 |||
 DB 1 GGCADGPTLRWISFCGG 18

RESULT 9

ID ADJ73058 standard; peptide; 18 AA.

XX ADJ73058;

XX 06-MAY-2004 (first entry)

XX TPO mimetic peptide sequence SegID 512.

XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;

KM cardiovascular; infectious; malignant; neurologic disease; anaemia;

KM immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;

XX TPO.

OS Synthetic.

XX WO2003084477-A2.

XX 16-OCT-2003.

XX 24-MAR-2003; 2003WO-US009139.

XX 29-MAR-2002; 2002US-0368791P.

XX (CENZ) CENTOCOR INC.

PI Heavner GA, Knight DM, Scallion BJ, Chrayeb J;

XX WPI; 2003-804237/75.

PT New CDR mimetibody comprising a portion of a heavy or light chain

PT variable region comprising human framework or ligand binding region,

PT useful for preparing a composition for treating e.g., immune,

PT cardiovascular or neurologic disease.

XX Disclosure; SEQ ID NO 512; 97pp; English.

XX This invention relates to novel mammalian CDR mimetibodies, specific

CC portions or variants thereof. Specifically, it refers to an antibody

CC fragment where a protein has been inserted into, or replaces a portion

CC of, one or more CDR regions, such that each CDR mimetibody comprises at

CC least one portion of a heavy chain or light chain variable region, which

CC itself comprises at least one human framework region and at least one

CC ligand binding region (LBR). The present invention describes human

CC mimetibodies, including modified immunoglobulins and cleavage products

CC that can be useful in gene therapy and the generation of transgenic

CC plants and animals. Furthermore, the CDR mimetibody is useful for

CC preparing compositions for modulating, treating or reducing the symptoms

CC of immune, cardiovascular, infectious, malignant and/or neurologic

CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,

CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This

CC peptide sequence is a TPO mimetic peptide sequence used to make a

CC mimetibody of the invention.

RESULT 10
 ADJ52693
 ID ADJ52693 standard; peptide; 18 AA.

XX ADJ52693;

XX 06-MAY-2004 (first entry)

XX CHI deleted mimetibody-related peptide SegID512.

XX CHI deleted mimetibody; immunosuppressive; cardiovascular; cardiant;

KM hypotensive; neuroprotective; nootropic; antibacterial; virucide;

KM fungicide; gene therapy; immune disorder; cardiovascular disease;

KM arrhythmia; hypertension; heart failure; neurodegenerative;

KM multiple sclerosis; dementia; Alzheimer's disease; anaemia;

KM cancerous condition; infectious disease; bacterial infection;

XX viral infection; fungal infection.

XX Unidentified.

OS Synthetic.

XX WO2004002417-A2.

XX 08-JUN-2004.

XX 27-JUN-2003; 2003WO-US020347.

XX 28-JUN-2002; 2002US-0392431P.

XX (CENZ) CENTOCOR INC.

PI Heavner GA, Knight DM, Chrayeb J, Scallion BJ, Neespor TC;

XX Kutowski KA;

XX WPI; 2004-082870/08.

PT New CHI-deleted mimetibody polypeptides and nucleic acids, useful for

PT modulating, treating, alleviating, preventing an immune, cardiovascular,

PT or neurodegenerative disease or disorder, anaemia, cancer, or infectious

PT diseases.

XX Claim 2; SEQ ID NO 512; 129pp; English.

XX This invention relates to CHI deleted mimetibodies (and the DNA sequences

CC which encode them), compositions, methods and uses. The invention may be

CC useful for the development of compounds with an immunosuppressive,

CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,

CC antibacterial, virucide or fungicide activity. In addition, the disclosed

CC sequences may prove useful for gene therapy. The CHI-deleted mimetibody

CC is useful for diagnosing or treating a disease condition in a cell,

CC tissue, organ or animal, specifically for modulating, treating,

CC alleviating, preventing the incidence or reducing the symptoms of an

CC immune, cardiovascular (for example arrhythmia, hypertension or heart

CC failure), or neurodegenerative (for example multiple sclerosis, dementia

CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous

CC conditions, or infectious diseases (for example bacterial, viral or

CC fungal infection). The present sequence is that of a peptide which may be

CC used during the creation of a mimetibody of the invention.

Query Match 95.6%; Score 109; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.6e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWISFCGG 18
 |||
 DB 1 GGCADGPTLRWISFCGG 18

RESULT 11

ADJ51654
 ID ADJ51654 standard; peptide, 18 AA.
 XX
 AC ADJ51654;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE CH1 deleted mimetibody-related peptide SeqID512.
 XX
 KW CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
 KW dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
 KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KW antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
 KW ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
 KW TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KW dental disorder; oral disorder; dermatological disorder; ear disorder;
 KW nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KW gastrointestinal disorder; gynaecological disorder; hepatic disorder;
 KW obstructive disorder; haematologic disorder; immunological disorder;
 KW allergic disorder; infectious disorder; musculoskeletal disorder;
 KW oncological disorder; neurological disorder; nutritional disorder;
 KW ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KW renal disorder; pulmonary disorder.
 XX
 OS Unidentified.
 OS Synthetic.
 OS
 PN WO2004002424-A2.
 XX
 PD 08-JAN-2004.
 XX
 PF 30-JUN-2003; 2003WO-US020495.
 XX
 PR 28-JUN-2002; 2002US-0392431P.
 PR 19-SEP-2002; 2002US-0412144P.
 XX
 XX (GENZ) CENTOCOR INC.
 PA Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Neespor TC;
 PI Kucloski KA;
 PI Kucloski KA;
 DR WPI; 2004-082872/08.
 XX
 PT New CH1 deleted mimetibody polypeptide and nucleic acid, useful for
 PT diagnosing, preventing or treating cardiovascular, dermatologic,
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
 PT nutritional disorders.
 PS
 PS Claim 15, SEQ ID NO 512; 123pp; English.
 XX
 CC This invention relates to CH1 deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an osteopathic,
 CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
 CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
 CC immunomodulator, antiallergic, muscular-Gen, cytostatic,
 CC antiinflammatory, neuroleptic, ophthalmological, nephrotropic or
 CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
 CC modulator or cytokine-agonist. The methods and compositions of the
 CC present invention are useful for the diagnosis, prevention and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the CH1 deleted mimetibody, such as a bone or joint,
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
 CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
 CC obstructive, haematologic, immunological, allergic, infectious,
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
 CC pediatric, psychiatric, renal or pulmonary disorders. The present
 CC sequence is that of a peptide which may be used during the creation of a
 CC mimetibody of the invention.
 XX
 XX Sequence 18 AA;
 Query Match 95.6%; Score 109; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 6.6e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGCGDPTLRWISFCGG 18
 DB 1 GGCGDPTLRWISFCGG 18
 RESULT 12
 AAW09466
 ID AAW09466 standard; protein; 14 AA.
 XX
 AC AAW09466;
 XX
 DT 10-SEP-1997 (first entry)
 XX
 DE Thrombopoietin receptor binding compound cyclic peptide.
 KW Haematology; thrombocytopenia; TPO; TR; proliferation; cyclic;
 KW bone marrow transfusion; chemotherapy; radiation therapy.
 XX
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Disulfide-bond 1. 14
 FT Modified-site 1 /note= "In acetyl form"
 FT Modified-site 14 /note= "In amide form"
 FT
 FT
 FT
 PN WO9640189-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US008998.
 XX
 PR 07-JUN-1995; 95US-00472371.
 PR 07-JUN-1995; 95US-004723604.
 PR 07-JUN-1995; 95US-00476168.
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00484090.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RM, Cwirja SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX
 DR WPI; 1997-051883/05.
 XX
 CC Thrombopoietin receptor-binding/activating peptide(s) and peptide
 CC mimetic(s) - useful in treatment of haematological disorders, esp.
 CC thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Claim 30; Page 91; 106pp; English.
 XX
 CC The present sequence is a compound which binds to thrombopoietin (TPO)
 CC receptor (TR). The compound can be used for treating patients suffering
 CC from haematological disorders and thrombocytopenia resulting from
 CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide
 CC may also be used to maintain the proliferation and growth of TPO-
 CC dependent cell lines and for use in biological research, for detecting
 CC TPO receptors on living cells
 XX
 XX Sequence 14 AA;
 Query Match 74.6%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e-05; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0;
 QY 3 CADGPTLRWISFC 16
 DB 1 CADGPTLRWISFC 14

RESULT 13
ID AAM09462 standard; protein; 14 AA.
XX AAM09462;
AC
XX 10-SEP-1997 (first entry)
DT
XX Thrombopoietin receptor binding compound peptide.
DE
XX Haematology; thrombocytopenia; TPO; TR; proliferation;
KW bone marrow transfusion; chemotherapy; radiation therapy.
KW
OS Synthetic.
XX
Key Location/Qualifiers
FH Misc-difference 1..14
FT /note= "Preferably linkages are selected from: -
FT CH2OC(O)NR-, phosphonate; -CH2S(O)2NR-, -CH2NR-, -C(O)NR6
FT FT -NRC(O)NH; where R is hydrogen or lower alkyl and R6 is
FT lower alkyl"
FT 1
FT /note= "Preferably N-terminus is selected from: -NRn1; -
FT NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NHR; succinimide;
FT benzoyloxycarbonyl-NH; benzoyloxycarbonyl-NH with 1-3
FT substitutions on the phenyl ring selected from lower
FT alkyl, lower alkoxy, chloro, bromo; where R and R1 are
FT independently selected from hydrogen and lower alkyl"
FT 14
FT /note= "Preferably C-terminus is -C(O)R2 where R2 is
FT selected from hydroxy, lower alkoxy, and -NR3R4, where R3
FT and R4 are independently selected from hydrogen and lower
FT alkyl, and where the nitrogen atom of the -NR3R4 group
FT can optionally be the amine group of the N-terminus of
FT the peptide forming a cyclic peptide"
XX
XX WO9640189-A1.
PN
XX 19-DEC-1996.
PD
XX
PF 05-JUN-1996; 96MO-US008998.
PR
XX 07-JUN-1995; 95US-00472371.
PR 07-JUN-1995; 95US-00473604.
PR 07-JUN-1995; 95US-00476168.
PR 07-JUN-1995; 95US-00478128.
PR 07-JUN-1995; 95US-00484090.
PR 07-JUN-1995; 95US-00485301.
PR
XX (GLAXO) GLAXO GROUP LTD.
PA
XX Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS,
PI Mathaeakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
PI XX MPI, 1997-051883/05.
DR
XX Thrombopoietin receptor-binding/activating peptide(s) and peptide
PT mimetic(s) - useful in treatment of haematological disorders, esp.
PT thrombocytopenia resulting from chemotherapy, etc.
XX
PS Claim 18; Page 89; 106pp; English.
XX
CC The present sequence is a compound which binds to thrombopoietin (TPO)
CC receptor (TR). It has a molecular weight of < 8000 Da, and a binding
CC affinity to TR as expressed by an IC50 of no more than about 100 mM. The
CC compound (especially if modified, see features table) can be used for
CC treating patients suffering from haematological disorders and
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC marrow transplants. The peptide may also be used to maintain the
CC proliferation and growth of TPO-dependent cell lines and for use in
CC biological research, for detecting TPO receptors on living cells

[illegible]

XX 07-JUN-1996; 96WO-US009623.
 PF
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 PI Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 DR WPI; 1997-052226/05.
 XX
 PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Disclosure; Page 26; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 XX
 SQ Sequence 14 AA;
 5Q
 Query Match 74.6%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CADGPTLRWISFC 16
 Db 1 CADGPTLRWISFC 14
 Dd
 RESULT 18
 AAW33029
 ID AAW33029 standard; peptide; 14 AA.
 XX
 AC AAW33029;
 XX
 DT 11-MAR-1998 (first entry)
 XX
 DE Thrombopoietin receptor binding peptide.
 XX
 KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 PN WO9640750-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009623.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 PI Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 DR WPI; 1997-052226/05.
 XX
 PT Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Claim 19; Page 89; 106pp; English.
 XX
 CC The present peptide binds the thrombopoietin receptor (TR), has a
 CC molecular weight of less than 8000 Da and a TR binding affinity as
 CC expressed by an IC50 of no more than about 100 microm. It can be used to
 CC treat disorders which are susceptible to treatment with a thrombopoietin
 CC agonist, preferably haematological disorders and thrombocytopenia
 CC resulting from chemotherapy, radiation therapy or bone marrow
 CC transfusions. It can also be used diagnostically, e.g. to investigate the
 CC mechanism of thrombopoietin signal transduction and receptor activation,
 CC or to maintain the proliferation and growth of thrombopoietin dependent
 CC cell lines
 XX
 SQ Sequence 14 AA;
 5Q
 Query Match 74.6%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CADGPTLRWISFC 16
 Db 1 CADGPTLRWISFC 14
 Dd
 RESULT 19
 AAW35401
 ID AAW35401 standard; peptide; 14 AA.
 XX
 AC AAW35401;
 XX
 DT 11-MAR-1998 (first entry)
 XX
 DE Thrombopoietin receptor binding peptide.
 XX
 KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH Disulfide-bond 1..14
 FT Modified-site 14
 FT /note= "NH2-D-Cys"
 XX
 PN WO9640750-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009623.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 PI Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 DR WPI; 1997-052226/05.
 XX
 PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Example 6; Page 63; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a

CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

XX Sequence 14 AA;

Query Match 74.6%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFC 16
 Db 1 CADGPTLRWISFC 14

RESULT 20

AAW36647
 ID AAW36647 standard; peptide; 14 AA.

XX AAW36647;

DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

XX Synthetic.

PN WO9640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

PI Dower WJ, Barret RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

XX Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX Disclosure; Page 26; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be

XX used to treat disorders which are susceptible to treatment with a

CC thrombopoietin agonist, preferably haematological disorders and

CC marrow transfusions. It can also be used diagnostically, e.g. to

CC investigate the mechanism of thrombopoietin signal transduction and

CC receptor activation, or to maintain the proliferation and growth of

CC thrombopoietin dependent cell lines

Db |||||
 1 CADGPTLRWISFC 14

RESULT 21

AAW35400
 ID AAW35400 standard; peptide; 14 AA.

XX AAW35400;

DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

XX Synthetic.

PN WO9640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

PI Dower WJ, Barret RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

XX Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX Example 6; Page 63; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be

XX used to treat disorders which are susceptible to treatment with a

CC thrombopoietin agonist, preferably haematological disorders and

CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone

CC marrow transfusions. It can also be used diagnostically, e.g. to

CC investigate the mechanism of thrombopoietin signal transduction and

CC receptor activation, or to maintain the proliferation and growth of

CC thrombopoietin dependent cell lines

XX Sequence 14 AA;

Query Match 74.6%; Score 85; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFC 16
 Db 1 CADGPTLRWISFC 14

RESULT 22

AAW33032
 ID AAW33032 standard; peptide; 14 AA.

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XX AC AAW3032;
XX DT 11-MAR-1998 (first entry)
XX DE Thrombopoietin receptor binding peptide.
XX KW Thrombopoietin receptor; binding peptide; treatment; agonist;
XX KW haematological disorder; thrombocytopenia; chemotherapy;
XX KW radiation therapy; bone marrow transfusion; diagnosis;
XX KW signal transduction; receptor activation; cell culture.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 1..14
XX FT Modified-site /note="acylated"
XX FT Modified-site 14
XX FT /note="amidated"
XX PN MO9640750-A1.
XX PD 19-DEC-1996.
XX PF 07-JUN-1996; 96WO-US009623.
XX PR 07-JUN-1995; 95US-00478128.
XX PR 07-JUN-1995; 95US-00485301.
XX PA (GLAXO ) GLAXO GROUP LTD.
XX PI Power WJ, Barret RM, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
XX PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX DR WPI; 1997-052226/05.
XX PT Peptides and peptide mimetics which bind to and activate the
XX PT thrombopoietin receptor - useful in treatment of haematological
XX PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX CS Claim 30; Page 91; 106pp; English.
XX CC The present peptide binds the thrombopoietin receptor (TR), has a
XX CC molecular weight of less than 8000 Da and a TR binding affinity as
XX CC expressed by an IC50 of no more than about 100 microm. It can be used to
XX CC treat disorders which are susceptible to treatment with a thrombopoietin
XX CC agonist, preferably haematological disorders and thrombocytopenia
XX CC resulting from chemotherapy, radiation therapy or bone marrow
XX CC transfusions. It can also be used diagnostically, e.g. to investigate the
XX CC mechanism of thrombopoietin signal transduction and receptor activation,
XX CC or to maintain the proliferation and growth of thrombopoietin dependent
XX CC cell lines
XX SQ Sequence 14 AA;
XX QY Query Match 74.6%; Score 85; DB 2; Length 14;
XX DB Best Local Similarity 100.0%; Pred. No. 1.7e-05;
XX DB Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 3 CADGPTLRWISFC 16
XX DB 1 CADGPTLRWISFC 14
XX RESULT 23
XX ID AAB17014 standard; peptide; 14 AA.
XX AC AAB17014;
XX DE 31-OCT-2000 (first entry)
XX DT
XX

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DE TPO-mimetic peptide sequence SEQ ID NO:70.
XX KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
XX KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
XX KW immunosuppressive; EPO; TPO; CRIA4; mimetic; IL-1; TNF; antagonist; MMP;
XX KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
XX KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
XX KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
XX KW thrombolysis; pharmaceutical.
XX OS Synthetic.
XX PN WO200024782-A2.
XX PD 04-MAY-2000.
XX PF 25-OCT-1999; 99WO-US025044.
XX PR 23-OCT-1998; 98US-0105371P.
XX PR 22-OCT-1999; 99US-00428082.
XX PA (AMGEN-) AMGEN INC.
XX PI Feige U, Liu C, Cheatham J, Boone TC;
XX DR WPI; 2000-350702/30.
XX PT Novel composition of matter comprising an Fc domain and pharmacologically
XX PT active peptides, useful for treating cancer and autoimmune diseases.
XX CS Claim 19; Page 218; 608pp; English.
XX CC The present invention describes composition of matter (I) comprising an
XX CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
XX CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
XX CC independently selected from -(L1)-c-P1, -(L1)c-P1-(L2)-d-P2, -(L1)c-P1-
XX CC (L2)-d-P2-(L3)-e-P3, or -(L1)c-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,
XX CC P3, and P4 = are each independently sequences of pharmacologically active
XX CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
XX CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
XX CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
XX CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
XX CC cells from the present invention can be used for producing pharmaceutical
XX CC compositions. The compositions are useful for treating cancer, asthma,
XX CC thrombolysis, or autoimmune diseases. The use of an Fc domain (rather than
XX CC a Fab domain) can provide a longer half-life or incorporate functions
XX CC such as Fc receptor binding, protein A binding, complement fixation, and
XX CC possibly placental transfer. AAB69443 to AAB69526 and AAB16955 to
XX CC AAB19003 represent nucleotide and amino acid sequences used in the
XX CC exemplification of the present invention
XX SQ Sequence 14 AA;
XX QY Query Match 74.6%; Score 85; DB 3; Length 14;
XX DB Best Local Similarity 100.0%; Pred. No. 1.7e-05;
XX DB Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 3 CADGPTLRWISFC 16
XX DB 1 CADGPTLRWISFC 14
XX RESULT 24
XX ID AAU25826 standard; peptide; 14 AA.
XX AC AAU25826;
XX DE 17-DEC-2001 (first entry)
XX DT Human thrombopoietin receptor (TPO-R) activator peptide #12.
XX KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

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KM haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
KM bone marrow transplantation; hematological disorder; platelet disorder;
KM enzyme-linked immunosorbent assay; in situ staining; biological fluid;
KM tissue homogenate; fluorescence-activated cell sorting; Western blotting;
KM in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.
XX
OS Homo sapiens.
XX
PN US6251864-B1.
XX
PD 26-JUN-2001.
XX
PF 01-MAR-2000; 2000US-00516704.
XX
PR 07-JUN-1995; 95US-00478128.
PR 07-JUN-1995; 95US-00485301.
PR 07-JUN-1996; 96WO-US009623.
PR 15-AUG-1996; 96US-00699027.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Dower WJ, Barrett RW, Cwirja SE, Gates CM, Schatz PJ,
PI Balasubramanian P, Wagstrom CR, Hendren RM, Deprince RB, Poddaturi S;
PI Yin Q;
XX
DR WPI; 2001-564142/63.
XX
PT Activating thrombopoietin receptors in cells, used to treat
PT thrombocytopenia and hematological disorders, comprises contacting cells
PT with peptides and peptide mimetics attached to hydrophilic polymers.
XX
PS Disclosure; Col 67-68; 128pp; English.
XX
SQ Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
CC of activating thrombopoietin receptors in cells comprise contacting the
CC cells with effective amounts of peptides and peptide mimetics attached to
CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
CC as that due to chemotherapy, radiation therapy or bone-marrow
CC transplantation and to prevent thrombocytopenia in patients at risk. The
CC sequences are used to treat and prevent haematological disorders
CC including thrombocytopenia and platelet disorders. They are used in vitro
CC as unique tools for understanding the biological role of thrombopoietin
CC (TPO) and to develop other compounds that bind to and activate the TPO
CC receptor. The peptides can be used to detect TPO receptors on living
CC cells and fixed cells, in biological fluids, in tissue homogenates, and
CC in purified or natural biological materials. They may also be used for in
CC situ staining, fluorescence-activated cell sorting, Western blotting and
CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
CC be used for in vitro expansion of megakaryocytes and their committed
CC progenitors alone or in conjunction with additional cytokines
XX
SQ Sequence 14 AA;
XX
Query Match 74.6%; Score 85; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CADGPTLRWISFC 16
DB 1 CADGPTLRWISFC 14

RESULT 25
AAU25852
ID AAU25852 standard; peptide; 14 AA.
XX
AC AAU25852;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human thrombopoietin receptor (TPO-R) activator peptide #38.

KM Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
KM haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
KM bone marrow transplantation; hematological disorder; platelet disorder;
KM enzyme-linked immunosorbent assay; in situ staining; biological fluid;
KM tissue homogenate; fluorescence-activated cell sorting; Western blotting;
KM in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.
XX
OS Homo sapiens.
XX
PN US6251864-B1.
XX
PD 26-JUN-2001.
XX
PF 01-MAR-2000; 2000US-00516704.
XX
PR 07-JUN-1995; 95US-00478128.
PR 07-JUN-1995; 95US-00485301.
PR 07-JUN-1996; 96WO-US009623.
PR 15-AUG-1996; 96US-00699027.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Dower WJ, Barrett RW, Cwirja SE, Gates CM, Schatz PJ,
PI Balasubramanian P, Wagstrom CR, Hendren RM, Deprince RB, Poddaturi S;
PI Yin Q;
XX
DR WPI; 2001-564142/63.
XX
PT Activating thrombopoietin receptors in cells, used to treat
PT thrombocytopenia and hematological disorders, comprises contacting cells
PT with peptides and peptide mimetics attached to hydrophilic polymers.
XX
PS Disclosure; Col 20; 128pp; English.
XX
SQ Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
CC of activating thrombopoietin receptors in cells comprise contacting the
CC cells with effective amounts of peptides and peptide mimetics attached to
CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
CC as that due to chemotherapy, radiation therapy or bone-marrow
CC transplantation and to prevent thrombocytopenia in patients at risk. The
CC sequences are used to treat and prevent haematological disorders
CC including thrombocytopenia and platelet disorders. They are used in vitro
CC as unique tools for understanding the biological role of thrombopoietin
CC (TPO) and to develop other compounds that bind to and activate the TPO
CC receptor. The peptides can be used to detect TPO receptors on living
CC cells and fixed cells, in biological fluids, in tissue homogenates, and
CC in purified or natural biological materials. They may also be used for in
CC situ staining, fluorescence-activated cell sorting, Western blotting and
CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
CC be used for in vitro expansion of megakaryocytes and their committed
CC progenitors alone or in conjunction with additional cytokines
XX
SQ Sequence 14 AA;
XX
Query Match 74.6%; Score 85; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CADGPTLRWISFC 16
DB 1 CADGPTLRWISFC 14

RESULT 26
AAU25866
ID AAU25866 standard; peptide; 14 AA.
XX
AC AAU25866;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human thrombopoietin receptor (TPO-R) activator peptide #52.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; Iacti gene.
 XX Homo sapiens.
 XX US6251864-B1.
 XX 26-JUN-2001.
 XX 01-MAR-2000; 2000US-00516704.
 XX 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX (GLAXO) GLAXO GROUP LTD.
 PA Dower WJ, Barrett RM, Cwiryla SE, Gates CM, Schatz PJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RM, Deprince RB, Poddaturi S;
 PI Yin Q;
 DR WPI; 2001-564142/63.
 XX Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX Disclosure; Col 20; 128pp; English.
 XX Sequences ANU25815-ANU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX Sequence 14 AA;
 SQ
 Query Match 74.6%; Score 85; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CADGPTLRWISFC 16
 DB 1 CADGPTLRWISFC 14
 RESULT 27
 ABB72900
 ID ABB72900 standard; peptide; 14 AA.
 XX ABB72900;
 AC ABB72900;
 XX 05-APR-2002 (first entry)
 DT

DE TPO mimetic peptide SEQ ID NO:70.
 XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
 XX erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumor; immunosuppressive;
 KW cytostatic; antineumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX Homo sapiens.
 XX Synthetic.
 OS WO200183525-A2.
 XX 08-NOV-2001.
 PD 02-MAY-2001; 2001WO-US014310.
 XX 03-MAY-2000; 2000US-00563286.
 XX (AMGEN-) AMGEN INC.
 PA Feige U, Liu C, Cheatham JC, Boone TC, Gudae JM;
 PI WPI; 2002-130313/17.
 DR Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 XX Claim 39; Page 44; 176pp; English.
 PS The present invention describes a vehicle-peptide molecule (I) or its
 XX multimers. (I) can have antiinflammatory, antitumor, immunosuppressive,
 CC cyostatic, antineumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (II) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABB35695 to ABB35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention
 XX Sequence 14 AA;
 SQ
 Query Match 74.6%; Score 85; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 CADGPTLRWISFC 16
 DB 1 CADGPTLRWISFC 14
 RESULT 28

ADJ73051	ID	ADJ73051 standard; peptide; 14 AA.
XX		
AC	ADJ73051;	
XX		
DT	06-MAY-2004	(first entry)
XX		
DE	TPO mimetic peptide sequence Seqid 505.	
XX		
KM	mimetic; CDR mimetibody; gene therapy; transgenic; immune;	
KW	cardiovascular; infectious; malignant; neurologic disease; anaemia;	
KM	immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;	
TPC.		
XX		
OS	Synthetic.	
XX		
PN	WO2003084477-A2.	
PD	16-OCT-2003.	
XX		
PP	24-MAR-2003; 2003WO-US009139.	
PR	29-MAR-2002; 2002US-0368791P.	
PA	(CENZ) CENTOCOR INC.	
PI	Heavner GA, Knight DM, Scallion BJ, Ghrayeb J;	
DR	WPI; 2003-804237/75.	
PT	New CDR mimetibody comprising a portion of a heavy or light chain	
PT	variable region comprising human framework or ligand binding region,	
PT	useful for preparing a composition for treating e.g., immune,	
XX	cardiovascular or neurologic disease.	
XX		
PS	Disclosure; SEQ ID NO 505; 97pp; English.	
XX		
CC	This invention relates to novel mammalian CDR mimetibodies, specific	
CC	portions or variants thereof. Specifically, it refers to an antibody	
CC	fragment where a protein has been inserted into, or replaces a portion	
CC	of, one or more CDR regions, such that each CDR mimetibody comprises at	
CC	least one portion of a heavy chain or light chain variable region, which	
CC	itself comprises at least one human framework region and at least one	
CC	ligand binding region (LBR). The present invention describes human	
CC	mimetibodies, including modified immunoglobulins and cleavage products	
CC	that can be useful in gene therapy and the generation of transgenic	
CC	plants and animals. Furthermore, the CDR mimetibody is useful for	
CC	preparing compositions for modulating, treating or reducing the symptoms	
CC	of immune, cardiovascular, infectious, malignant and/or neurologic	
CC	diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,	
CC	cardiant, antimicrobial, cytostatic and neuroprotective activities. This	
CC	peptide sequence is a TPO mimetic peptide sequence used to make a	
CC	mimetibody of the invention.	
XX		
SQ	Sequence 14 AA:	
	Query Match	74.6%; Score 85; DB 7; Length 14;
	Best Local Similarity	100.0%; Pred. No. 1.7e-05;
	Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	3 CADGPTLRWISFC 16	
DB	1 CADGPTLRWISFC 14	
RESULT 29		
ID	ADJ52686	
XX	ADJ52686 standard; peptide; 14 AA.	
XX		
AC	ADJ52686;	
DT	06-MAY-2004	(first entry)
XX		

DE	CH1 deleted mimetibody-related peptide SeqID505.
XX	
KM	CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
KM	hypotensive; neuroprotective; nootropic; antibacterial; virucide;
KM	fungicide; gene therapy; immune disorder; cardiovascular disease;
KM	arrhythmia; hypertension; heart failure; neurodegenerative;
KM	multiple sclerosis; dementia; Alzheimer's disease; anaemia;
KM	cancerous condition; infectious disease; bacterial infection;
KM	viral infection; fungal infection.
XX	
OS	Unidentified.
OS	Synthetic.
XX	
PN	WO2004002417-A2.
XX	
PD	08-JAN-2004.
XX	
PF	27-JUN-2003; 2003WO-US020347.
XX	
PR	28-JUN-2002; 2002US-0392431P.
XX	
PA	(GEN2) CENTOCOR INC.
XX	
PI	Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Neespor TC;
XX	Kuculoglu KA;
XX	WPI; 2004-082870/08.
XX	
PT	New CH1-deleted mimetibody polypeptides and nucleic acids, useful for
PT	modulating, treating, alleviating, preventing an immune, cardiovascular,
PT	or neurodegenerative disease or disorder, anemia, cancer, or infectious
PT	diseases.
XX	
PS	Claim 2; SEQ ID NO 505; 129pp; English.
XX	
CC	This invention relates to CH1 deleted mimetibodies (and the DNA sequences
CC	which encode them), compositions, methods and uses. The invention may be
CC	useful for the development of compounds with an immunosuppressive,
CC	cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
CC	antibacterial, virucide or fungicide activity. In addition, the disclosed
CC	sequences may prove useful for gene therapy. The CH1-deleted mimetibody
CC	is useful for diagnosing or treating a disease condition in a cell,
CC	tissue, organ or animal, specifically for modulating, treating,
CC	alleviating, preventing the incidence or reducing the symptoms of an
CC	immune, cardiovascular (for example arrhythmia, hypertension or heart
CC	failure), or neurodegenerative (for example multiple sclerosis, dementia
CC	or Alzheimer's disease) diseases or disorders, anaemia, cancerous
CC	conditions, or infectious diseases (for example bacterial, viral or
CC	fungal infection). The present sequence is that of a peptide which may be
CC	used during the creation of a mimetibody of the invention.
XX	
SQ	Sequence 14 AA;
XX	
Query Match	74.6%; Score 85; DB 8; Length 14;
Best Local Similarity	100.0%; Pred. NO. 1.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Oy	3 CADGPTLRWISFC 16
Db	1 CADGPTLRWISFC 14
XX	
RESULT 30	
ID	ADJ51647
ID	ADJ51647 standard; peptide; 14 AA.
XX	
AC	ADJ51647;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	CH1 deleted mimetibody-related peptide SeqID505.
XX	
KM	CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;

KM dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
 KM gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KM antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
 KM ophthalmological; nephrotoxic; respiratory-Gen; tumour necrosis factor;
 KM TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KM dental disorder; oral disorder; dermatological disorder; ear disorder;
 KM nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KM gastrointestinal disorder; gynaecological disorder; hepatic disorder;
 KM obstetric disorder; haematological disorder; immunological disorder;
 KM allergic disorder; infectious disorder; musculoskeletal disorder;
 KM oncological disorder; neurological disorder; nutritional disorder;
 KM ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KM renal disorder; pulmonary disorder.
 KM Unidentified.
 OS Synthetic.
 XX
 XX
 PN WO2004002424-A2.
 XX
 XX 08-JAN-2004.
 PD
 XX 30-JUN-2003; 2003WO-US020495.
 PF
 XX 28-JUN-2002; 2002US-0392441P.
 PR 19-SEP-2002; 2002US-0412144P.
 XX
 XX (CENZ) CENTOCOR INC.
 XX
 PI Heaver GA, Knight DM, Ghayeb J, Scallion BJ, Nespor TC;
 PI Kutolowski KA,
 XX
 DR WPI; 2004-082872/08.
 XX
 XX
 PT New CHI deleted mimetibody polypeptide and nucleic acid, useful for
 PT diagnosing, preventing or treating cardiovascular, dermatologic,
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
 PT nutritional disorders.
 XX
 XX
 PS Claim 15; SEQ ID NO 505; 123pp; English.
 XX
 XX This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an osteopathic,
 CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
 CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
 CC immunomodulator, antiallergic, muscular-Gen, cytostatic,
 CC antiinflammatory, neuroleptic, ophthalmological, nephrotoxic or
 CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
 CC modulator or cytokine-agonist. The methods and compositions of the
 CC present invention are useful for the diagnosis, prevention and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the CHI deleted mimetibody, such as a bone or joint,
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
 CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
 CC obstetric, haematologic, immunological, allergic, infectious,
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
 CC pediatric, psychiatric, renal or pulmonary disorders. The present
 CC sequence is that of a peptide which may be used during the creation of a
 CC mimetibody of the invention.
 CC
 SQ Sequence 14 AA;
 XX
 XX
 Query Match 74.6%; Score 85; DB 8; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID AAM09467 standard; protein; 13 AA.
 XX
 XX AAM09467;
 AC
 XX
 XX 10-SEP-1997 (first entry)
 DT
 XX Thrombopoietin receptor binding compound cyclic peptide.
 DE
 XX Haematology; thrombocytopenia; TPO; TR; proliferation; cyclic;
 KM bone marrow transfusion; chemotherapy; radiation therapy.
 XX
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "The Ala is linked with the modified Cys at
 FT position 13"
 FT Modified-site 14
 FT /label= OTHER
 FT /note= "S-carboxymethyl-cysteine alpha-carboxamide;
 FT forming a linkage onto the Ala at position one with the
 FT delta C of this residue"
 XX
 XX
 PN WO640189-A1.
 XX
 XX 19-DEC-1996.
 PD
 XX 05-JUN-1996; 96WO-US008998.
 PF
 XX 07-JUN-1995; 95US-00472371.
 PR 07-JUN-1995; 95US-00473604.
 PR 07-JUN-1995; 95US-00476168.
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00484090.
 PR 07-JUN-1995; 95US-00485301.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 PA
 XX Dower WJ, Barrett RW, Cwirila SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 PI
 XX WPI; 1997-051883/05.
 DR
 XX Thrombopoietin receptor-binding/activating peptide(s) and peptide
 PT mimetic(s) - useful in treatment of haematological disorders, esp.
 PT thrombocytopenia resulting from chemotherapy, etc.
 XX
 XX
 PS Claim 30; Page 91; 106pp; English.
 XX
 XX The present sequence is a compound which binds to thrombopoietin (TPO)
 CC receptor (TR). The compound can be used for treating patients suffering
 CC from haematological disorders and thrombocytopenia resulting from
 CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide
 CC may also be used to maintain the proliferation and growth of TPO-
 CC dependent cell lines and for use in biological research, for detecting
 CC TPO receptors on living cells
 CC
 SQ Sequence 13 AA;
 XX
 XX
 Query Match 66.7%; Score 76; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX 11-MAR-1998 (first entry)
DT Thrombopoietin receptor binding peptide.
DE
XX Thrombopoietin receptor; binding peptide; treatment; agonist;
KW haematological disorder; thrombocytopaenia; chemotherapy;
KM radiation therapy; bone marrow transfusion; diagnosis;
KW signal transduction; receptor activation; cell culture.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "COCH2-alanine linked via CH2 group to Cys13"
FT Modified-site 13 /note= "NH2-cytosine linked via sulphoxidised thiol group to Ala1"
FT
FT
XX WO9640750-A1.
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US009623.
XX
XX 07-JUN-1995; 95US-00478128.
XX 07-JUN-1995; 95US-00485301.
XX
XX (GLAXO ) GLAXO GROUP LTD.
XX
XX Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Mattheakis LC, Schatz PJ, Magstrom CR, Wrighton NC;
XX
XX WPI; 1997-052226/05.
XX
XX Peptides and peptide mimetics which bind to and activate the
PT thrombopoietin receptor - useful in treatment of haematological
PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX
XX Example 6; Page 63; 106pp; English.
XX
XX The present peptide, which binds the thrombopoietin receptor (TR), can be
CC used to treat disorders which are susceptible to treatment with a
CC thrombopoietin agonist, preferably haematological disorders and
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC marrow transfusions. It can also be used diagnostically, e.g. to
CC investigate the mechanism of thrombopoietin signal transduction and
CC receptor activation, or to maintain the proliferation and growth of
CC thrombopoietin dependent cell lines
XX
XX Sequence 13 AA;
SQ
Query Match 66.7%; Score 76; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ADGPTLRWISFC 16
DB 1 ADGPTLRWISFC 13

```

```

KW radiation therapy; bone marrow transfusion; diagnosis;
KW signal transduction; receptor activation; cell culture.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Cross-links 1 /note= "linked via disulfide bond to Cys1 of identical peptide"
FT Modified-site 13 /note= "NH2-Phe"
FT
FT
XX WO9640750-A1.
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US009623.
XX
XX 07-JUN-1995; 95US-00478128.
XX 07-JUN-1995; 95US-00485301.
XX
XX (GLAXO ) GLAXO GROUP LTD.
XX
XX Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Mattheakis LC, Schatz PJ, Magstrom CR, Wrighton NC;
XX
XX WPI; 1997-052226/05.
XX
XX Peptides and peptide mimetics which bind to and activate the
PT thrombopoietin receptor - useful in treatment of haematological
PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX
XX Example 9; Page 73; 106pp; English.
XX
XX The present peptide, which binds the thrombopoietin receptor (TR), can be
CC used to treat disorders which are susceptible to treatment with a
CC thrombopoietin agonist, preferably haematological disorders and
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC marrow transfusions. It can also be used diagnostically, e.g. to
CC investigate the mechanism of thrombopoietin signal transduction and
CC receptor activation, or to maintain the proliferation and growth of
CC thrombopoietin dependent cell lines
XX
XX Sequence 13 AA;
SQ
Query Match 66.7%; Score 76; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CADGPTLRWISF 15
DB 1 CADGPTLRWISF 13

```

```

RESULT 33
AAW35417
ID AAW35417 standard; peptide; 13 AA.
XX
XX AAW35417;
AC
XX 11-MAR-1998 (first entry)
DT
XX Thrombopoietin receptor binding peptide.
DE
XX Thrombopoietin receptor; binding peptide; treatment; agonist;
KW haematological disorder; thrombocytopaenia; chemotherapy;

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```

RESULT 34
AAW33033
ID AAW33033 standard; peptide; 13 AA.
XX
XX AAW33033;
AC
XX 11-MAR-1998 (first entry)
DT
XX Thrombopoietin receptor binding peptide.
DE
XX Thrombopoietin receptor; binding peptide; treatment; agonist;
KW haematological disorder; thrombocytopaenia; chemotherapy;
KW radiation therapy; bone marrow transfusion; diagnosis;
KW signal transduction; receptor activation; cell culture.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1

```

```

FT      /note= "COCH2-alanine linked via CH2 group to Cys13"
FT      Modified-site
FT      13
FT      /note= "NH2-cytosine linked via thiol group to Ala1"
XX
XX
PN      WO9640750-A1.
PD      19-DEC-1996.
XX
XX      07-JUN-1996;
XX      96WO-US009623.
XX
XX      07-JUN-1996;
XX      96WO-US009623.
XX
XX      07-JUN-1995;
XX      95US-00478128.
XX      07-JUN-1995;
XX      95US-00485301.
XX
XX      (GLAX ) GLAXO GROUP LTD.
XX
XX      Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
XX      Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX      WPI, 1997-052226/05.
XX
XX      Peptides and peptide mimetics which bind to and activate the
XX      thrombopoietin receptor - useful in treatment of haematological
XX      disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX
XX      Claim 30; Page 91; 106pp; English.
XX
XX      The present peptide binds the thrombopoietin receptor (TR), has a
XX      molecular weight of less than 8000 Da and a TR binding affinity as
XX      expressed by an IC50 of no more than about 100 microm. It can be used to
XX      treat disorders which are susceptible to treatment with a thrombopoietin
XX      agonist, preferably haematological disorders and thrombocytopenia
XX      resulting from chemotherapy, radiation therapy or bone marrow
XX      CC transfusions. It can also be used diagnostically, e.g. to investigate the
XX      mechanism of thrombopoietin signal transduction and receptor activation,
XX      or to maintain the proliferation and growth of thrombopoietin dependent
XX      cell lines
XX
XX      Sequence 13 AA;
XX
SQ
Query Match      66.7%; Score 76; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 ADGPTLRWISFC 16
      |||||
      1 ADGPTLRWISFC 13
DB
RESULT 35
AAW35413
ID      AAW35413 standard; peptide; 13 AA.
XX
XX      AAW35413;
AC
XX      11-MAR-1998 (first entry)
XX
XX      Thrombopoietin receptor binding peptide.
XX
XX      Thrombopoietin receptor; binding peptide; treatment; agonist;
XX      haematological disorder; thrombocytopenia; chemotherapy;
XX      radiation therapy; bone marrow transfusion; diagnosis;
XX      signal transduction; receptor activation; cell culture.
XX
XX      Synthetic.
XX
XX      Key
XX      Modified-site      Location/Qualifiers
XX      FT      1
XX      FT      /note= "Br-Ala"
XX      FT      Modified-site      13
XX      FT      /note= "NH2-Cys"
XX      PN      WO9640750-A1.

```

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PD      19-DEC-1996.
XX
XX      07-JUN-1996;
XX      96WO-US009623.
XX
XX      07-JUN-1995;
XX      95US-00478128.
XX      07-JUN-1995;
XX      95US-00485301.
XX
XX      (GLAX ) GLAXO GROUP LTD.
XX
XX      Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
XX      Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX      WPI, 1997-052226/05.
XX
XX      Peptides and peptide mimetics which bind to and activate the
XX      thrombopoietin receptor - useful in treatment of haematological
XX      disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX
XX      Example 9; Page 73; 106pp; English.
XX
XX      The present peptide, which binds the thrombopoietin receptor (TR), can be
XX      used to treat disorders which are susceptible to treatment with a
XX      thrombopoietin agonist, preferably haematological disorders and
XX      thrombocytopenia resulting from chemotherapy, radiation therapy or bone
XX      marrow transfusions. It can also be used diagnostically, e.g. to
XX      investigate the mechanism of thrombopoietin signal transduction and
XX      receptor activation, or to maintain the proliferation and growth of
XX      thrombopoietin dependent cell lines
XX
XX      Sequence 13 AA;
XX
SQ
Query Match      66.7%; Score 76; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 ADGPTLRWISFC 16
      |||||
      1 ADGPTLRWISFC 13
DB
RESULT 36
AAW35406
ID      AAW35406 standard; peptide; 13 AA.
XX
XX      AAW35406;
AC
XX      11-MAR-1998 (first entry)
XX
XX      Thrombopoietin receptor binding peptide.
XX
XX      Thrombopoietin receptor; binding peptide; treatment; agonist;
XX      haematological disorder; thrombocytopenia; chemotherapy;
XX      radiation therapy; bone marrow transfusion; diagnosis;
XX      signal transduction; receptor activation; cell culture.
XX
XX      Synthetic.
XX
XX      Key
XX      Modified-site      Location/Qualifiers
XX      FT      1
XX      FT      /note= "CO-CH (Ph)-alanine linked via CH group to Cys13"
XX      FT      Modified-site      13
XX      FT      /note= "NH2-cytosine linked via thiol group to Ala1"
XX      PN      WO9640750-A1.
XX
XX      19-DEC-1996.
XX
XX      07-JUN-1996;
XX      96WO-US009623.
XX
XX      07-JUN-1995;
XX      95US-00478128.
XX      07-JUN-1995;
XX      95US-00485301.
XX
XX      (GLAX ) GLAXO GROUP LTD.

```

XX Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX WPI; 1997-052226/05.
 DR
 XX Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Example 6; Page 64; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 CC
 SQ Sequence 13 AA;
 Query Match 66.7%; Score 76; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00033; Mismatches 0; Gaps 0;
 Matches 13; Conservative 0; Indels 0; Gaps 0;
 QY 4 ADGPTLRWISFC 16
 |||||
 1 ADGPTLRWISFC 13
 Db
 RESULT 37
 AAW35422
 ID AAW35422 standard; peptide; 13 AA.
 XX
 AC AAW35422;
 XX
 DT 11-MAR-1998 (first entry)
 XX
 DE Thrombopoietin receptor binding peptide.
 XX
 KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "optionally acylated"
 FT Cross-links 13 /note= "linked via disulfide bond to Cys13 of identical
 FT peptide"
 FT
 XX WO9640750-A1.
 PN
 XX 19-DEC-1996.
 PD
 XX 07-JUN-1996; 96WO-US009623.
 PF
 XX 07-JUN-1995; 95US-00478128.
 PR
 XX 07-JUN-1995; 95US-00485301.
 PA
 XX (GLAX) GLAXO GROUP LTD.
 XX Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX WPI; 1997-052226/05.
 DR
 XX Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 XX Example 9; Page 74; 106pp; English.
 PS
 XX The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 CC
 SQ Sequence 13 AA;
 Query Match 66.7%; Score 76; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00033; Mismatches 0; Gaps 0;
 Matches 13; Conservative 0; Indels 0; Gaps 0;
 QY 4 ADGPTLRWISFC 16
 |||||
 1 ADGPTLRWISFC 13
 Db
 RESULT 38
 AAW35397
 ID AAW35397 standard; peptide; 13 AA.
 XX
 AC AAW35397;
 XX
 DT 11-MAR-1998 (first entry)
 XX
 DE Thrombopoietin receptor binding peptide.
 XX
 KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "COCH2-alanine linked via CH2 group to Cys13"
 FT Modified-site 13 /note= "NH2-cytosine linked via thiol group to Ala1"
 FT
 XX WO9640750-A1.
 PN
 XX 19-DEC-1996.
 PD
 XX 07-JUN-1996; 96WO-US009623.
 PF
 XX 07-JUN-1995; 95US-00478128.
 PR
 XX 07-JUN-1995; 95US-00485301.
 PA
 XX (GLAX) GLAXO GROUP LTD.
 XX Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX WPI; 1997-052226/05.
 DR
 XX Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Example 6; Page 63; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and

CC thrombocytopaenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

XX Sequence 13 AA;

Query Match 66.7%; Score 76; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00033;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ADGPTLRWISFC 16
 |||||
 1 ADGPTLRWISFC 13

Db

RESULT 39

AAU25997

ID AAU25997 standard; peptide; 13 AA.

XX AAU25997;

AC

17-DEC-2001 (first entry)

DT

XX

Human thrombopoietin receptor (TPO-R) activator peptide #183.

DE

XX

Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

XX haemostatic; thrombocytopaenia; chemotherapy; radiation therapy; ELISA;

KW bone marrow transplantation; haematological disorder; platelet disorder;

KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;

KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;

KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.

XX

XX Homo sapiens.

OS

US6251864-B1.

PN

26-JUN-2001.

PD

01-MAR-2000; 2000US-00516704.

PF

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

PR 07-JUN-1996; 96WO-US009623.

PR 15-AUG-1996; 96US-00699027.

XX

(GLAX) GLAXO GROUP LTD.

PA

XX Dower WJ, Barrett RW, Cwirja SE, Gates CM, Schatz PJ;

XX Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;

PI Yin Q;

PI WPI; 2001-564142/63.

DR

XX

XX

PT Activating thrombopoietin receptors in cells, used to treat

PT thrombocytopaenia and hematological disorders, comprises contacting cells

PT with peptides and peptide mimetics attached to hydrophilic polymers.

XX

XX Disclosure; Col 143-144; 128pp; English.

XX

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that

CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods

CC of activating thrombopoietin receptors in cells comprise contacting the

CC cells with effective amounts of peptides and peptide mimetics attached to

CC hydrophilic polymers. The methods are used to treat thrombocytopaenia such

CC as that due to chemotherapy, radiation therapy or bone-marrow

CC transplantation and to prevent thrombocytopaenia in patients at risk. The

CC sequences are used to treat and prevent hematological disorders

CC including thrombocytopaenia and platelet disorders. They are used in vitro

CC as unique tools for understanding the biological role of thrombopoietin

CC (TPO) and to develop other compounds that bind to and activate the TPO

CC receptor. The peptides can be used to detect TPO receptors on living

CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines

XX Sequence 13 AA;

Query Match 66.7%; Score 76; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00033;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CADGPTLRWISF 15
 |||||
 1 CADGPTLRWISF 13

Db

RESULT 40

AAU25984

ID AAU25984 standard; peptide; 13 AA.

XX

XX

AC

17-DEC-2001 (first entry)

DT

XX

XX

DE

Human thrombopoietin receptor (TPO-R) activator peptide #170.

XX

XX

Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

KW haemostatic; thrombocytopaenia; chemotherapy; radiation therapy; ELISA;

KW bone marrow transplantation; haematological disorder; platelet disorder;

KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;

KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;

KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.

XX

XX Homo sapiens.

OS

US6251864-B1.

PN

26-JUN-2001.

PD

01-MAR-2000; 2000US-00516704.

PF

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

PR 07-JUN-1996; 96WO-US009623.

PR 15-AUG-1996; 96US-00699027.

XX

(GLAX) GLAXO GROUP LTD.

PA

XX Dower WJ, Barrett RW, Cwirja SE, Gates CM, Schatz PJ;

XX Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;

PI Yin Q;

PI WPI; 2001-564142/63.

DR

XX

XX

PT Activating thrombopoietin receptors in cells, used to treat

PT thrombocytopaenia and hematological disorders, comprises contacting cells

PT with peptides and peptide mimetics attached to hydrophilic polymers.

XX

XX Disclosure; Col 137; 128pp; English.

XX

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that

CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods

CC of activating thrombopoietin receptors in cells comprise contacting the

CC cells with effective amounts of peptides and peptide mimetics attached to

CC hydrophilic polymers. The methods are used to treat thrombocytopaenia such

CC as that due to chemotherapy, radiation therapy or bone-marrow

CC transplantation and to prevent thrombocytopaenia in patients at risk. The

CC sequences are used to treat and prevent hematological disorders

CC including thrombocytopaenia and platelet disorders. They are used in vitro

CC as unique tools for understanding the biological role of thrombopoietin

CC (TPO) and to develop other compounds that bind to and activate the TPO

CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines

XX Sequence 13 AA;

Query Match 66.7%; Score 76; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ADGPTLRWISFC 16
 |||||
 1 ADGPTLRWISFC 13

RESULT 41

AAW35398 ID AAW35398 standard; peptide; 14 AA.

XX AC AAW35398;

DT 11-MAR-1998 (first entry)

XX Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopaenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1. .14

FT Modified-site /note= "Homocysteine"

FT Modified-site 14 /note= "NH2-Cys"

XX W09640750-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009623.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

XX Dower WJ, Barret RW, Cwirla SB, Duffin DJ, Gates CM, Johnson SS;
 PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

XX Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopaenia resulting from chemotherapy, etc.

XX Example 6; Page 63; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopaenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

XX Sequence 14 AA;

Query Match 66.7%; Score 76; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ADGPTLRWISFC 16
 |||||
 2 ADGPTLRWISFC 14

RESULT 42

AAW35396 ID AAW35396 standard; peptide; 14 AA.

XX AC AAW35396;

DT 11-MAR-1998 (first entry)

XX Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopaenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1. .14

FT Modified-site /note= "Penicillamine"

FT Modified-site 14 /note= "NH2-Cys"

XX W09640750-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009623.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

XX Dower WJ, Barret RW, Cwirla SB, Duffin DJ, Gates CM, Johnson SS;
 PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

XX Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopaenia resulting from chemotherapy, etc.

XX Example 6; Page 63; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopaenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

XX Sequence 14 AA;

Query Match 66.7%; Score 76; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ADGPTLREWISFC 16
 XX |||||
 XX 2 ADGPTLREWISFC 14

RESULT 43

ID AAM35402 standard; peptide; 14 AA.

AC AAM35402;

DT 11-MAR-1998 (first entry)

XX Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

KW hematological disorder; thrombocytopenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

XX signal transduction; receptor activation; cell culture.

OS Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1. .14

FT Modified-site /note= "D-form residue, Penicillamine"

FT Modified-site 14

FT Modified-site /note= "NH2-D-Cys"

XX WO9640750-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009623.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

XX Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

DR WPI; 1997-052226/05.

XX Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of hematological

PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX Example 6; Page 64; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be

CC used to treat disorders which are susceptible to treatment with a

CC thrombopoietin agonist, preferably hematological disorders and

CC thrombocytopenia resulting from chemotherapy; radiation therapy or bone

CC marrow transfusions. It can also be used diagnostically, e.g. to

CC investigate the mechanism of thrombopoietin signal transduction and

CC receptor activation, or to maintain the proliferation and growth of

CC thrombopoietin dependent cell lines

XX Sequence 14 AA;

SQ

Query Match 66.7%; Score 76; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00036;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ADGPTLREWISFC 16

XX |||||

XX 2 ADGPTLREWISFC 14

RESULT 44

AU25987

ID AU25987 standard; peptide; 14 AA.

AC AU25987;

DT 18-DEC-2001 (first entry)

XX Human thrombopoietin receptor (TPO-R) activator peptide #173.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;

KW bone marrow transplantation; hematological disorder; platelet disorder;

KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;

KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;

KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.

OS Homo sapiens.

XX US6251864-B1.

XX 26-JUN-2001.

XX 01-MAR-2000; 2000US-00516704.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

XX 07-JUN-1996; 96WO-US009623.

XX 15-AUG-1996; 96US-00699027.

XX (GLAX) GLAXO GROUP LTD.

XX Dower WJ, Barrett RM, Cwiria SE, Gates CM, Schatz PJ;

PI Balasubramanian P, Wagstrom CR, Hendren RM, Depierre RB, Podduturi S;

PI yin Q;

DR WPI; 2001-564142/63.

XX Activating thrombopoietin receptors in cells, used to treat

PT thrombocytopenia and hematological disorders, comprises contacting cells

PT with peptides and peptide mimetics attached to hydrophilic polymers.

XX Disclosure; Col 139; 128pp; English.

XX Sequences AU25815-AU26049 represent peptides and peptide mimetics that

CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods

CC of activating thrombopoietin receptors in cells comprise contacting the

CC cells with effective amounts of peptides and peptide mimetics attached to

CC hydrophilic polymers. The methods are used to treat thrombocytopenia such

CC as that due to chemotherapy, radiation therapy or bone-marrow

CC transplantation and to prevent thrombocytopenia in patients at risk. The

CC sequences are used to treat and prevent hematological disorders

CC including thrombocytopenia and platelet disorders. They are used in vitro

CC as unique tools for understanding the biological role of thrombopoietin

CC (TPO) and to develop other compounds that bind to and activate the TPO

CC receptor. The peptides can be used to detect TPO receptors on living

CC cells and fixed cells, in biological fluids, in tissue homogenates, and

CC in purified or natural biological materials. They may also be used for in

CC situ staining, fluorescence-activated cell sorting, Western blotting and

CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can

CC be used for in vitro expansion of megakaryocytes and their committed

CC progenitors alone or in conjunction with additional cytokines

XX Sequence 14 AA;

SQ

Query Match 66.7%; Score 76; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00036;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CADGPTLREWISF 15

XX |||||

XX 1 CADGPTLREWISF 13

RESULT 45

AU25987

Search completed: September 1, 2005, 16:12:10
Job time : 87.3453 secs

```

AAU25983
ID AAU25983 standard; peptide: 14 AA.
XX
AC AAU25983;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human thrombopoietin receptor (TPO-R) activator peptide #169.
XX
KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
KW bone marrow transplantation; haematological disorder; platelet disorder;
KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; Iaci gene.
XX
OS Homo sapiens.
XX
PN US651864-B1.
XX
PD 26-JUN-2001.
XX
PF 01-MAR-2000; 2000US-00516704.
XX
PR 07-JUN-1995; 95US-00478128.
PR 07-JUN-1995; 95US-00485301.
PR 07-JUN-1996; 96WO-US009623.
PR 15-AUG-1996; 96US-00699027.
XX
PA (GLAXO ) GLAXO GROUP LTD.
XX
PI Dower WJ, Barreclt RM, Cwiria SE, Gates CM, Schatz PJ,
PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;
PI Yin Q;
XX
DR WPI: 2001-564142/63.
XX
PT Activating thrombopoietin receptors in cells, used to treat
PT thrombocytopenia and hematological disorders, comprises contacting cells
PT with peptides and peptide mimetics attached to hydrophilic polymers.
XX
PS Disclosure; Col 135-137; 128pp; English.
XX
CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
CC of activating thrombopoietin receptors in cells comprise contacting the
CC cells with effective amounts of peptides and peptide mimetics attached to
CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
CC as that due to chemotherapy, radiation therapy or bone-marrow
CC transplantation and to prevent thrombocytopenia in patients at risk. The
CC sequences are used to treat and prevent haematological disorders
CC including thrombocytopenia and platelet disorders. They are used in vitro
CC as unique tools for understanding the biological role of thrombopoietin
CC (TPO) and to develop other compounds that bind to and activate the TPO
CC receptor. The peptides can be used to detect TPO receptors on living
CC cells and fixed cells, in biological fluids, in tissue homogenates, and
CC in purified or natural biological materials. They may also be used for in
CC situ staining, fluorescence-activated cell sorting, Western blotting and
CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
CC be used for in vitro expansion of megakaryocytes and their committed
CC progenitors alone or in conjunction with additional cytokines
XX
SQ Sequence 14 AA;

Query Match 56.7%; Score 76; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 ADGPTLRWISFC 16
|||||
2 ADGPTLRWISFC 14

```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2005, 15:57:33 ; Search time 14.4892 Seconds
(without alignment)
126.171 Million cell updates/sec

Title: US-10-083-768-8

Perfect score: 114
Sequence: 1 GGCCADGPTLRWISFCGSK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	43.0	245	2	T47701
2	47	41.2	475	2	T33943
3	46	40.4	346	2	A58583
4	45	39.5	108	2	T49731
5	45	39.5	180	2	T44944
6	45	39.5	421	2	T22969
7	45	39.5	499	2	S51089
8	44	38.6	346	2	T19008
9	44	38.6	371	2	D75266
10	44	38.6	490	2	T08084
11	44	38.6	526	2	A86440
12	44	38.6	974	2	S34189
13	44	38.6	1022	1	S00503
14	44	38.6	1023	2	A24414
15	44	38.2	376	2	T39685
16	43.5	38.2	1499	2	A88813
17	43	37.7	113	2	D72595
18	43	37.7	115	2	T15386
19	43	37.7	192	1	A24902
20	43	37.7	230	2	I48685
21	43	37.7	233	2	A82768
22	43	37.7	246	2	T15988
23	43	37.7	268	2	D97548
24	43	37.7	276	2	A38654
25	43	37.7	434	2	S21324
26	43	37.7	629	2	A82497
27	43	37.7	953	2	S54478
28	43	37.7	1010	2	B37227
29	43	37.7	1010	2	B37227

30	43	37.7	1013	1	S00801	Na+/K+-exchanging
31	43	37.7	1013	2	C24639	Na+/K+-exchanging
32	43	37.7	1017	2	A57227	Na+/K+-exchanging
33	43	37.7	1020	2	A34474	Na+/K+-exchanging
34	43	37.7	1020	2	B24639	Na+/K+-exchanging
35	43	37.7	1021	1	PWSHNA	Na+/K+-exchanging
36	43	37.7	1021	1	S04630	Na+/K+-exchanging
37	43	37.7	1021	2	A28139	Na+/K+-exchanging
38	43	37.7	1021	2	B24862	Na+/K+-exchanging
39	43	37.7	1022	2	S49127	Na+/K+-exchanging
40	43	37.7	1023	1	A24639	Na+/K+-exchanging
41	43	37.7	1023	1	S24650	Na+/K+-exchanging
42	43	37.7	1025	2	A60444	Na+/K+-exchanging
43	43	37.7	1027	1	PMCCMA	Na+/K+-exchanging
44	43	37.7	1038	1	S03632	Na+/K+-exchanging
45	42.5	37.3	210	2	A42687	neurotrophin-4 pre
46	42.5	37.3	353	2	T32638	hypothetical prote
47	42.5	37.3	1004	2	JH0470	Na+/K+-exchanging
48	42.5	37.3	1302	2	T00038	hypothetical prote
49	42	36.8	98	2	A70301	ribosomal protein
50	42	36.8	141	2	AH2829	conserved hypothet
51	42	36.8	141	2	F97607	hypothetical prote
52	42	36.8	192	1	S28148	erythropoietin pre
53	42	36.8	312	2	F86876	hypothetical prote
54	42	36.8	440	2	F81555	glutamate-1-semial
55	42	36.8	440	2	B86508	glutamate-1-semial
56	42	36.8	440	2	G72114	glutamate-1-semial
57	42	36.8	473	2	T31717	hypothetical prote
58	42	36.8	522	2	D69226	hypothetical prote
59	42	36.8	522	2	S62941	probable membrane
60	42	36.8	725	2	A11544	conserved hypothet
61	42	36.8	816	2	T08978	serine proteinase
62	42	36.8	842	2	T12091	serine phosphoryla
63	41.5	36.4	108	2	G82991	thioredoxin PA5240
64	41.5	36.4	108	2	G45522	similar to gibbere
65	41.5	36.4	209	2	B42687	neurotrophin-4 pre
66	41.5	36.4	359	2	T15470	hypothetical prote
67	41	36.0	132	1	G69256	conserved hypothet
68	41	36.0	189	2	C71943	hypothetical prote
69	41	36.0	189	2	S07755	hypothetical prote
70	41	36.0	206	2	T22345	hypothetical prote
71	41	36.0	239	2	AC2745	glycerophosphoryl
72	41	36.0	245	2	JC7273	inducible mast cel
73	41	36.0	246	2	B97526	hypothetical prote
74	41	36.0	273	2	H70849	hypothetical prote
75	41	36.0	274	2	A45754	tryptase (BC 3.4.2
76	41	36.0	275	2	C35863	tryptase (BC 3.4.2
77	41	36.0	298	2	T23362	hypothetical prote
78	41	36.0	410	1	DEPSXA	3-methyl-2-oxobuta
79	41	36.0	410	2	C83365	2-oxoisovalerate d
80	41	36.0	473	2	B84853	hypothetical prote
81	41	36.0	494	2	H82489	conserved hypothet
82	41	36.0	576	2	C88950	protein R09B5.11 l
83	41	36.0	593	2	S45281	coagulation factor
84	41	36.0	618	2	T48193	hypothetical prote
85	41	36.0	916	2	H72372	exonuclease ABC c
86	41	36.0	929	2	S75098	hypothetical prote
87	41	36.0	955	2	T10947	search phosphoryla
88	41	36.0	966	1	PHOAG	search phosphoryla
89	41	36.0	971	2	T09210	search phosphoryla
90	41	36.0	1000	2	S77243	protein p27F5.11 l
91	41	36.0	1313	2	B96509	hypothetical prote
92	41	36.0	1522	2	C96578	hypothetical prote
93	41	36.0	1616	2	T17884	S-layer protein -
94	40.5	35.5	369	2	B84542	hypothetical prote
95	40.5	35.5	1101	2	T16840	hypothetical prote
96	40.5	35.5	1363	2	T43220	insulin-like growt
97	40	35.1	152	2	S21826	T-cell receptor be
98	40	35.1	155	2	S23629	hypothetical prote
99	40	35.1	157	2	B83066	hypothetical prote
100	40	35.1	169	1	ICMS2	interleukin-2 prec

ALIGNMENTS

RESULT 1

T47701 translation initiation factor eIF-6-like protein [imported] - Arabidopsis thaliana

N/Alternate names: protein F1116.30

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C/Accession: T47701

R/Bones, V.; Wurmbach, E.; Dzyronek, H.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.

submitted to the Protein Sequence Database, March 2000

A/Reference number: Z24473

A/Accession: T47701

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-245 <BEN>

A/Cross-references: UNIPROT:Q9M060; EMBL:AL161667

A/Experimental source: cultivar Columbia; BAC clone F1116

C/Genetics:

A/Map position: 3

A/Intons: 4/1; 36/2; 65/1; 80/1; 123/3; 160/3

C/Superfamily: conserved hypothetical protein YPR016c

Query Match

Best Local Similarity 57.1%; Pred. No. 9.2;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 ADGPTLRWISFCG 17

DB 194 AAGTVDWTSFCG 207

RESULT 2

T33943 hypothetical protein C01B4.7 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C/Accession: T33943

R/Smith, A.; Wameley, P.; Fromack, W.

submitted to the EMBL Data Library, February 1999

A/Description: The sequence of C. elegans cosmid C01B4.

A/Reference number: Z21443

A/Accession: T33943

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-475 <SMI>

A/Cross-references: UNIPROT:Q9UAT5; EMBL:AF125952; PIDN:AAD14699.1; GSPDB:GN00023; CESP:

A/Experimental source: strain Bristol N2; clone C01B4

C/Genetics:

A/Map position: 5

A/Intons: 45/2; 80/1; 118/2; 189/3; 239/2; 340/3; 433/3

Query Match

Best Local Similarity 50.0%; Pred. No. 33;

Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFCG 18

DB 268 CTDRCVLSAWVSFLGG 283

RESULT 3

A58583 testostosterone-resistant immunity-associated protein IAP38 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C/Accession: A58583

R/Kneucken, J.; Schmitt-Wrede, H.P.; Markmann-Mulisch, U.; Wunderlich, F.

Biochem. Biophys. Res. Commun. 230, 167-170, 1997

A/Title: Novel gene expressed in spleen cells mediating acquired testosterone-resistant

A/Reference number: A58583; MUID:97148595; PMID:9020038

A/Accession: A58583

A/Molecule type: mRNA

A/Residues: 1-346 <KRU>

A/Cross-references: UNIPROT:P70224; GB:Y08026; NID:g1550784; PIDN:CAA69283.1; PID:g1550

C/Experimental source: spleen cell

C/Comment: This protein is a plasma membrane protein with two membrane-spanning domains

C/Genetics:

A/Accession: IAP38

F:148-167/Domain: transmembrane #status predicted <TW1>

F:320-335/Domain: transmembrane #status predicted <TW2>

Query Match

Best Local Similarity 41.2%; Pred. No. 35;

Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFCGK 19

DB 213 CTDRALRDLVVAECGR 229

RESULT 4

T49731 hypothetical protein B24B19.30 [imported] - Neurospora crassa

C/Species: Neurospora crassa

C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C/Accession: T49731

R/Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura

submitted to the Protein Sequence Database, May 2000

A/Reference number: Z25022

A/Accession: T49731

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-108 <SCH>

A/Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.30

A/Experimental source: BAC clone B24B19; strain OR74A

C/Genetics:

A/Map position: 6

A/Intons: 7; 118/2; 189/3; 239/2; 340/3; 433/3

C/Superfamily: Neurospora crassa hypothetical protein B24B19.30

Query Match

Best Local Similarity 39.5%; Pred. No. 17;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFC 16

DB 70 CQCQPIRLRWMLSWC 83

RESULT 5

T44944 hypothetical protein 5 [imported] - Natronobacterium pharaonis

C/Species: Natronobacterium pharaonis

C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C/Accession: T44944

R/Mattar, S.; Engelhard, W.

Eur. J. Biochem. 250, 332-341, 1997

A/Title: Cytochrome b23 from Natronobacterium pharaonis: An archaeal four-subunit cyto

A/Reference number: Z22876; MUID:9808958; PMID:9428682

A/Accession: T44944

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-180 <MAT>

A/Cross-references: UNIPROT:Q07291; EMBL:Y10500; PIDN:CAA71527.1

A/Experimental source: strain SP1/28

C/Genetics:

A/Map position: 5

A/Intons: 45/2; 80/1; 118/2; 189/3; 239/2; 340/3; 433/3

C/Superfamily: conserved hypothetical protein AF1745

Query Match

Best Local Similarity 39.5%; Pred. No. 27;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 9 LREWISFCG 17
 Db 116 LLEWISFCG 124

RESULT 6

T22969
 hypothetical protein F59A1.13 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T22969

R:Mottimore, B.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19644

A:Accession: T22969

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-421 <WIL>

A:Cross-references: UNIPROT:O9XUV7; EMBL:Z81557; PIDN:CA804538.1; GSPDB:GN00023; CESP:FS

A:Experimental source: clone F59A1

C:Genetics:

A:Gene: CESP:F59A1.13

A:Map position: 5

A:introns: 27/1; 116/1; 245/3; 286/3; 340/3; 381/3

Query Match 39.5%; Score 45; DB 2; Length 421;
 Best Local Similarity 50.0%; Pred. No. 58;
 Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 3 CADGPTLREWISFCG 18
 Db 214 CTDGTVLVGMISVFCG 229

RESULT 7

S51089
 ammonium transport protein MEP2 - yeast (Saccharomyces cerevisiae)

N:Alternate names: NH3 permease; protein JTA499; protein N1207; protein N1820; protein X

C:Species: Saccharomyces cerevisiae

C:Date: 10-May-1998 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C:Accession: S51089; S55142; S59247; S63087

R:Marini, A.M.; Andre, B.

submitted to the EMBL Data Library, December 1994

A:Reference number: S51089

A:Accession: S51089

A:Molecule type: DNA

A:Residues: 1-499 <MAR>

A:Cross-references: UNIPROT:P41948; EMBL:X83608; NID:G619513; PIDN:CA858587.1; PID:G6195

R:Mallet, L.; Bussereau, F.; Jacquet, M.

submitted to the EMBL Data Library, November 1994

A:Description: A 43.5 kb fragment of the chromosome XIV.

A:Reference number: S55136

A:Accession: S55142

A:Molecule type: DNA

A:Residues: 1-499 <MAL>

A:Cross-references: EMBL:Z46843; NID:G861113; PIDN:CA86884.1; PID:G854496

R:Mallet, L.; Bussereau, F.; Jacquet, M.

submitted to the EMBL Data Library, November 1994

A:Reference number: S59241; MUID:96109932; PMID:8619318

A:Accession: S59247

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-499 <MAW>

A:Cross-references: EMBL:Z46843; NID:G861113; PIDN:CA86884.1; PID:G854496

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994

R:Mallet, L.; Bussereau, F.; Jacquet, M.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S63069

A:Accession: S63087

A:Molecule type: DNA

A:Residues: 1-499 <MAF>
 A:Cross-references: EMBL:Z71418; NID:G1302090; PIDN:CA96025.1; PID:G1302091; MIPS:YNL1

A:Experimental source: strain S286C

C:Genetics:

A:Gene: SGD:MEP2

A:Cross-references: SGD:S0005086; MIPS:YNL142W

A:Map position: 14L

C:Function:

A:Description: ammonium transport

C:Superfamily: ammonium transport protein

C:Keywords: ammonium transport; transmembrane protein

F:35-51/Domain: transmembrane #status predicted <TM1>

F:62-78/Domain: transmembrane #status predicted <TM2>

F:123-139/Domain: transmembrane #status predicted <TM3>

F:154-170/Domain: transmembrane #status predicted <TM4>

F:228-244/Domain: transmembrane #status predicted <TM5>

F:288-304/Domain: transmembrane #status predicted <TM6>

F:306-322/Domain: transmembrane #status predicted <TM7>

F:397-413/Domain: transmembrane #status predicted <TM8>

Query Match 39.5%; Score 45; DB 2; Length 499;
 Best Local Similarity 38.5%; Pred. No. 68;
 Matches 10; Conservative 1; Mismatches 7; Indels 8; Gaps 1;

Qy 1 GGCADGPTLREWISF-----CGG 18
 Db 247 GGSAGNATIRAWYSIMGTNLAAACGG 272

RESULT 8

T19008
 hypothetical protein C06C6.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T19008

R:McMurray, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19059

A:Accession: T19008

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-346 <WIL>

A:Cross-references: UNIPROT:O62030; EMBL:Z93374; PIDN:CA807554.1; GSPDB:GN00023; CESP:G

A:Experimental source: clone C06C6

C:Genetics:

A:Gene: CESP:C06C6.2

A:Map position: 5

A:introns: 109/1; 135/2; 160/2; 310/1

Query Match 38.6%; Score 44; DB 2; Length 346;
 Best Local Similarity 56.2%; Pred. No. 68;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GCADGPTLREWISFCG 17
 Db 183 GLADGSTIYNWDSFIG 198

RESULT 9

D75266
 cell division protein, FtsW/RodZ/SpoVE family - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: D75266

R:White, O.; Eissen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: D75266

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-371 <WHI>
A:Cross-references: UNIPROT:Q9RRJ3; GB:AE002079; GB:AE000513; NID:G6460315; PIDN:AAE1203
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2497
A:Map position: 1
C:Superfamily: rod shape-determining protein

Query Match 38.6%; Score 44; DB 2; Length 371;
Best Local Similarity 43.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 GCADGPTLRWISFCG 17
Db 77 GSGDPSGVRWRLSTAG 92

RESULT 10
T09084
Phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)

C:Species: Chlamydomonas reinhardtii
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09084
R:Molendijk, A.J.; Irvine, R.F.
Plant Mol. Biol. 37, 53-66, 1998

A>Title: Inositolide signalling in Chlamydomonas: Characterization of a phosphatidylinositol
A:Reference number: Z16411; MUID:98281574; PMID:9620264

A:Accession: T09084
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-490 <MOL>

A:Cross-references: UNIPROT:O04270; EMBL:U97663; NID:G2109290; PIDN:AACS0018.1; PID:G210
A:Experimental source: strain CW-15
C:Genetics:

A:Introns: 265/3; 331/3; 370/3; 455/1; 481/3

Query Match 38.6%; Score 44; DB 2; Length 490;
Best Local Similarity 50.0%; Pred. No. 94;
Matches 10; Conservative 3; Mismatches 3; Indels 4; Gaps 2;

QY 1 GGCA--DGPTLR--EWISFC 16
Db 244 GGSSPFGDSTARKWDEMLTFC 263

RESULT 11

A86440
58.8K hypothetical protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: A86440
R:Thelloglou, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A86440
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-526 <STO>

A:Cross-references: UNIPROT:Q9C868; GB:AB005172; NID:G11054679; PIDN:AA627899.1; GSPDB:C
C:Genetics:

A:Map position: 1

Query Match 38.6%; Score 44; DB 2; Length 526;
Best Local Similarity 44.4%; Pred. No. 1e+02;

Matches 8; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
QY 1 GCADGPT--LRWISFC 16
Db 395 GGRVGRGSPPLINQWIEFC 412

RESULT 12

S34189
starch phosphorylase (EC 2.4.1.1) L - potato

C:Species: Solanum tuberosum (potato)
C>Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: S53489; S34189
R:Sommerwald, U.; Baener, A.; Greve, B.; Steup, M.

Plant Mol. Biol. 27, 567-576, 1995

A>Title: A second L-type isozyme of potato glucan phosphorylase: cloning, antisense inh
A:Reference number: S53489; MUID:95201249; PMID:7894019

A:Accession: S53489
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-974 <S02>

A:Cross-references: UNIPROT:P53535; EMBL:X73684; NID:G3133348; PIDN:CAA52036.1; PID:G313
C:Superfamily: glucan phosphorylase

C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphat
F:820/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 38.6%; Score 44; DB 2; Length 974;
Best Local Similarity 58.3%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 DGPTLRWISFC 16
Db 619 NGVTPRRWLSFC 630

RESULT 13

S00503
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - Pacific electric ray

C:Species: Torpedo californica (Pacific electric ray)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C:Accession: S00503; S28885; S29880
R:Kamakura, K.; Noguchi, S.; Noda, M.; Takahashi, H.; Ohta, T.; Kawamura, M.; Nojima, H

Nature 316, 733-736, 1985
A>Title: Primary structure of the alpha-subunit of Torpedo californica (Na(+)+K(+))ATPa
A:Reference number: S00503; MUID:8526307; PMID:2893905

A:Accession: S00503
A:Molecule type: mRNA

A:Residues: 1-1022 <KAW1>
A:Cross-references: UNIPROT:P05025; EMBL:X02810; NID:G64399; PIDN:CAA26578.1; PID:G6440

A:Accession: S28885
A:Molecule type: protein
A:Residues: 228-240/431-438;535-550;671-690;1011-1022 <KAW2>

R:Ohta, T.; Nagano, K.; Yoshida, M.
Proc. Natl. Acad. Sci. U.S.A. 83, 2071-2075, 1986

A>Title: The active site structure of Na(+)/K(+)-transporting ATPase: location of the 5
A:Reference number: S29880; MUID:86177549; PMID:3008150

A:Accession: S29880
A:Molecule type: protein

A:Residues: 386-402;502-512;671-689;887-906 <OHT>
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans

F:96-120/Domain: transmembrane #status predicted <TM1>
F:110-149/Domain: transmembrane #status predicted <TM2>
F:150-290/Domain: intracellular #status predicted <INT2>

F:291-313/Domain: transmembrane #status predicted <TM3>
F:320-348/Domain: transmembrane #status predicted <TM4>
F:349-785/Domain: intracellular #status predicted <INT3>

F:566-782/Domain: ATPase nucleotide-binding domain homology <ATNH>
F:786-809/Domain: transmembrane #status predicted <TM5>
F:848-873/Domain: transmembrane #status predicted <TM6>

F:874-951/Domain: intracellular #status predicted <INT4>
F:952-977/Domain: transmembrane #status predicted <TM7>
F:978-1022/Domain: extracellular #status predicted <EXT>

F:376/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:507/Binding site: ATP (Lys) #status predicted
 F:716,720,725/Active site: Asp, Asp, Lys #status predicted

Query Match 38.6%; Score 44; DB 1; Length 1022;
 Best Local Similarity 70.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16
 Db 84 PTPPEWIKFC 93

RESULT 14

A24414
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - human
 N:Alternate names: sodium pump; sodium/potassium transporting ATPase alpha-A chain
 C:Species: Homo sapiens (man)
 C>Date: 02-Jun-1988 #sequence revision 02-Jun-1988 #text_change 09-Jul-2004
 C:Accession: A24414; A27795; A39910; I60116; S09171
 R:Kawakami, K.; Ohta, T.; Nojima, H.; Nagano, K.
 J. Biochem. 100, 389-397, 1986
 A:Title: Primary structure of the alpha-subunit of human Na,K-ATPase deduced from cDNA
 A:Reference number: A24414; MUID:87057096; PMID:2430951
 A:Accession: A24414
 A:Molecule type: mRNA
 A:Residues: 1-1023 <XAM>
 A:Cross-references: UNIPROT:P05023; EMBL:X04297; NID:g28926; PIDN:CAA27840.1; PID:g28927
 R:Shull, M.M.; Lingrel, J.B.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
 A:Title: Multiple genes encode the human Na,K-ATPase catalytic subunit.
 A:Reference number: A94158; MUID:87231946; PMID:3035563
 A:Accession: A27795
 A:Molecule type: DNA
 A:Residues: 168-189;213-214,'X',216-244 <SHU>
 R:Chehab, F.F.; Kan, Y.W.; Law, M.L.; Hartz, J.; Kao, F.T.; Blostein, R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7901-7905, 1987
 A:Title: Human placental Na,K-ATPase alpha subunit: cDNA cloning, tissue expression, D
 A:Reference number: A39910; MUID:88068506; PMID:2891135
 A:Accession: A39910
 A:Molecule type: preliminary
 A:Status: preliminary
 A:Residues: 199-942 <CHE>
 A:Cross-references: GB:J03007
 R:Shull, M.M.; Pugh, D.G.; Lingrel, J.B.
 Genomics 6, 451-460, 1990
 A:Title: The human Na,K-ATPase alpha 1 gene: characterization of the 5'-flanking region
 A:Reference number: I60116; MUID:90228961; PMID:1970326
 A:Accession: I60116
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-61 <RES>
 A:Cross-references: GB:M30310; NID:g179206; PIDN:AAA51801.1; PID:g179208
 C:Genetics:
 A:Gene: GDB:ATP1A1
 A:Cross-references: GDB:119711; OMTM:182310
 A:Map position: 1p13-1p11
 C:Superfamily: Na+/K+-translocating ATPase alpha chain; ATPase nucleotide-binding domain
 C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
 F:6-1022/Product: Na+/K+-translocating ATPase alpha-1 chain #status predicted <MAT>
 F:6-95/Domain: Intracellular #status predicted <INT1>
 F:96-130/Domain: transmembrane #status predicted <TM1>
 F:130-149/Domain: transmembrane #status predicted <TM2>
 F:150-200/Domain: intracellular #status predicted <INT2>
 F:291-313/Domain: transmembrane #status predicted <TM3>
 F:320-348/Domain: transmembrane #status predicted <TM4>
 F:349-766/Domain: intracellular #status predicted <INT3>
 F:587-783/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:787-810/Domain: transmembrane #status predicted <TM5>
 F:849-874/Domain: transmembrane #status predicted <TM6>
 F:875-952/Domain: intracellular #status predicted <INT4>
 F:953-978/Domain: transmembrane #status predicted <TM7>
 F:979-1023/Domain: extracellular #status predicted <EXT>

F:376/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:508/Binding site: ATP (Lys) #status predicted
 F:717,721,726/Active site: Asp, Asp, Lys #status predicted

Query Match 38.6%; Score 44; DB 2; Length 1023;
 Best Local Similarity 70.0%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16
 Db 84 PTPPEWIKFC 93

RESULT 15

T39685
 conserved hypothetical protein SPBC1778.03c - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T39685
 R:Oliver, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, March 1998
 A:Reference number: Z21869
 A:Accession: T39685
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-376 <OLI>
 A:Cross-references: UNIPROT:Q9Y7J0; EMBL:AL049489; PIDN:CAB39798.1; GSPDB:GN00067; SPDB
 A:Experimental source: strain 972h; cosmid cl778
 C:Genetics:
 A:Gene: SPDB:SPBC1778.03c
 A:Map position: 2
 A:introns: 11/2

Query Match 38.2%; Score 43.5; DB 2; Length 376;
 Best Local Similarity 42.9%; Pred. No. 87;
 Matches 9; Conservative 3; Mismatches 6; Indels 3; Gaps 1;

QY 1 GGCADGPTLRBWS---FCGG 18
 Db 164 GACAFARSIDWISRYRCPG 184

RESULT 16

A89813
 glutamate synthase large subunit [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C>Date: 10-May-2001 #sequence revision 10-May-2001 #text_change 16-Aug-2004
 C:Accession: A89813
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
 ma, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: A89813
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1499 <RUR>
 A:Cross-references: UNIPROT:Q99WD1; GB:BA000018; PID:g13700362; PIDN:BA041660.1; GSPDB:
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: gltB
 C:Superfamily: Glutamate synthase, large subunit

Query Match 38.2%; Score 43.5; DB 2; Length 1499;
 Best Local Similarity 64.3%; Pred. No. 3.1e+02;
 Matches 9; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 5 DGPTLRMISFCGG 18
 Db 339 DGPTM---ISFCNG 349

```
RESULT 17
D72595
hypothetical protein APE1229 - Aeropyrum pernix (strain K1)
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: D72595
R/Kawababyaai, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takai-
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A/Reference number: A72450; MUID:9310339; PMID:10382966
A/Accession: D72595
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-113 <KMW>
A/Cross-references: UNIPROT:Q9YCM9; DDBJ:AP000061; NID:95104821; PIDN:BAAB0218.1; PID:Q1
A/Experimental source: strain K1
C/Genetics:
A/Gene: APE1229

Query Match          37.7%; Score 43; DB 2; Length 113;
Best Local Similarity 61.5%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 GPTLRWISFCG 18
    |||:|||||
Db 21 GEARLRCWPSFCG 33

RESULT 18
T15386
hypothetical protein CO3B1.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15386
R/Martin, V.
Submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid CO3B1.
A/Reference number: Z18340
A/Accession: T15386
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-115 <MAR>
A/Cross-references: UNIPROT:Q11110; EMBL:U40952; NID:91072237; PID:91072244; PIDN:AAA817
C/Genetics:
A/Gene: CESP:CO3B1.3
A/Introns: 80/1

Query Match          37.7%; Score 43; DB 2; Length 115;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFCG 17
    |||:|||||
Db 68 CAGGEVHHWACFCG 82

RESULT 19
A24902
erythropoietin precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 25-Oct-1997 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C/Accession: A24902; A24901
R/Shoemaker, C.B.; Miltsock, L.D.
Mol. Cell. Biol. 6, 849-858, 1986
A/Title: Murine erythropoietin gene: cloning, expression, and human gene homology.
A/Reference number: A24902; MUID:87039105; PMID:3773894
A/Accession: A24902
A/Molecule type: DNA
A/Residues: 1-192 <SHO>
A/Cross-references: UNIPROT:P07321
A/Note: the authors translated the codon TTA for residue 12 as Phe, TTA for residue 43 as
R; McDonald, J.D.; Lin, F.K.; Goldwasser, E.
```

```
Mol. Cell. Biol. 6, 842-848, 1986
A/Title: Cloning, sequencing, and evolutionary analysis of the mouse erythropoietin gene
A/Reference number: A24901; MUID:87039104; PMID:3022133
A/Accession: A24901
A/Molecule type: DNA
A/Residues: 1-67, 'P', 69-192 <MCD>
A/Cross-references: GB:M12930; NID:9193086; PIDN:AAA7570.1; PID:9387152
C/Comment: Erythropoietin is produced by kidney or liver of adult mammals and by liver c
C/Genetics:
A/Introns: 5/1; 52/3; 81/3; 141/3
C/Function:
A/Description: the primary inducer of erythrocyte formation
C/Superfamily: erythropoietin
C/Keywords: erythropoiesis; glycoprotein; hormone; kidney; liver
F/1-26/Domain: signal sequence #status predicted <SIG>
F/27-192/Product: erythropoietin #status predicted <MAT>
F/33-187, 55-165/Disulfide bonds: #status predicted
F/50, 64, 109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          37.7%; Score 43; DB 1; Length 192;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 GCADGPTLRWISFCG 19
    |||:|||||
Db 54 GCAEGPRLSENITVADTK 71

RESULT 20
I46885
mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I46885; S43172
R/Huang, R.; Hellman, L.
Immunogenetics 40, 397-414, 1994
A/Title: Genes for mast-cell serine protease and their molecular evolution.
A/Reference number: I46884; MUID:95048582; PMID:7959952
A/Accession: I46885
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-230 <RES>
A/Cross-references: UNIPROT:P1845; EMBL:X78542; NID:9468809; PIDN:CAA55288.1; PID:9468
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; serine proteinase
F/32-230/Domain: trypsin homology #status atypical <TRY>

Query Match          37.7%; Score 43; DB 2; Length 230;
Best Local Similarity 70.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 LRWISFCG 18
    |||:|||||
Db 53 LNYWIHFCCG 62

RESULT 21
AB2768
lipote liposynthesis protein B [imported] - Agrobacterium tumefaciens (strain C58, Dupo
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AB2768
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guentherer, D.; Kulyavin, T.; Levy, R.; Li, M.; Mclel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AB2768
A/Status: preliminary
A/Molecule type: DNA
```


A;Residues: 1-233 <KTR>
A;Cross-references: UNIPROT:Q8UF44; GB:AE008688; PIDN:AA42560.1; PID:G17739983; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: 11pB
A;Map position: circular chromosome
C;Superfamily: Becherichia coli lipocate-protein ligase 11pB

Query Match 37.7%; Score 43; DB 2; Length 233;
Best Local Similarity 43.5%; Pred. No. 66;
Matches 10; Conservative 3; Mismatches 4; Indels 6; Gaps 1;

QY 1 GGCAD-----GPTLRWISFCG 17
DB 148 GGMADKIALGIRLRKWSFPG 170

RESULT 22

T19988
hypothetical protein C47B2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19988
R;Keshaw, J.
submitted to the EMBL Data Library, October 1997
A;Reference number: Z19208
A;Accession: T19988
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-246 <WIL>
A;Cross-references: UNIPROT:O62106; EMBL:Z99709; PIDN:CA316860.1; GSPDB:GN00019; CESP:CA
A;Experimental source: clone C47B2
C;Genetics:
A;Gene: CESP:C47B2.5
A;Map position: 1
A;Intons: 91/3; 127/3
C;Superfamily: conserved hypothetical protein YPR016c

Query Match 37.7%; Score 43; DB 2; Length 246;
Best Local Similarity 41.7%; Pred. No. 70;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 6 GPTLRWISFCG 17
DB 196 GMYVNDWVAFPG 207

RESULT 23

T01012
probable translation initiation factor [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T517.12
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01012; H84821
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, November 1997
A;Description: Arabidopsis thaliana chromosome II BAC T517 genomic sequence.
A;Reference number: Z14152

A;Accession: T01012
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-247 <ROU>
A;Cross-references: UNIPROT:O22290; EMBL:AC003000; NID:G2642152; PIDN:AA87131.1; PID:G2
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Koffel, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Taiton, L.;
euser, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-769, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84821
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-247 <SNO>
A;Cross-references: GB:AE002093; NID:G2642164; PIDN:AA87131.1; GSPDB:GN00139
C;Genetics:
A;Gene: T517.12; At2g39820
A;Map position: 2
A;Intons: 4/1; 38/2; 82/1; 162/3
C;Superfamily: conserved hypothetical protein YPR016c

Query Match 37.7%; Score 43; DB 2; Length 247;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 GPTLRWISFCG 17
DB 198 GLTVNDWTAFPG 209

RESULT 24

D97548
lipocate-protein ligase b (lipocate biosynthesis protein b) [imported] - Agrobacterium tu
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97548
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: D97548
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-268 <KTR>
A;Cross-references: UNIPROT:Q8UF44; GB:AE007869; PIDN:AAK87341.1; PID:G15156641; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: AGR C.2865
A;Map position: circular chromosome
C;Superfamily: Becherichia coli lipocate-protein ligase 11pB

Query Match 37.7%; Score 43; DB 2; Length 268;
Best Local Similarity 43.5%; Pred. No. 75;
Matches 10; Conservative 3; Mismatches 4; Indels 6; Gaps 1;

QY 1 GGCAD-----GPTLRWISFCG 17
DB 183 GGMADKIALGIRLRKWSFPG 205

RESULT 25

A38654
mast cell proteinase 6 (BC 3.4.21.-) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Feb-1992 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A38654; B38654; D35646; I59478
R;Remold, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E.
J. Biol. Chem. 266, 3847-3853, 1991

A;Title: Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription by p
A;Reference number: A38654; MUID:91139682; PMID:1995638
A;Accession: A38654
A;Molecule type: DNA
A;Residues: 1-276 <REV>
A;Cross-references: UNIPROT:P21845; GB:M57625; NID:G200506; PIDN:AA39987.1; PID:G20050
A;Note: the authors translated the codon GGC for residue 24 as Ala, GAG for residue 37
as Gly, GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly
A;Accession: B38654
A;Molecule type: mRNA
A;Residues: 1-276 <RE2>
A;Cross-references: GB:M57626; NID:G200508; PIDN:AA39988.1; PID:G200509
R;Remold, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990
A;Title: Different mouse mast cell populations express various combinations of at least
A;Reference number: A35646; MUID:90222202; PMID:2326280
A;Accession: D35646
A;Status: preliminary
A;Molecule type: protein

A:Residues: 32-54 <RES>
R:Hang, R.; Abrik, M.; Gobl, A.E.; Nilsson, G.; Aveskog, M.; Larsson, L.G.; Nilsson, Scand J. Immunol 38, 359-367, 1993
A:Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and A:Reference number: 159478; MUID:94023807; PMID:8210998
A:Accession: 159478
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-276 <RES>
A:Cross-references: GB:L31853; NID:g473480; PIDN:AAA39725.1; PID:g473481
C:Genetics:
A:Gene: MCP-6
A:Introns: 24/1; 79/2; 168/1; 222/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase; zymogen
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-31/Domain: activation peptide #status predicted <ACT>
F:32-276/Product: mast cell proteinase 6 #status experimental <MAT>
F:32-268/Domain: trypsin homology <TRY>
F:75,122,225/Active site: His, Asp, Ser #status predicted

Query Match 37.7%; Score 43; DB 2; Length 276;
Best Local Similarity 70.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 9 LREWISFCGG 18
|||
|||
Db 53 LNYWIHFCGG 62

RESULT 26
S21374
probable beta-glucosidase - Ruminococcus flavefaciens
C:Species: Ruminococcus flavefaciens
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S21324
R:Hang, C.M.; Asmurdson, R.V.; Yu, P.L.
submitted to the EMBL Data Library, September 1990
A:Description: Nucleotide sequence of a cellulase gene complex from Ruminococcus flavefaciens
A:Reference number: S21323
A:Accession: S21324
A:Molecule type: DNA
A:Residues: 1-434 <HND>
A:Cross-references: UNIPROT:Q52748; EMBL:X56082; NID:g46152; PIDN:CA39560.1; PID:e33392
A:Note: the coding region was assigned by the authors; it does not start with ATG and over A:Note: the authors designated this protein as beta-glucosidase

Query Match 37.7%; Score 43; DB 2; Length 434;
Best Local Similarity 50.0%; Pred. No. 1,2e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 6 GPTLEWISFCGGK 19
|||
|||
Db 75 GPSYGYWYTCGGK 88

RESULT 27
AE2497
Hypothetical protein alr7157 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120a1
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE2497
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriguichin, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Nucleic Acids Res. 8, 205-211, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE2497
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-629 <KUR>
A:Cross-references: UNIPROT:Q8YK1; GB:BA000020; PIDN:BA078241.1; PID:g17135695; GSPDB:C01

```

A:Experimental source: strain FCC 7120
C:Genetics:
A:Gene: alr7157
A:Genome: plasmid

Query Match      37.7%; Score 43; DB 2; Length 629;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY      9 LREWISFCGK 19
      ||::|||
Db      215 LKQWNEFCAGK 225

RESULT 28
S54478
probable membrane protein YMR266w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YMR156.08
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
R:Lye, G.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54014
A:Accession: S54478
A:Molecule type: DNA
A:Residues: 1-953 <LYE>
A:Cross-references: UNIPROT:Q03516; EMBL:Z49260; NID:g809081; PID:g809089; GSFDB:GN0001
A:Experimental source: strain AB972
C:Genetics:
A:Gene: SGD:RSN1; MIPS:YMR266w
A:Cross-references: SGD:S0004879
A:Map position: 13R
C:Superfamily: yeast probable membrane protein YOL084w
C:Keywords: transmembrane protein
F:32-48/Domain: transmembrane #status predicted <TM1>
F:106-122/Domain: transmembrane #status predicted <TM2>
F:152-168/Domain: transmembrane #status predicted <TM3>
F:395-411/Domain: transmembrane #status predicted <TM4>
F:435-451/Domain: transmembrane #status predicted <TM5>
F:545-561/Domain: transmembrane #status predicted <TM6>
F:599-625/Domain: transmembrane #status predicted <TM7>
F:646-662/Domain: transmembrane #status predicted <TM8>
F:668-684/Domain: transmembrane #status predicted <TM9>

Query Match      37.7%; Score 43; DB 2; Length 953;
Best Local Similarity 41.2%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY      1 GGCADGPTLRWISFCG 17
      ||::|||
Db      558 GAFDGTVRKKMRFCG 574

RESULT 29
B37227
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - chicken
C:Species: Gallus gallus (chicken)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C:Accession: B37227; I50395
R:Takeyasu, K.; Lemae, V.; Fambrough, D.M.
Am. J. Physiol. 259, C619-C630, 1990
Article: Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms in evolution.
A:Reference number: A37227; MUID:91023019; PMID:2171348
A:Accession: B37227
A:Molecule type: mRNA
A:Residues: 1-1010 <TM2>
A:Cross-references: UNIPROT:P24798; GB:M59960; NID:g212407; PTDN:AAA48982.1; PID:g212407
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium t
F:574-770/Domain: ATPase nucleotide-binding domain homology <ATN>
F:202-470/Binding site: carboxylate (Asn) (covalent) #status predicted
F:363/Active site: Asp (separtylphosphate intermediate) #status predicted

```

F:495/Binding site: ATP (Lys) #status predicted

Query Match 37.7%; Score 43; DB 2; Length 1010;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 7 PTLREWSFC 16
Db 71 PTPREWKFC 80

RESULT 30

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: S00801; S04019; A27397; S02275
R:Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Broudé, N.E.; Ushkaryov, Y.A.; Melkov, A.M.; S
dyanov, N.N.; Sverdlov, E.D.
FEBS Lett. 233, 87-94, 1988
A:Title: Family of human Na,K-ATPase genes. Structure of the gene for the catalytic subu
A:Reference number: S00801; MUID:88255304; PMID:2838329
A:Accession: S00801

A:Molecule type: DNA
A:Residues: 1-1013 <OVC>
A:Cross-references: UNIPROT:P13637; EMBL:M37456
R:Sverdlov, E.D.; Monastyrskaya, G.S.; Broudé, N.E.; Ushkaryov, Y.A.; Melkov, A.M.; Smir
ov, N.N.; Ovchinnikov, Y.A.
Dokl. Biochem. 297, 426-431, 1987
A:Title: Family of human Na(+),K(+)-ATPase genes. Structure of the gene of isoform alpha
A:Reference number: S04019
A:Accession: S04019

A:Molecule type: DNA
A:Residues: 1,'EIH','3-1013 <SVE1>
A:Cross-references: EMBL:X1910; NID:928963
A:Note: The authors translated the codon TTC for residue 283 as Ser and TCT for residue
A:Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk S
R:Sverdlov, E.D.; Monastyrskaya, G.S.; Broudé, N.E.; Ushkaryov, Y.A.; Allikmets, R.L.; M
elkov, A.M.; Sverdlov, E.D.; Modyanov, N.N.; Ovchinnikov, Y.A.
FEBS Lett. 217, 275-278, 1987
A:Title: The family of human Na,K-ATPase genes. No less than five genes and/or pseudog
A:Reference number: A27397; MUID:87247232; PMID:3036582
A:Accession: A27397

A:Molecule type: mRNA
A:Residues: 243-434 <SVE2>
A:Cross-references: GB:M27570
C:Genetics:
A:Gene: GDB:ATP1A3
A:Cross-references: GDB:119713; OMIM:182350
A:Map position: 19q13.2-19q13.2
A:Introns: 2/3; 31/3; 51/3; 119/3; 157/3; 202/3; 242/1; 331/3; 398/1; 435/2; 479/3; 544/
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F:86-110/Domain: transmembrane #status predicted <TM1>
F:120-119/Domain: transmembrane #status predicted <TM2>
F:140-280/Domain: intracellular #status predicted <INT2>
F:281-303/Domain: transmembrane #status predicted <TM3>
F:310-338/Domain: intracellular #status predicted <INT3>
F:339-776/Domain: intracellular #status predicted <INT4>
F:577-773/Domain: ATPase nucleotide-binding domain homology <ATN>
F:777-800/Domain: transmembrane #status predicted <TM5>
F:839-864/Domain: transmembrane #status predicted <TM6>
F:865-942/Domain: intracellular #status predicted <INT4>
F:943-968/Domain: transmembrane #status predicted <TM7>
F:965-1013/Domain: extracellular #status predicted <EXT>
F:366/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:498/Binding site: Asp (Lys) #status predicted
F:707,711,716/Active site: Asp, Asp, Lys #status predicted

Query Match 37.7%; Score 43; DB 1; Length 1013;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 7 PTLREWSFC 16
Db 74 PTPREWKFC 83

RESULT 31

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - rat
C:Accession: C24639
N:Alternate names: Na+/K+-transporting ATPase alpha (III) chain
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence revision 23-Apr-1993 #text_change 09-Jul-2004
C:Accession: C24639; S00514; B27180; A60470
R:Shull, G.E.; Greeb, J.; Lingrel, J.B.
Biochemistry 25, 8125-8132, 1986

A:Title: Molecular cloning of three distinct forms of the Na,K-ATPase alpha-subunit f
A:Reference number: A90512; MUID:87128908; PMID:3028470
A:Accession: C24639
A:Molecule type: mRNA
A:Residues: 1-1013 <SHU>
A:Cross-references: UNIPROT:P06687; EMBL:M4513; NID:9203030; PIDN:AAA40777.1; PID:9203
A:Note: In the authors' translation 405-Ser is shown after residue 409 and, consequentl
R:Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Kojima, T.; Ohta, T.;
J. Biochem. 102, 43-58, 1987
A:Title: Primary structures of two types of alpha-subunit of rat brain Na(+),K(+)-ATPase
A:Reference number: S00460; MUID:88032933; PMID:2822682
A:Accession: S00514

A:Molecule type: mRNA
A:Residues: 1-907,'C','909-1013 <HAR>
A:Cross-references: EMBL:X05883; NID:955769; PIDN:CAA29307.1; PID:955770
R:Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard, B.
J. Cell Biol. 105, 1855-1865, 1987
A:Title: Three differentially expressed Na,K-ATPase alpha subunit isoforms: structural
A:Reference number: A92749; MUID:88033255; PMID:2822726
A:Accession: B27180

A:Molecule type: mRNA
A:Residues: 1,'NL','4-103','R','105-113','E','115-127','G','129-148','Q','150-151','T','153-165','D
A:Cross-references: EMBL:M26648; NID:9205633; PIDN:AAA1672.1; PID:9205634
A:Note: The authors translated the codon CAG for residue 149 as Glu, GGC for residue 19
R:Han, Y.M.; Goldetti, G.
Biochemistry 28, 569-573, 1989
A:Title: Rat brain has the alpha3 form of the (Na+,K+)ATPase.
A:Reference number: A60470; MUID:89229049; PMID:2540801
A:Accession: A60470

A:Molecule type: protein
A:Residues: 117-132;586-595,'X','597-601 <HSU>
C:Comment: The alpha-3 form appears to be highly ouabain-inhibitable, as is alpha-2 but
C:Genetics:
A:Gene: NKX3
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans

F:86-110/Domain: transmembrane #status predicted <TM1>
F:120-119/Domain: transmembrane #status predicted <TM2>
F:140-280/Domain: intracellular #status predicted <INT2>
F:281-303/Domain: transmembrane #status predicted <TM3>
F:310-338/Domain: intracellular #status predicted <INT3>
F:339-776/Domain: intracellular #status predicted <INT4>
F:577-773/Domain: ATPase nucleotide-binding domain homology <ATN>
F:777-800/Domain: transmembrane #status predicted <TM5>
F:839-864/Domain: transmembrane #status predicted <TM6>
F:865-942/Domain: intracellular #status predicted <INT4>
F:943-968/Domain: transmembrane #status predicted <TM7>
F:965-1013/Domain: extracellular #status predicted <EXT>
F:366/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:498/Binding site: Asp (Lys) #status predicted
F:707,711,716/Active site: Asp, Asp, Lys #status predicted

Query Match 37.7%; Score 43; DB 2; Length 1013;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 7 PTLREWSFC 16
Db 74 PTPREWKFC 83

RESULT 32

A37227
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - chicken
C/Species: Gallus gallus (chicken)
C/Date: 16-Sep-1992 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: I50394; A37227
R/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F/6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MNT>
F/6-93/Domain: intracellular #status predicted <INT1>
F/94-118/Domain: transmembrane #status predicted <TM1>
F/128-147/Domain: transmembrane #status predicted <TM2>
F/148-288/Domain: intracellular #status predicted <INT2>
F/289-311/Domain: transmembrane #status predicted <TM3>
F/318-346/Domain: transmembrane #status predicted <TM4>
F/347-783/Domain: intracellular #status predicted <INT3>
F/584-780/Domain: ATPase nucleotide-binding domain homology <ATN>
F/784-807/Domain: transmembrane #status predicted <TM5>
F/846-871/Domain: transmembrane #status predicted <TM6>
F/872-949/Domain: intracellular #status predicted <INT4>
F/950-975/Domain: transmembrane #status predicted <TM7>
F/976-1020/Domain: extracellular #status predicted <EXT>
F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/505/Binding site: Asp (Lys) #status predicted
F/714,718,723/Active site: Asp, Asp, Lys #status predicted

A/Accession: I50394
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1017 <TA>
A/Cross-references: UNIPROT:P2797; GB:M5959; NID:g212405; PIDN:AAA48981.1; PID:g212406
R/Keywords: ATP; glycoprotein; hydrolase; phosphoprotein
F/581-777/Domain: ATPase nucleotide-binding domain homology <ATN>
F/210,478/Binding site: carboxylate (Asn) (covalent) #status predicted
F/371/Active site: Asp (aspartylphosphate intermediate) #status predicted

A/Accession: A37227
A/Molecule type: mRNA
A/Residues: 3-1017 <TA>
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; glycoprotein; hydrolase; phosphoprotein
F/581-777/Domain: ATPase nucleotide-binding domain homology <ATN>
F/210,478/Binding site: carboxylate (Asn) (covalent) #status predicted
F/371/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match

Best Local Similarity 37.7%; Score 43; DB 2; Length 1017;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16
DB 79 PTLPEWVKFC 88

RESULT 33

A34474
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - human
N/Alternate names: Na+/K+-exchanging ATPase alpha chain-4; sodium/potassium transporting
C/Species: Homo sapiens (man)
C/Date: 15-Jun-1990 #sequence revision 15-Jun-1990 #text_change 09-Jul-2004
C/Accession: A34474; B27795; D27397
R/Keywords: ATP; glycoprotein; hydrolase; phosphoprotein
F/581-777/Domain: ATPase nucleotide-binding domain homology <ATN>
F/210,478/Binding site: carboxylate (Asn) (covalent) #status predicted
F/371/Active site: Asp (aspartylphosphate intermediate) #status predicted

A/Accession: A34474
A/Molecule type: DNA
A/Residues: 1-1020 <SHU>
A/Cross-references: UNIPROT:P50993; GB:J05096; NID:g179164; PIDN:AAA51797.1; PID:g179165
R/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F/6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MNT>
F/6-93/Domain: intracellular #status predicted <INT1>
F/94-119/Domain: transmembrane #status predicted <TM1>
F/128-147/Domain: transmembrane #status predicted <TM2>
F/148-288/Domain: intracellular #status predicted <INT2>
F/289-311/Domain: transmembrane #status predicted <TM3>
F/318-346/Domain: transmembrane #status predicted <TM4>
F/347-783/Domain: intracellular #status predicted <INT3>
F/584-780/Domain: ATPase nucleotide-binding domain homology <ATN>
F/784-807/Domain: transmembrane #status predicted <TM5>
F/846-871/Domain: transmembrane #status predicted <TM6>
F/872-949/Domain: intracellular #status predicted <INT4>
F/950-975/Domain: transmembrane #status predicted <TM7>
F/976-1020/Domain: extracellular #status predicted <EXT>
F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/505/Binding site: Asp (Lys) #status predicted
F/714,718,723/Active site: Asp, Asp, Lys #status predicted

A/Reference number: A94158; MUID:87231946; PMID:3035563
A/Accession: B27795
A/Molecule type: DNA
A/Residues: 211-249 <SH2>
A/Cross-references: GB:M16795; NID:g179196; PIDN:AAA51799.1; PID:g553194
R/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F/6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MNT>
F/6-93/Domain: intracellular #status predicted <INT1>
F/94-119/Domain: transmembrane #status predicted <TM1>
F/128-147/Domain: transmembrane #status predicted <TM2>
F/148-288/Domain: intracellular #status predicted <INT2>
F/289-311/Domain: transmembrane #status predicted <TM3>
F/318-346/Domain: transmembrane #status predicted <TM4>
F/347-783/Domain: intracellular #status predicted <INT3>
F/584-780/Domain: ATPase nucleotide-binding domain homology <ATN>
F/784-807/Domain: transmembrane #status predicted <TM5>
F/846-871/Domain: transmembrane #status predicted <TM6>
F/872-949/Domain: intracellular #status predicted <INT4>
F/950-975/Domain: transmembrane #status predicted <TM7>
F/976-1020/Domain: extracellular #status predicted <EXT>
F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/505/Binding site: Asp (Lys) #status predicted
F/714,718,723/Active site: Asp, Asp, Lys #status predicted

A/Reference number: A27397; MUID:87247232; PMID:3036582
A/Accession: D27397
A/Molecule type: DNA
A/Residues: 251-442 <SVE>
A/Cross-references: GB:M27571
C/Genetics:
A/Gene: GDB:ATP1A2

A/Cross-references: GDB:119712; OMIM:182340

A/Map position: 1q21-1q23
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F/6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MNT>
F/6-93/Domain: intracellular #status predicted <INT1>
F/94-118/Domain: transmembrane #status predicted <TM1>
F/128-147/Domain: transmembrane #status predicted <TM2>
F/148-288/Domain: intracellular #status predicted <INT2>
F/289-311/Domain: transmembrane #status predicted <TM3>
F/318-346/Domain: transmembrane #status predicted <TM4>
F/347-783/Domain: intracellular #status predicted <INT3>
F/584-780/Domain: ATPase nucleotide-binding domain homology <ATN>
F/784-807/Domain: transmembrane #status predicted <TM5>
F/846-871/Domain: transmembrane #status predicted <TM6>
F/872-949/Domain: intracellular #status predicted <INT4>
F/950-975/Domain: transmembrane #status predicted <TM7>
F/976-1020/Domain: extracellular #status predicted <EXT>
F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/505/Binding site: Asp (Lys) #status predicted
F/714,718,723/Active site: Asp, Asp, Lys #status predicted

Query Match

Best Local Similarity 37.7%; Score 43; DB 2; Length 1020;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16
DB 82 PTLPEWVKFC 91

RESULT 34

B24639
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - rat
N/Alternate names: Na+/K+-transporting ATPase alpha-plus chain
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text_change 09-Jul-2004
C/Accession: B24639
R/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F/6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MNT>
F/6-93/Domain: intracellular #status predicted <INT1>
F/94-119/Domain: transmembrane #status predicted <TM1>
F/128-147/Domain: transmembrane #status predicted <TM2>
F/148-288/Domain: intracellular #status predicted <INT2>
F/289-311/Domain: transmembrane #status predicted <TM3>
F/318-346/Domain: transmembrane #status predicted <TM4>
F/347-783/Domain: intracellular #status predicted <INT3>
F/584-780/Domain: ATPase nucleotide-binding domain homology <ATN>
F/784-807/Domain: transmembrane #status predicted <TM5>
F/846-871/Domain: transmembrane #status predicted <TM6>
F/872-949/Domain: intracellular #status predicted <INT4>
F/950-975/Domain: transmembrane #status predicted <TM7>
F/976-1020/Domain: extracellular #status predicted <EXT>
F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/505/Binding site: Asp (Lys) #status predicted
F/714,718,723/Active site: Asp, Asp, Lys #status predicted

A/Accession: B24639
A/Molecule type: mRNA
A/Residues: 1-1020 <SHU>
A/Cross-references: UNIPROT:P06666; EMBL:M14512; NID:g203028; PIDN:AAA40776.1; PID:g203
C/Genetics:
A/Gene: NIKRA2
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F/6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MNT>
F/6-93/Domain: intracellular #status predicted <INT1>
F/94-119/Domain: transmembrane #status predicted <TM1>
F/128-147/Domain: transmembrane #status predicted <TM2>
F/148-288/Domain: intracellular #status predicted <INT2>
F/289-311/Domain: transmembrane #status predicted <TM3>
F/318-346/Domain: transmembrane #status predicted <TM4>
F/347-783/Domain: intracellular #status predicted <INT3>
F/584-780/Domain: ATPase nucleotide-binding domain homology <ATN>
F/784-807/Domain: transmembrane #status predicted <TM5>
F/846-871/Domain: transmembrane #status predicted <TM6>
F/872-949/Domain: intracellular #status predicted <INT4>
F/950-975/Domain: transmembrane #status predicted <TM7>
F/976-1020/Domain: extracellular #status predicted <EXT>
F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/505/Binding site: Asp (Lys) #status predicted
F/714,718,723/Active site: Asp, Asp, Lys #status predicted

Query Match

Best Local Similarity 37.7%; Score 43; DB 2; Length 1020;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLREWISFC 16

Db 82 PTPBWKFC 91

RESULT 35

PMSHNA

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - sheep
N/Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha chain
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004

C/Accession: A01074; A35426

R/Shull, G.E.; Schwartz, A.; Lingrel, J.B.

Nature 316, 691-695, 1985

A/Title: Amino-acid sequence of the catalytic subunit of the (Na(+)+K(+)) ATPase deduced

A/Reference number: A01074; MUID:85296299; PMID:2993903

A/Accession: A01074

A/Molecule type: mRNA

A/Residues: 1-1021 <SHU>

A/Cross-references: UNIPROT:P04074; GB:X02813; NID:g1205; PIDN:CAA26581.1; PID:g1206

J./Hinz, H.R.; Kitley, T.D.

J. Biol. Chem. 265, 10260-10265, 1990

A/Title: Lysine 480 is an essential residue in the putative ATP site of lamb kidney (Na, K)-ATPase

A/Reference number: A35426; MUID:90285144; PMID:2162343

A/Accession: A35426

A/Status: preliminary

A/Molecule type: protein

A/Residues: 475-492 <HIN>

C/Comment: This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP to ADP and inorganic phosphate, providing the energy for active transport of sodium and potassium across the cell membrane.

C/Comment: This enzyme is specifically inhibited by cardiac glycosides such as digoxin and ouabain.

C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain

C/Keywords: ATP; hydrolyase; phosphoprotein; potassium transport; sodium transport; transmembrane

F/6-1021/Product: Na+/K+-transporting ATPase alpha chain #status predicted <MAT>

F/94-118/Domain: transmembrane #status predicted <TM1>

F/128-144/Domain: transmembrane #status predicted <TM2>

F/288-311/Domain: transmembrane #status predicted <TM3>

F/318-346/Domain: transmembrane #status predicted <TM4>

F/585-781/Domain: ATPase nucleotide-binding domain homology <ATN>

F/785-808/Domain: transmembrane #status predicted <TM5>

F/847-872/Domain: transmembrane #status predicted <TM6>

F/951-976/Domain: transmembrane #status predicted <TM7>

F/315/Binding site: cardiac glycoside (TTP) #status predicted

F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted

F/506/Binding site: ATP (Lys) #status predicted

Query Match 37.7%; Score 43; DB 1; Length 1021;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLBWKFC 16
Db 82 PTPBWKFC 91

RESULT 36

S04630

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - horse

C/Species: Equus caballus (domestic horse)

C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C/Accession: S04630

R/Kano, I.; Nagai, F.; Satoh, K.; Ushiyama, K.; Nakao, T.; Kano, K.

FEBS Lett. 250, 91-98, 1989

A/Title: Structure of the alpha(1) subunit of horse Na,K-ATPase gene.

A/Reference number: S04630; MUID:89290042; PMID:2544461

A/Accession: S04630

A/Molecule type: DNA

A/Residues: 1-1021 <KAN>

A/Cross-references: UNIPROT:P18907; EMBL:X16773; NID:g1010; PIDN:CAA34716.1; PID:g871026

C/Genetics:

A/Intron: 4/3; 39/3; 59/3; 127/3; 165/3; 210/3; 250/1; 339/3; 406/1; 442/3; 487/3; 552/3

C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain

C/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp

F/6-1021/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>

F/6-93/Domain: intracellular #status predicted <INT1>

F/94-118/Domain: transmembrane #status predicted <TM1>

F/128-147/Domain: transmembrane #status predicted <TM2>

F/148-288/Domain: intracellular #status predicted <INT2>

F/289-311/Domain: transmembrane #status predicted <TM3>

F/318-346/Domain: transmembrane #status predicted <TM4>

F/347-784/Domain: intracellular #status predicted <INT3>

F/585-781/Domain: ATPase nucleotide-binding domain homology <ATN>

F/785-808/Domain: transmembrane #status predicted <TM5>

F/847-872/Domain: transmembrane #status predicted <TM6>

F/873-950/Domain: intracellular #status predicted <INT4>

F/951-976/Domain: transmembrane #status predicted <TM7>

F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted

F/506/Binding site: ATP (Lys) #status predicted

F/715, 719, 724/Active site: Asp, Asp, Lys #status predicted

Query Match 37.7%; Score 43; DB 1; Length 1021;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLBWKFC 16
Db 82 PTPBWKFC 91

RESULT 37

A28199

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - chicken

C/Species: Gallus gallus (chicken)

C/Date: 21-Sep-1988 #sequence_revision 21-Sep-1988 #text_change 09-Jul-2004

C/Accession: A28199

R/Takeyasu, K.; Tamkun, M.W.; Renaud, K.J.; Fambrough, D.M.

J. Biol. Chem. 263, 4347-4354, 1988

A/Title: Ouabain-sensitive (Na(+)+K(+))-ATPase activity expressed in mouse L cells by

A/Reference number: A28199; MUID:88153759; PMID:2831227

A/Accession: A28199

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-1021 <YAK>

A/Cross-references: UNIPROT:P09572; GB:J03230; NID:g211219; PIDN:AAA48607.1; PID:g211222

C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain

C/Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein

F/585-781/Domain: ATPase nucleotide-binding domain homology <ATN>

F/213, 481/Binding site: carboxylate (Asn) (covalent) #status predicted

F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted

F/506/Binding site: ATP (Lys) #status predicted

Query Match 37.7%; Score 43; DB 2; Length 1021;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 PTLBWKFC 16
Db 82 PTPBWKFC 91

RESULT 38

B24862

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - pig

N/Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha chain

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004

C/Accession: B24862; I46572; A35504; S00011; S00502; S02569; S29762

R/Ovchinnikov, Y.A.; Modayany, N.N.; Broude, N.E.; Petrunkin, K.B.; Grishin, A.V.; Arza

FEBS Lett. 201, 237-245, 1986

A/Title: Pig kidney Na+,K+-ATPase. Primary structure and spatial organization.

A/Reference number: A91361; MUID:86220813; PMID:2423371

A/Accession: B24862

A/Molecule type: mRNA

A/Residues: 1-1021 <OVCC>

A/Cross-references: UNIPROT:P05024; EMBL:X03938; NID:g1897; PIDN:CAA27576.1; PID:g1898

A/Note: the authors translated the codon TCC for residue 391 as Phe. TCG for residue 723
 A/Note: part of this sequence, including the amino and carboxyl end of the mature protein
 R/Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Arsenyan, S.G.; Broute, N.E.; Petrunkin, K.E.;
 Dohl. Biochem. 283, 270-272, 1985
 A/Title: Amino acid sequence of the 17-kilodalton fragment of the cytoplasmic region of
 A/Reference number: 146572
 A/Accession: 146572
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 469-617 <OVCL>
 A/Cross-references: GB:M32512; NID:g164385; PIDN:AAA31004.1; PID:g164386
 R/Karlish, S.J.D.; Goldshleger, R.; Stein, W.D.
 Proc. Natl. Acad. Sci. U.S.A. 87, 4566-4570, 1990
 A/Title: A 19-kDa C-terminal tryptic fragment of the alpha chain of Na/K-ATPase is essen
 A/Reference number: A35504; MUID:90280416; PMID:2162048
 A/Accession: A35504
 A/Molecule type: protein
 A/Residues: 836-845, 'R', 847-851 <KAR>
 R/Ovchinnikov, Y.A.; Arzamazova, N.M.; Arystarkhova, E.A.; Gevondyan, N.M.; Aldanova, N.
 FEBS Lett. 217, 269-274, 1987
 A/Title: Detailed structural analysis of exposed domains of membrane-bound Na⁺, K⁺-ATPase
 A/Reference number: S00011; MUID:8724231; PMID:3036581
 A/Contents: annotation; membrane topology
 R/Ovchinnikov, Y.A.; Luneva, N.M.; Arystarkhova, E.A.; Gevondyan, N.M.; Arzamazova, N.M.
 FEBS Lett. 227, 230-234, 1988
 A/Title: Topology of Na, K-ATPase: identification of the extra- and intracellular hydroph
 A/Reference number: S02569; MUID:88112252; PMID:2448169
 A/Contents: annotation; membrane topology
 C/Superfamily: Na⁺/K⁺-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 A/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
 F/6-1021/Product: Na⁺/K⁺-transporting ATPase alpha chain #status experimental <MAT>
 F/6-93/Domain: intracellular #status predicted <INT1>
 F/94-118/Domain: transmembrane #status predicted <TM1>
 F/128-147/Domain: transmembrane #status predicted <INT2>
 F/168-268/Domain: intracellular #status predicted <INT2>
 F/289-311/Domain: transmembrane #status predicted <TM>
 F/318-346/Domain: transmembrane #status predicted <TM>
 F/347-784/Domain: intracellular #status predicted <INT3>
 F/585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
 F/785-808/Domain: transmembrane #status predicted <TM5>
 F/847-872/Domain: transmembrane #status predicted <TM6>
 F/951-976/Domain: intracellular #status predicted <INT4>
 F/977-1021/Domain: extracellular #status predicted <EXT>
 F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F/506/Binding site: ATP (Lys) #status predicted
 F/715,719,724/Active site: Asp, Asp, Lys #status predicted

Query Match 37.7%; Score 43; DB 2; Length 1021;
 Best Local Similarity 60.0%; Pred. No. 2.6e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PTLREWISFC 16
 Db 82 PTPREWVKFC 91

RESULT 39
 Na⁺/K⁺-exchanging ATPase (EC 3.6.3.9) alpha chain - European eel
 C/Species: Anguilla anguilla (European eel)
 C/Date: 01-Feb-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
 C/Accession: S49127
 R/Cutler, C.; Sanders, J.L.; Cramb, G.
 submitted to the EMBL Data Library, November 1993
 A/Reference number: S45093
 A/Accession: S49127
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1022 <CUT>
 A/Cross-references: UNIPROT:Q92030; EMBL:X76108; NID:g509405; PIDN:CAA53714.1; PID:g5094
 C/Superfamily: Na⁺/K⁺-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 A/Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; transmem

F/586-782/Domain: ATPase nucleotide-binding domain homology <ATN>
 F/214,482/Binding site: carboxylate (asn) (covalent) #status predicted
 F/375/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F/507/Binding site: ATP (Lys) #status predicted

Query Match 37.7%; Score 43; DB 2; Length 1022;
 Best Local Similarity 60.0%; Pred. No. 2.6e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PTLREWISFC 16
 Db 83 PTPREWVKFC 92

RESULT 40
 Na⁺/K⁺-exchanging ATPase (EC 3.6.3.9) alpha-1 chain [validated] - rat
 N/Alternate names: Na⁺/K⁺-transporting ATPase alpha chain, kidney-type
 N/Contents: Na⁺/K⁺-transporting ATPase alpha-s chain
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
 C/Accession: A24639; S00460; A27180; S11020; A25171; S29877; S10758
 R/Shull, G.E.; Greb, J.; Lingrel, J.B.
 Biochemistry 25, 8125-8132, 1986
 A/Title: Molecular cloning of three distinct forms of the Na⁺, K⁺-ATPase alpha-subunit f.
 A/Reference number: A90512; MUID:87128908; PMID:3028470
 A/Accession: A24639
 A/Molecule type: mRNA
 A/Residues: 1-1023 <SHU>
 A/Cross-references: UNIPROT:P06685; EMBL:M4511; NID:g203026; PIDN:AAA40775.1; PID:g2030
 R/Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Ohta, T.; I
 J. Biochem. 102, 43-58, 1987
 A/Title: Primary structures of two types of alpha-subunit of rat brain Na⁺(+), K⁺(+)-ATPase
 A/Reference number: S00460; MUID:88032933; PMID:2822682
 A/Accession: S00460
 A/Molecule type: mRNA
 A/Residues: 1-1023 <HAR>
 A/Cross-references: EMBL:X05882; NID:g55771; PIDN:CAA29306.1; PID:g55772
 R/Hertera, V.U.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard, B.
 J. Cell Biol. 105, 1855-1865, 1987
 A/Title: Three differentially expressed Na, K-ATPase alpha subunit isoforms: structural
 A/Reference number: A92749; MUID:88033255; PMID:2822726
 A/Accession: A27180
 A/Molecule type: mRNA
 A/Residues: 1-67, 'PV', 70-174, 'E', 176-187, 'V', 189-334, 'V', 336-1023 <HER>
 A/Cross-references: EMBL:M28647; NID:g205631; PIDN:AAA41671.1; PID:g205632
 R/Yagawa, Y.; Kawakami, K.; Nagano, K.
 Biochim. Biophys. Acta 1049, 286-292, 1990
 A/Title: Cloning and analysis of the 5'-flanking region of rat Na⁺(+)/K⁺(+)-ATPase alpha-
 A/Reference number: S11020; MUID:90344872; PMID:2166579
 A/Accession: S11020
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 1-41 <YAG>
 A/Cross-references: EMBL:X53233
 R/Schneider, J.W.; Mercer, R.W.; Caplan, M.; Emanuel, J.R.; Sweadner, K.J.; Benz Jr., B
 Proc. Natl. Acad. Sci. U.S.A. 82, 6357-6361, 1985
 A/Title: Molecular cloning of rat brain Na, K-ATPase alpha-subunit cDNA.
 A/Reference number: A25171; MUID:85298352; PMID:2994074
 A/Accession: A25171
 A/Molecule type: mRNA
 A/Residues: 489-533 <SCH>
 R/Lytton, J.
 Biochem. Biophys. Res. Commun. 132, 764-769, 1985
 A/Title: The catalytic subunits of the Na⁺(+), K⁺(+)-ATPase alpha and alpha(+) isozymes
 A/Reference number: S29877; MUID:86050667; PMID:2998384
 A/Accession: S29877
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 6-19 <LYT>
 R/Kurihara, K.; Hosoi, K.; Kodama, A.; Ueha, T.
 Biochim. Biophys. Acta 1039, 234-240, 1990
 A/Title: A new electrophoretic variant of alpha subunit of Na⁺(+)/K⁺(+)-ATPase from the s

A:Reference number: S10758; MUID:90304196; PMID:2163680
A:Accession: S10758
A:Molecule type: protein
A:Residues: 6 'X', 8-10, 'X', 12-16 <KUR>
A:Experimental source: submandibular gland
A>Note: designated alpha-S form, thought to arise from alpha-1 chain by post-translational
C:Genetics:
A:Gene: NKAAL
A:Introns: 4/3
A>Note: the list of introns may be incomplete
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F:6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status experimental <MAT>
F:96-120/Domain: intracellular #status predicted <INT1>
F:130-149/Domain: transmembrane #status predicted <TM1>
F:150-280/Domain: intracellular #status predicted <INT2>
F:291-313/Domain: transmembrane #status predicted <TM3>
F:320-348/Domain: intracellular #status predicted <TM4>
F:349-786/Domain: intracellular #status predicted <INT3>
F:587-783/Domain: ATPase nucleotide-binding domain homology <ATN>
F:787-810/Domain: transmembrane #status predicted <TM5>
F:849-874/Domain: transmembrane #status predicted <TM6>
F:875-952/Domain: intracellular #status predicted <INT4>
F:953-978/Domain: transmembrane #status predicted <TM7>
F:979-1023/Domain: extracellular #status predicted <EXT>
F:376/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:508/Binding site: Asp (Lys) #status predicted
F:717,721,726/Active site: Asp, Asp, Lys #status predicted

Query Match 37.7%; Score 43; DB 1; Length 1023;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PTLREWISFC 16
Db 84 PTLREWVFC 93

RESULT 41
S24650
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - giant toad
C:Species: Bufo marinus (giant toad)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: A43451; S24650
R:Jaissner, F.; Canessa, C.M.; Horibarger, J.D.; Rossier, B.C.
J. Biol. Chem. 267, 16895-16903, 1992
A:Title: Primary sequence and functional expression of a novel ouabain-resistant Na,K-AT
A:Reference number: A43451; MUID:92380991; PMID:1380956
A:Accession: A43451
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1023 <JAI>
A:Cross-references: UNIPROT:P30714; EMBL:Z11798; NID:962491; PIDN:CAA77842.1; PID:962492
A:Experimental source: urinary bladder cell line TBM 18-23
A>Note: submitted to the EMBL Data Library, March 1992
A:Note: sequence extracted from NCBI backbone (NCBI:P111876)
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F:6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>
F:96-120/Domain: transmembrane #status predicted <TM1>
F:130-149/Domain: intracellular #status predicted <INT1>
F:150-290/Domain: transmembrane #status predicted <TM2>
F:291-313/Domain: transmembrane #status predicted <TM3>
F:320-348/Domain: intracellular #status predicted <TM4>
F:349-786/Domain: intracellular #status predicted <INT3>
F:587-783/Domain: ATPase nucleotide-binding domain homology <ATN>
F:787-810/Domain: transmembrane #status predicted <TM5>
F:849-874/Domain: transmembrane #status predicted <TM6>
F:875-952/Domain: intracellular #status predicted <INT4>
F:953-978/Domain: transmembrane #status predicted <TM7>
F:979-1023/Domain: extracellular #status predicted <EXT>

F:376/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:508/Binding site: ATP (Lys) #status predicted
F:717,721,726/Active site: Asp, Asp, Lys #status predicted

Query Match 37.7%; Score 43; DB 1; Length 1023;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PTLREWISFC 16
Db 84 PTLREWVFC 93

RESULT 42
A60444
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - African clawed frog
N:Alternate names: sodium pump alpha chain
C:Species: Xenopus laevis (African clawed frog)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C:Accession: A60444
R:Verrey, F.; Kallouz, P.; Schaefer, E.; Fuentes, P.; Geering, K.; Rossier, B.C.; Kraet
Am. J. Physiol. 256, F1034-F1043, 1989
A:Title: Primary sequence of Xenopus laevis Na(+)-K(+)-ATPase and its localization in
A:Reference number: A60444; MUID:89285429; PMID:2544104
A:Accession: A60444
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1025 <VER>
A:Cross-references: UNIPROT:Q92123; GB:U0108; NID:9499225; PIDN:AAA19022.1; PID:949922
C:Comment: The alpha chain is the catalytic chain.
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium t
F:589-785/Domain: intracellular #status predicted <INT3>
F:217,485/Binding site: carboxylate (Asn) (covalent) #status predicted
F:376/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:510/Binding site: ATP (Lys) #status predicted

Query Match 37.7%; Score 43; DB 2; Length 1025;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PTLREWISFC 16
Db 86 PTLREWVFC 95

RESULT 43
PWCMM
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - white sucker
C:Species: Catostomus commersoni (white sucker)
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C:Accession: S14740
R:Schoenrock, C.; Morley, S.D.; Okawara, Y.; Lederis, K.; Richter, D.
J. Biol. Chem. Hoppe-Seyler 372, 279-286, 1991
A:Title: Sodium and potassium ATPase of the teleost fish Catostomus commersoni. Sequen
A:Reference number: S14740; MUID:91282983; PMID:1711856
A:Accession: S14740
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1027 <SCH>
A:Cross-references: UNIPROT:P25489; EMBL:X58629; NID:962641; PIDN:CAA41483.1; PID:9626
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP; hydrolase; ion transport; phosphoprotein; potassium transport; sodium
F:99-124/Domain: transmembrane #status predicted <TM1>
F:133-152/Domain: transmembrane #status predicted <TM2>
F:153-293/Domain: intracellular #status predicted <INT2>
F:294-316/Domain: transmembrane #status predicted <TM3>
F:323-351/Domain: transmembrane #status predicted <TM4>
F:352-790/Domain: intracellular #status predicted <INT3>
F:591-787/Domain: ATPase nucleotide-binding domain homology <ATN>
F:791-814/Domain: transmembrane #status predicted <TM5>
F:853-878/Domain: transmembrane #status predicted <TM6>
F:879-956/Domain: intracellular #status predicted <INT4>
F:957-982/Domain: transmembrane #status predicted <TM7>

F,963-1027/Domain: extracellular #status predicted <EXT>
 F,319/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F,512/Binding site: ATP (Lys) #status predicted
 F,721,725,730/Active site: Asp, Asp, Lys #status predicted

Query Match 37.7%; Score 43; DB 1; Length 1027;
 Best Local Similarity 60.0%; Pred. No. 2.6e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 PTLREWISFC 16
 |||:|
 Db 87 PTPPEWVKFC 96

RESULT 44

S03632 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - fruit fly (*Drosophila melanogaster*)

N/Alternate names: sodium pump alpha chain

C/Species: *Drosophila melanogaster*

C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C/Accession: S03632; S07049

R/Leibovitz, R.M.; Takeyasu, K.; Fambrough, D.M.

EMBO J. 8, 193-202, 1989

A/Title: Molecular characterization and expression of the (Na+K)-ATPase alpha-subunit in

A/Reference number: S03632; MUID:89231618; PMID:2540956

A/Accession: S03632

A/Molecule type: mRNA

A/Residues: 1-1038 <LEB>

A/Cross-references: UNIPROT:P13607; EMBL:X14476

A/Note: the sequence from Fig. 9 is inconsistent with that from Fig. 8 in having 89-Asp,

R/Varadi, A.; Gilmore-Hebert, M.; Benz Jr., E.J.

FEBS Lett. 258, 203-207, 1989

A/Title: Amplification of the phosphorylation site - ATP-binding site cDNA fragment of

A/Reference number: S07049; MUID:90092469; PMID:2557235

A/Accession: S07049

A/Molecule type: mRNA

A/Residues: 397-521 <VAR>

A/Cross-references: EMBL:X17471

A/Note: the authors translated the codon ACC for residue 3 as Asn and AAT for residue 89

C/Genetics:

A/Gene: FlyBase:Atp-alpha

A/Cross-references: FlyBase:FBgn0002921

A/Map position: 3R 93B

C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain

C/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp

F,113-135/Domain: transmembrane #status predicted <TM1>

F,146-165/Domain: transmembrane #status predicted <TM2>

F,166-305/Domain: intracellular #status predicted <INT2>

F,306-328/Domain: transmembrane #status predicted <TM3>

F,335-363/Domain: transmembrane #status predicted <TM4>

F,364-801/Domain: intracellular #status predicted <INT3>

F,602-798/Domain: ATPase nucleotide-binding domain homology <ATN>

F,802-825/Domain: transmembrane #status predicted <TM5>

F,864-889/Domain: transmembrane #status predicted <TM6>

F,890-966/Domain: intracellular #status predicted <INT4>

F,967-993/Domain: transmembrane #status predicted <TM7>

F,994-1038/Domain: extracellular #status predicted <EXT>

F,391/Active site: Asp (aspartylphosphate intermediate) #status predicted

F,523/Binding site: ATP (Lys) #status predicted

F,732,736,741/Active site: Asp, Asp, Lys #status predicted

Query Match 37.7%; Score 43; DB 1; Length 1038;

Best Local Similarity 44.4%; Pred. No. 2.6e+02;

Matches 8; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

Qy 5 DGPTLR-----EWISFC 16
 |||:|
 Db 93 DGPTLRPPKQTPPEWVKFC 110

RESULT 45

A42687

neurotrophin-4 precursor - human

N/Alternate names: neurotrophin-5

C/Species: *Homo sapiens* (man)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: A42687; JH0503

R/ID, N.Y.; Ibanez, C.F.; Nye, S.H.; McClain, J.; Jones, P.F.; Gies, D.R.; Belluscio, L

Proc. Natl. Acad. Sci. U.S.A. 89, 3060-3064, 1992

A/Title: Mammalian neurotrophin-4: structure, chromosomal localization, tissue distribu

A/Reference number: A42687; MUID:92212967; PMID:1313578

A/Accession: A42687

A/Molecule type: DNA

A/Residues: 1-210 <RP1>

A/Cross-references: UNIPROT:P34130; GB:M86528; NID:9190264; PIDN:AAA60154.1; PID:919026

A/Note: sequence extracted from NCBI backbone (NCBIN:93810, NCBI:P.93811)

R/Berkemeier, L.R.; Winslow, J.W.; Kaplan, D.R.; Nikolic, K.; Goeddel, D.V.; Rosenthal

Neuron 7, 857-866, 1991

A/Title: Neurotrophin-5: a novel neurotrophic factor that activates trk and trkB.

A/Reference number: JH0503; MUID:92075279; PMID:1742028

A/Accession: JH0503

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 1-210 <BER>

C/Comment: The neurotrophins stimulate autophosphorylation and transduce signals throug

C/Genetics:

A/Gene: GDB:NRF5

A/Cross-references: GDB:134723; OMIM:162662

A/Map position: 19pter-19qter

C/Superfamily: nerve growth factor beta chain

C/Keywords: glycoprotein

F,1-24/Domain: signal sequence #status predicted <SIG>

F,25-80/Domain: propeptide #status predicted <PRO>

F,81-210/Product: neurotrophin-4 #status predicted <NEU>

F,76/Binding site: carbonylrate (Asn) (covalent) #status predicted

Query Match 37.3%; Score 42.5; DB 2; Length 210;

Best Local Similarity 47.4%; Pred. No. 71;

Matches 9; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

Qy 1 GGCADGPTLRWISFCGCK 19
 |||:|
 Db 156 GGCR-GVDRRHVWVSECKAK 173

Search completed: September 1, 2005, 16:22:51
 Job time : 15.4892 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:37 ; Search time 70.6691 Seconds
(without alignments)
137.677 Million cell updates/sec

Title: US-10-083-768-8

Perfect score: 114
Sequence: 1 GGCAAGPTLRWISFCGK 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	56	49.1	297	2 Q7UQ84	Q7UQ84 rhodoptrel
2	55.5	48.7	934	2 Q9NEX6	Q9NEX6 caenothabdi
3	51	44.7	386	1 ETR1_CANTR	Q8WZM3 candida tro
4	51	44.7	386	1 ETR2_CANTR	Q8WZM4 candida tro
5	50.5	44.3	387	2 Q98A97	Q8KJF9 rhizobium 1
6	50.5	44.3	389	2 Q8KJF9	Q8KJF9 rhizobium 1
7	49.5	43.4	405	2 Q9KIE9	Q9KIE9 streptomyc
8	49	43.0	245	2 Q9M060	Q9M060 arabidopsis
9	49	43.0	349	2 Q7V2B2	Q7V2B2 prochloroco
10	48	42.1	319	2 Q9RKM5	Q9RKM5 streptomyc
11	48	42.1	342	2 Q6VMH4	Q6VMH4 streptomyc
12	48	42.1	461	2 Q7J2M7	Q7J2M7 mycobacteri
13	48	42.1	1123	2 Q7QC63	Q7QC63 anophelies g
14	47.5	41.7	238	2 Q7ULR5	Q7ULR5 rhodoptrel
15	47.5	41.7	283	2 Q82CW2	Q82CW2 streptomyc
16	47	41.2	94	2 Q6MX73	Q6MX73 azoarcus sp
17	47	41.2	129	2 Q8DHX7	Q8DHX7 synecococc
18	47	41.2	271	2 Q8SPB8	Q8SPB8 bradyrhizob
19	47	41.2	475	2 Q9UAT5	Q9UAT5 caenothabdi
20	47	41.2	821	2 Q966D4	Q966D4 caenothabdi
21	47	41.2	956	2 Q6CLJ9	Q6CLJ9 kluyveromyc
22	47	41.2	1926	2 Q9Y8B3	Q9Y8B3 paracoccidi
23	46.5	40.8	166	2 Q6KGG9	Q6KGG9 bacterioph
24	46.5	40.8	426	2 Q89HJ8	Q89HJ8 bradyrhizob
25	46	40.4	97	2 Q8FPCA	Q8FPCA corynebacte
26	46	40.4	117	2 Q7MV49	Q7MV49 porphyromon
27	46	40.4	159	2 Q8N852	Q8N852 homo sapien
28	46	40.4	162	2 Q63KH8	Q63KH8 burkholderi
29	46	40.4	196	2 Q7VWMS	Q7VWMS burkholderi
30	46	40.4	196	2 Q7W9X1	Q7W9X1 burkholderi
31	46	40.4	245	2 Q8GVPS	Q8GVPS oryza sativ

32	46	40.4	275	2 O13090	O13090 pleurodeles
33	46	40.4	277	1 IMPI_MOUSE	P70224 mus musculu
34	46	40.4	312	2 Q9ND50	Q9ND50 trypanosoma
35	46	40.4	347	2 Q7PP6	Q7PP6 anophelies g
36	46	40.4	403	2 Q88N02	Q88N02 pseudomonas
37	46	40.4	443	2 Q9P858	Q9P858 phaeosphaer
38	46	40.4	482	2 Q6A1R0	Q6A1R0 desulfotale
39	46	40.4	540	2 Q82L10	Q82L10 streptomyc
40	46	40.4	926	1 AASS_HUMAN	Q94R5 homo sapien
41	46	40.4	1902	2 Q9Y878	Q9Y878 coccidioid
42	45.5	39.9	309	2 Q8XZNS	Q8XZNS talstonia s
43	45.5	39.9	485	2 Q8SC10	Q8SC10 propionibac
44	45	39.5	108	2 Q7RUA5	Q7RUA5 neurospora
45	45	39.5	146	2 Q6ZTT4	Q6ZTT4 homo sapien
46	45	39.5	173	2 Q8C4M6	Q8C4M6 mus musculu
47	45	39.5	180	2 Q07291	Q07291 natronomona
48	45	39.5	201	2 Q75LB6	Q75LB6 oryza sativ
49	45	39.5	209	2 Q6N1X5	Q6N1X5 rhodopsedu
50	45	39.5	290	2 Q88HF5	Q88HF5 pseudomonas
51	45	39.5	290	2 Q89JF5	Q89JF5 bradyrhizob
52	45	39.5	338	2 Q82CX1	Q82CX1 streptomyc
53	45	39.5	367	2 Q64BD6	Q64BD6 uncultured
54	45	39.5	379	2 Q7SXV0	Q7SXV0 brachydantio
55	45	39.5	385	2 Q7XMK0	Q7XMK0 oryza sativ
56	45	39.5	410	2 Q629V1	Q629V1 burkholderi
57	45	39.5	410	2 Q63HZ6	Q63HZ6 burkholderi
58	45	39.5	421	2 Q8XUV7	Q8XUV7 caenothabdi
59	45	39.5	499	1 MEP2_YEAST	Q9XUV7 saccharomyc
60	45	39.5	594	2 Q7SHC4	Q7SHC4 neurospora
61	45	39.5	721	2 Q6K4D2	Q6K4D2 oryza sativ
62	45	39.5	769	2 Q70804	Q70804 tt virus. 1
63	45	39.5	894	2 Q63UA1	Q63UA1 burkholderi
64	45	39.5	1134	2 Q8P378	Q8P378 xanthomonas
65	45	39.5	1335	1 RFOR_HUMAN	Q8H122 homo sapien
66	45	39.5	175	2 Q7XQ02	Q7XQ02 oryza sativ
67	44.5	39.0	175	2 Q7XQ02	Q7XQ02 oryza sativ
68	44.5	39.0	248	2 Q7PXF4	Q7PXF4 anophelies g
69	44.5	39.0	271	2 Q72J02	Q72J02 thermus the
70	44.5	39.0	282	2 Q7QCK2	Q7QCK2 anophelies g
71	44.5	39.0	429	2 Q8AVB0	Q8AVB0 brachydantio
72	44.5	39.0	497	2 Q7QIK7	Q7QIK7 anophelies g
73	44.5	39.0	818	2 Q6PBA6	Q6PBA6 brachydantio
74	44.5	39.0	1067	2 Q6MZ09	Q6MZ09 aspergillus
75	44.5	39.0	1142	2 Q8IT12	Q8IT12 trypanosoma
76	44.5	39.0	1183	2 Q7NLS9	Q7NLS9 gloeobacter
77	44	38.6	173	2 Q6ZAD7	Q6ZAD7 oryza sativ
78	44	38.6	173	2 Q6QHD2	Q6QHD2 gallid herp
79	44	38.6	197	2 Q6RL14	Q6RL14 gallid herp
80	44	38.6	197	2 Q6R8A0	Q6R8A0 sodalis glo
81	44	38.6	209	2 Q7L059	Q7L059 streptomyc
82	44	38.6	210	2 Q69PA9	Q69PA9 oryza sativ
83	44	38.6	238	2 Q7QKA0	Q7QKA0 anophelies g
84	44	38.6	292	2 Q67642	Q67642 gallid herp
85	44	38.6	298	2 Q86653	Q86653 gallid herp
86	44	38.6	304	2 Q82RG2	Q82RG2 streptomyc
87	44	38.6	310	2 Q7R8H2	Q7R8H2 lymphocyeti
88	44	38.6	346	2 Q62030	Q62030 caenothabdi
89	44	38.6	371	2 Q9RRJ3	Q9RRJ3 deinococcus
90	44	38.6	404	2 Q7QF40	Q7QF40 anophelies g
91	44	38.6	425	2 Q8PD03	Q8PD03 xanthomonas
92	44	38.6	450	2 Q75211	Q75211 ashbya goss
93	44	38.6	490	2 Q04270	Q04270 chlamydomon
94	44	38.6	519	2 Q7Y1N9	Q7Y1N9 oryza sativ
95	44	38.6	524	2 Q66GJ0	Q66GJ0 arabidopsis
96	44	38.6	524	2 Q84W33	Q84W33 arabidopsis
97	44	38.6	526	2 Q9C868	Q9C868 arabidopsis
98	44	38.6	537	2 Q63M37	Q63M37 burkholderi
99	44	38.6	613	2 Q7Y7Z5	Q7Y7Z5 burkholderi
100	44	38.6	613	2 Q9VGR8	Q9VGR8 dirosophila

ALIGNMENTS

```

RESULT 1
Q7UOE4 PRELIMINARY; PRT; 297 AA.
AC Q7UOE4;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=RB6375;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RP [1]
SEQUENCE FROM N.A.
RC STRAIN=1;
RA MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heltmann K., Rabus R.,
RA Schleener H., Aamann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR EMBL; BX294144; CAD74759.1; -.
DR InterPro; IPR001194; ATPase_a/bcentre.
DR InterPro; PS001169; GYF.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
DR PROSITE; PS50829; GYF.1
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 297 AA; 31805 MW; 475f670f02c7859b CRC64;

Query Match 49.1%; Score 56; DB 2; Length 297;
Best Local Similarity 69.2%; Pred. No. 2.5;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCADGPTLRWIS 14
| | | | | | | | | |
Db 173 GPADGPTMKOWIS 185

RESULT 2
Q9NEX6 PRELIMINARY; PRT; 934 AA.
AC Q9NEX6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein Y10588A.21.
GN ORNames=Y10588A.21;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RP [1]
SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Sulston J.E.;
RA Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL132876; CA48140.1; -.
DR WormBase; WBGen00013679; Y10588A.21.
DR WormPep; Y10588A.21; CR25162.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.

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KM Hypothetical protein.
SQ SEQUENCE 934 AA; 10485 MW; 5ED4E1D03DB06F24 CRC64;

Query Match 48.7%; Score 55.5; DB 2; Length 934;
Best Local Similarity 55.6%; Pred. No. 9.2;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 3 CADGPTLRW-1SFCCG 19
| | | | | | | | | |
Db 899 CVDGTRDWPVSFTG3E 916

RESULT 3
ETRL_CANTR STANDARD; PRT; 386 AA.
ID ETRL_CANTR
AC Q8WMZ3;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Enoyl-[acyl-carrier protein] reductase [NADPH, B-specific] 1,
DE mitochondrial precursor (EC 1.3.1.10).
GN Name=ETRL;
OS Candida tropicalis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5482;
RP [1]
SEQUENCE FROM N.A.; SEQUENCE OF 23-29, FUNCTION, SUBUNIT, AND
RP SUBCELLULAR LOCATION.
RC STRAIN=ATCC 20336;
RC MEDLINE=21400968; PubMed=11509667;
RX DOI=10.1128/MCB.21.18.6243-6253.2001;
RX Toroko J.M., Koivuranta K.T., Minalainen I.J., Yagi A.I., Schmitz W.,
RA Kastaniotis A.J., Alireme T.T., Gurvitz A., Hiltunen J.K.;
RT "Candida tropicalis Ecrip and Saccharomyces cerevisiae Ybr026p
RT (Mrf1p), 2-enoyl thioester reductases essential for mitochondrial
RT respiratory competence.";
RL Mol. Cell. Biol. 21:6243-6253 (2001).
RN [2]
SUBUNIT.
RC STRAIN=ATCC 20336;
RX PubMed=12890667; DOI=10.1074/jbc.M307664200;
RA Toroko J.M., Koivuranta K.T., Kastaniotis A.J., Alireme T.T.,
RA Glumoff T., Ilyes M., Hartig A., Gurvitz A., Hiltunen J.K.;
RT "Candida tropicalis expresses two mitochondrial 2-enoyl thioester
RT reductases that are able to form both homodimers and heterodimers.";
RL J. Biol. Chem. 278:41213-41220 (2003).
RN [3]
X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS), AND MUTAGENESIS OF TYR-79.
RX PubMed=12614607; DOI=10.1016/S0022-2836(03)00038-X;
RX Alireme T.T., Toroko J.M., Van den Plas S., Sormunen R.T.,
RA Kastaniotis A.J., Wierenga R.K., Hiltunen J.K.;
RT "Structure-function analysis of enoyl thioester reductase involved in
RT mitochondrial maintenance.";
RL J. Mol. Biol. 327:47-59 (2003).
CC -1- FUNCTION: Required for respiration and the maintenance of the
CC mitochondrial compartment. May have a role in the mitochondrial
CC synthesis of fatty acids.
CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NADP(+) = trans-
CC 2,3-dehydroacyl-[acyl-carrier protein] + NADPH.
CC -1- SUBUNIT: Homodimer and heterodimer with etrl2.
CC -1- SUBCELLULAR LOCATION: Mitochondrion.
CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
CC family. Quinone oxidoreductase subfamily.
CC -----
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CC -----

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DR EMBL: U94997; AAL55472.1; -.
DR PDB: 1GU7; X-ray; A/B=23-386.
DR PDB: 1GU7; X-ray; A/B=23-386.
DR PDB: 1GYR; X-ray; A/B/C=23-386.
DR InterPro: IPR02085; Adh zn family.
DR InterPro: IPR01032; GroES like.
DR Pfam: PF00107; ADH_zinc_N_1.
DR 3D-structure; Direct protein sequencing; Fatty acid biosynthesis;
KM Mitochondrion; NADP; Oxidoreductase; Transit peptide.
FT TRANSIT 1 22 Mitochondrion.
FT CHAIN 23 386 Enoyl-[acyl-carrier protein] reductase
FT SEQUENCE 386 AA; 42160 MW; FCBC174A240742D8 CRC64;
SQ SEQUENCE 386 AA; 42160 MW; FCBC174A240742D8 CRC64;

Query Match 44.7%; Score 51; DB 1; Length 386;
Best Local Similarity 57.1%; Pred. No. 19;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 GPTIREMISFCGK 19
DB 254 GPTIKWIKSGS 267

RESULT 4
ID ETR2_CANTR STANDARD; PRT; 386 AA.
AC 08WZM4;
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Enoyl-[acyl-carrier protein] reductase [NADPH, B-specific] 2,
DE Mitochondrial precursor (EC 1.3.1.10).
GN Name=ETR2;
OS Candida tropicalis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitospotic Saccharomycetales; Candida.
OX NCBI_TaxID=5482;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBUNIT.
RC STRAIN=ATCC 20336;
RA PubMed=12890667; DOI=10.1074/jbc.M307664200;
RA Toroko J.M., Kojivuranta K.T., Kastaniotis A.J., Airene T.T.,
RA Glumoff T., Iives M., Hartig A., Guryitz A., Hiltunen J.K.;
RT "Candida tropicalis expresses two mitochondrial 2-enoil thioester
RT reductases that are able to form both homodimers and heterodimers.";
RT J. Biol. Chem. 278:41213-41220(2003).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.11 ANGSTROMS).
RA Airene T.T., Toroko J.M., Hiltunen J.K.;
RT "Crystal structure of enoyl thioester reductase 2.";
RT Submitted (JUN-2002) to the PDB data bank.
CC -1- FUNCTION: Required for respiration and the maintenance of the
CC mitochondrial compartment. May have a role in the mitochondrial
CC synthesis of fatty acids.
CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + NADPH(+) = trans-
CC -2,3-dehydroacyl-[acyl-carrier protein] + NADPH.
CC -1- SUBUNIT: Homodimer and heterodimer with ETR1.
CC -1- SUBCELLULAR LOCATION: Mitochondrion (By similarity).
CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
CC family. Quinone oxidoreductase subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U94996; AAL55471.1; -.
DR PDB: 1HOK; X-ray; A/B=23-386.
DR InterPro: IPR02085; Adh_zn_family.

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DR InterPro: IPR01032; GroES like.
DR Pfam: PF00107; ADH_zinc_N_1.
DR 3D-structure; Fatty acid biosynthesis; Mitochondrion; NADP;
KM Oxidoreductase; Transit peptide.
FT TRANSIT 1 22 Mitochondrion (Potential).
FT CHAIN 23 386 Enoyl-[acyl-carrier protein] reductase
FT SEQUENCE 386 AA; 42116 MW; 91ABE0831F0C2E8 CRC64;

Query Match 44.7%; Score 51; DB 1; Length 386;
Best Local Similarity 57.1%; Pred. No. 19;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 GPTIREMISFCGK 19
DB 254 GPTIKWIKSGS 267

RESULT 5
ID 098A97 PRELIMINARY; PRT; 387 AA.
AC 098A97;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE M16096 protein.
GN OrderedLocustNames=m16096;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsuno M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RT DNA Res. 7:331-338(2000).
RN EMBL: AF003008; BAB52440.1; -.
DR HSSP; P77407; 1PQY.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro: IPR003673; CA1B BAIF.
DR Pfam: PF02515; COA_transf_3; 1.
KM Complete proteome.
SQ SEQUENCE 387 AA; 42226 MW; 64643BEC8F25518 CRC64;

Query Match 44.3%; Score 50.5; DB 2; Length 387;
Best Local Similarity 42.9%; Pred. No. 23;
Matches 9; Conservative 3; Mismatches 2; Indels 7; Gaps 1;

QY 3 CADGPTL-----REWISFC 16
DB 237 CADGEVIFSVQNDREWNFC 257

RESULT 6
ID 08KJF9 PRELIMINARY; PRT; 389 AA.
AC 08KJF9;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE PUTATIVE RACEMASE/DEHYDRATASE PROTEIN.
GN Name=m1181;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R7A;
RX DOI=10.1128/JB.184.11.3096-3095.2002;
RA Sullivan J.T., Trzebiatowski J.R., Cruckeank R.W., Gouzy J.,
  Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rosbach U.,
  Stuart G.S., Weaver J.E., Medby R.U., de Bruijn F.J., Ronson C.W.;
RT "Comparative sequence analysis of the symbiosis island of
  Mesorhizobium loti strain R7A.";
RL J. Bacteriol. 184:3086-3095(2002).
DR EMBL: AF672113; CAD31586.1; -.
DR HSSP: P77407; 1PQY.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR003673; CAIB_BAIF.
DR Pfam: PF02515; CoA_transf_3; 1.
SQ SEQUENCE 389 AA; 42703 MW; 6678D2C96A7E5204 CRC64;

Query Match 44.3%; Score 50.5; DB 2; Length 389;
Best Local Similarity 42.9%; Pred. No. 23;
Matches 9; Conservative 3; Mismatches 2; Indels 7; Gaps 1;

QY 3 CADGPTL-----REWISFC 16
Db 243 CADGKEVTFVSQNDREWMNFC 263

RESULT 7
O9K1E9 PRELIMINARY; PRT; 405 AA.
AC O9K1E9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE FkBE.
GN Name=FkBE;
OS Streptomyces hygroscopicus subsp. acromyceticus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomycetes.
OC NCBI_TaxID=132248;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20323220; PubMed=10863099; DOI=10.1016/S0378-1119(00)00171-2;
RA Wu K., Chung L., Revill W.P., Katz L., Reeves C.D.;
RT "The FK520 gene cluster of Streptomyces hygroscopicus var.
  acromyceticus (ATCC 14891) contains genes for biosynthesis of unusual
  RT polycyclic extender units.";
RL Gene 251:81-90(2000).
DR EMBL: AF235504; AAF6384.1; -.
DR HSSP: P77407; 1PQY.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR003673; CAIB_BAIF.
DR Pfam: PF02515; CoA_transf_3; 1.
SQ SEQUENCE 405 AA; 43696 MW; DC2569DFC914AD6F CRC64;

Query Match 43.4%; Score 49.5; DB 2; Length 405;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 10; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 5 DGPTL-----REWISFC 17
Db 252 DGOTINIGLONERWASFCG 271

RESULT 8
O9M060 PRELIMINARY; PRT; 245 AA.
AC O9M060;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Bkaryotic translation initiation factor 6 (EIF-6)-like protein
  DE (Ac3955620).

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GN Name=Flit6_30; Synonyms=At3955620;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Benes V., Wurmach E., Drzonek H., Ansoze W., Mewes H.W., Rudd S.,
  Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
  Dale J.M., Hayashizaki Y., Ishida J., Jones T., Kamita A.,
  Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
  Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
  Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
  Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
  Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
  RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamita A., Kawai J.,
  Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
  Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinzaki K.,
  Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL161667; CAB81587.1; -.
DR EMBL: BT009656; AAF75806.1; -.
DR EMBL: AY128351; AAM91554.1; -.
DR PIR: T47701; T47701.
DR HSSP: Q12522; 1G62.
DR GO: GO:0003743; P:translation initiation factor activity; IEA.
DR GO: GO:0006413; P:translational initiation; IEA.
DR InterPro: IPR002769; eIF6.
DR Pfam: PF01912; eIF-6; 1.
DR Pfam: PF006880; eIF6; 1.
DR Prodom: PD00654; eIF6; 1.
DR SMART: SM00654; eIF6; 1.
DR TIGRPFAM: TIGR00323; eIF-6; 1.
DR TIGRPFAM: TIGR00323; eIF-6; 1.
DR TIGRPFAM: TIGR00323; eIF-6; 1.
SQ SEQUENCE 245 AA; 26482 MW; 73369A2A657F390D CRC64;

Query Match 43.0%; Score 49; DB 2; Length 245;
Best Local Similarity 57.1%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 ADGPTLREWISFCG 17
Db 194 AAGMTVNDWTSFCG 207

RESULT 9
O7V2B2 PRELIMINARY; PRT; 349 AA.
ID O7V2B2;
AC O7V2B2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Dihydroorotase (EC 3.5.2.3).
GN Name=pyrC; Ordered locus names=PMW0569;
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

```

RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
 RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
 RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
 RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
 RA Webb E.A., Zinner E.R., Chisholm S.W.;
 RT "Genome divergence in two *Prochlorococcus* ecotypes reflects oceanic
 niche differentiation";
 RL Nature 424:1042-1047(2003).
 DR EMBL; BX572091; CAE19028.1; -.
 DR HSSP; P05020; 1079.
 DR GO; GO:0004151; F:dihydroorotase activity; IEA.
 DR GO; GO:0016787; P:hydrolase activity; IEA.
 DR GO; GO:0019856; P:pyrimidine base biosynthesis; IEA.
 DR InterPro; IPR006680; Amdohydro_1.
 DR InterPro; IPR004721; Dhodimr.
 DR InterPro; IPR002195; Dihydroorotase.
 DR Pfam; PF01979; Amdohydro_1; 1.
 DR TRGFAMs; TIGR00856; pyrC dimer; 1.
 DR PROSITE; PS00482; DIHYDROOROTASE_1; UNKNOWN_1.
 DR PROSITE; PS00483; DIHYDROOROTASE_2; 1.
 KM Complete proteome; Hydrolyase.
 SQ SEQUENCE 349 AA; 39958 MW; CC02F5AE02EC927 CRC64;

Query Match 43.0%; Score 49; DB 2; Length 349;
 Best Local Similarity 50.0%; Pred. No. 35;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GCADGPTLRWISFCG 17
 Db 243 GTDSAPHLRQWKAFCG 258

RESULT 10

Q9RKM5 PRELIMINARY; PRT; 319 AA.
 AC Q9RKM5;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Putative Meir family transcriptional regulator.
 GN ORFNames=SCD17.06c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 CX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(12) / M145;
 RX MEDLINE=2196410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wetzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RT *coelicolor* A3(12)";
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: Contains 1 HTH mer-r-type DNA-binding domain.
 DR EMBL; AL939118; CAB56383.1; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000551; HTH_MerR.
 DR InterPro; IPR009061; Putativ_DNA_bind.
 DR Pfam; PF00376; MerR; 1.
 DR PRINTS; PR00040; HTHMERR.
 DR SMART; SM00422; HTH_MER_1.
 DR PROSITE; PS0037; HTH_MER_2; 1.
 KM Complete proteome; DNA-binding.

SQ SEQUENCE 319 AA; 34841 MW; 1F51905A8BA5365E CRC64;

Query Match 42.1%; Score 48; DB 2; Length 319;
 Best Local Similarity 61.5%; Pred. No. 46;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GCADGPTLRWIS 14
 Db 255 GRPDGPELRWLA 267

RESULT 11

Q6VWH4 PRELIMINARY; PRT; 342 AA.
 AC Q6VWH4;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Putative SARF family pathway specific regulatory protein.
 GN Name=alpu;
 OS Streptomyces ambifaciens.
 OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 CX NCBI_TaxID=1889;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23877;
 RX PubMed=14742212;
 RA Pang X., Aigle B., Girardet J.M., Mangelot S., Pernodet J.L.,
 RA Decaris B., Leblond P.;
 RT "Functional angucycline-like antibiotic gene cluster in the terminal
 RT inverted repeats of the *Streptomyces ambifaciens* linear chromosome";
 RL Antimicrob. Agents Chemother. 48:575-588(2004).
 DR EMBL; AY338477; AAN30165.1; -.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0000156; F:two-component response regulator activity; IEA.
 DR GO; GO:0000160; P:two-component signal transduction system (p...); IEA.
 DR InterPro; IPR009059; b1_resp_regltr_C.
 DR InterPro; IPR005158; BTAD.
 DR InterPro; IPR001867; Trans_reg_C.
 DR Pfam; PF03704; BTAD; 1.
 DR Pfam; PF00486; Trans_reg_C; 1.
 SQ SEQUENCE 342 AA; 35639 MW; 945BC929E5ACEE3D CRC64;

Query Match 42.1%; Score 48; DB 2; Length 342;
 Best Local Similarity 46.7%; Pred. No. 50;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GCADGPTLRWISFC 16
 Db 112 GCGCGPSSRPLWBS 126

RESULT 12

Q73ZW7 PRELIMINARY; PRT; 461 AA.
 AC Q73ZW7;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocNames=MP1484c;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
 OC Corynebacterinae; Mycobacteriaceae; Mycobacterium.
 CX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K10;
 RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017232; AA030801.1; -.
 DR GO; GO:0005506; F:iron ion binding; IEA.

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DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0006725; P:aromatic compound metabolism; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR005806; R:Rieske reg.
DR InterPro: IPR001663; R:ring_hydroxyl_A.
DR Pfam: PF00355; R:Rieske_1.
DR PRINTS: PR00090; R:RINGDIOLINASE.
DR Complete proteome.
SQ SEQUENCE 461 AA; 52010 MW; 208B39A89C121839 CRC64;

Query Match 42.1%; Score 48; DB 2; Length 461;
Best Local Similarity 47.4%; Pred. No. 67;
Matches 9; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

Qy 1 GCGA-----DGPFLREMI 13
    |||||
    156 GCGCAWNLDDAPALRMM 174

RESULT 13
Q7QC63 PRELIMINARY; PRT; 1123 AA.
ID 070C63;
AC 070C63;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP1221.
GN Name=agCG53078; ORFNames=ENSAAGC00000018866;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAB01008859; EAA08177.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0008888; F:homocysteine S-methyltransferase activity; IEA.
DR GO: GO:0004672; F:protein kinase activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011009; K:kinase_like.
DR InterPro: IPR000719; P:prot_kinase.
DR InterPro: IPR003726; S:methyl_trans.
DR Pfam: PF00069; P:kinase_1.
DR Pfam: PF02574; S-methyl_trans_1.
DR ProDom: PD000001; P:prot_kinase_1.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
SQ SEQUENCE 1123 AA; 120006 MW; D3CC001D8D4882AF CRC64;

Query Match 42.1%; Score 48; DB 2; Length 1123;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ADGPFLREWISF 15
    |||||
    969 ADHPVRFWISF 980

Db 969 ADHPVRFWISF 980

RESULT 14
Q7UR5 PRELIMINARY; PRT; 238 AA.
ID Q7UR5;
AC Q7UR5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to phycoerythrin alpha phycoerythrin lyase Cgce (EC 4.---)
DE ).
GN Name=cgce; OrderedLocNames=RB9340;

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OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Firellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Hellmann K., Rabus R.,
RA Schlesner H., Aumann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Firellula sp.
RT strain 1."
RT Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL: BX294149; CAD76204.1; -.
DR GO: GO:0016829; F:lyase activity; IEA.
DR InterPro: IPR008938; ARM.
DR InterPro: IPR004155; ARM_lyase_HEAT.
DR Pfam: PF03130; HEAT_PBS_1.
DR SMART: SM00567; EZ_HEAT; 3.
DR Complete proteome; Lyase.
SQ SEQUENCE 238 AA; 26142 MW; B7CA7284593B0C72 CRC64;

Query Match 41.7%; Score 47.5; DB 2; Length 238;
Best Local Similarity 39.1%; Pred. No. 41;
Matches 9; Conservative 2; Mismatches 1; Indels 11; Gaps 1;

Qy 1 GCGADGP-----TLREW 12
    |||||
    29 GCGHDGPYALKHNPYFTMRGW 51

RESULT 15
Q82CW2 PRELIMINARY; PRT; 283 AA.
ID Q82CW2;
AC Q82CW2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative ICLR-family transcriptional regulator.
GN OrderedLocNames=SAV5226;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites."
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis."
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL: AP005042; BAC72938.1; -.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR005471; HTH_ICLR.
DR InterPro: IPR009058; Wing_hlx_DNA_bnd.
DR Pfam: PF01614; ICLR_1.
DR Complete proteome.
SQ SEQUENCE 283 AA; 30503 MW; F63B1705578EBE67 CRC64;

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RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Smith A., Wamsley P., Fronick W.;
RT "The sequence of C. elegans cosmid C01B4.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125952; AAD14699.1; -.
DR PIR; T33943; T33943.
DR WormBase; WBGene0015271; C01B4.7.
DR WormPep; C01B4.7; CE20476.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS50850; MFS; 1.
DR Hypothetical protein.
SQ SEQUENCE 475 AA; 53094 MW; 79095D45572AF535 CRC64;

Qy 3 CADGPTLRWISFCGG 18
Db 268 CTDRCVLSAWVSFLGG 283

Query Match 41.2%; Score 47; DB 2; Length 475;
Best Local Similarity 50.0%; Pred. No. 98;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

RESULT 20
Q966D4 PRELIMINARY; PRT; 821 AA.
AC Q966D4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein Y19D10A.4.
DE Name=Y19D10A.4; ORFNames=Y19D10A.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Johnson D.;
RT "The sequence of C. elegans cosmid Y19D10A.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;

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RA Waterston R.H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006722; AAK68417.1; -.
DR PDB; 1LUR; X-ray; A/B=483-821.
DR WormBase; WBGene0021219; Y19D10A.4.
DR WormPep; Y19D10A.4; CE21450.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004034; C:aldose 1-epimerase activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006012; P:galactose metabolism; IEA.
DR WormBase; Y19D10A.4; CE21450.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR008183; Ald1_epimerase.
DR InterPro; IPR011013; Gal_mut_like.
DR InterPro; IPR007114; MFS.
DR Pfam; PF01263; Aldose_epim; 1.
DR PROSITE; PS50850; MFS; 1.
DR Hypothetical protein.
SQ SEQUENCE 821 AA; 91593 MW; 923A788FC95D1A76 CRC64;

Query Match 41.2%; Score 47; DB 2; Length 821;
Best Local Similarity 50.0%; Pred. No. 17+02;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 3 CADGPTLRWISFCGG 18
Db 268 CTDRCVLSAWVSFLGG 283

RESULT 21
Q6CLJ9 PRELIMINARY; PRT; 956 AA.
AC Q6CLJ9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P40825 Saccharomyces cerevisiae YOR333c ALA1 alanyl-tRNA
synthetase.
OS ORFNames=KLU40F024319;
GN Kluyveromyces fragilis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=284590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neugeislise C., Talla E.,

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RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Blyksten C.,
 RA Boistrame A., Boyer J., Catolico L., Confalonieri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumas H., Groppi A.,
 RA Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerret A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Micaud J.M., Nikolski M., Ozias S., Ozier-Kalogeropoulos O.,
 RA Pelenz S., Potter S., Richard G.F., Straub M.L., Suleau A.,
 RA Swenne D., Tekala F., Wesolowski-Louvel M., Weschof E., Wirth B.,
 RA Zenioui-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Winkler P., Souciet J.L.,
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382126; CAG37897.1; -
 DR GO; GO:0004813; F:alanine-tRNA ligase activity; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0006419; P:amyl-tRNA aminoacylation; IEA.
 DR InterPro; IPR003156; Pesterase DHHA1.
 DR InterPro; IPR002318; tRNA-synt_2c.
 DR InterPro; IPR006193; tRNA-synt_Ala.
 DR Pfam; PF02272; DHHA1; 1.
 DR Pfam; PF01411; tRNA-synt_2c; 1.
 DR PRINTS; PRO0980; TRNASYNTHALA.
 DR TIGRFAMs; TIGR00344; alas; 1.
 DR PROSITE; PS0860; AA_TRNA_LIGASE_II_ALA; 1.
 DR Aminoacyl-tRNA synthetase.
 KW SEQUENCE 956 AA; 107100 MW; 4F5CE6855880A3C CRC64;
 SQ
 Query Match 41.2%; Score 47; DB 2; Length 956;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
 Matches 9; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
 Qy 5 DGPTLRW---ISFCGG 18
 Db 704 ENPTSEWQKXISFCGG 721
 RESULT 22
 Q9Y8B3 PRELIMINARY; PRT; 1926 AA.
 AC Q9Y8B3;
 DT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Glucan synthase.
 GN Name=Fks;
 OS Paracoccidioides brasiliensis.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Onygenales; mitosporic Onygenales; Paracoccidioides.
 CX NCBI_TaxID=121759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Pb01;
 RX MEDLINE=20171859; PubMed=10705373;
 RX DOI=10.1002/(SICI)1097-0061(20000330)16:5<451::AID-YEAS40>3.0.CO;2-O;
 RA Pereira M., Felipe M.S.S., Brigido M.M., Soares C.M.A., Azevedo M.O.;
 RT "Molecular cloning and characterization of a glucan synthase gene from
 RT the human pathogenic fungus Paracoccidioides brasiliensis."
 RL Yeast 16:451-462(2000)
 DR EMBL; AF148715; AAD37783.1; -
 DR GO; GO:0000148; C:1,3-beta-glucan synthase complex; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0003843; F:1,3-beta-glucan synthase activity; IEA.
 DR GO; GO:0006075; P:beta-1,3 glucan biosynthesis; IEA.
 DR InterPro; IPR003440; Glyco_trans_48.
 DR InterPro; IPR002114; HPT_Serp_S.

DR Pfam; PF02364; Glucan synthase; 1.
 DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN 1.
 SQ SEQUENCE 1926 AA; 220574 MW; BB098950FP2253DS CRC64;
 Query Match 41.2%; Score 47; DB 2; Length 1926;
 Best Local Similarity 46.7%; Pred. No. 3.9e+02;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 2 GCADPTLRWISFC 16
 Db 1374 GCADPTLRWISFC 1388
 RESULT 23
 Q6KG99 PRELIMINARY; PRT; 166 AA.
 AC Q6KG99;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Bacteriophage Felix 01.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales.
 CX NCBI_TaxID=77775;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strangmann N., Whitchard J.M., Pierson F.W., Kapur V., Weigt L.A.;
 RT "Bacteriophage Felix 01: Genetic Characterization."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF320576; AAQ14824.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 166 AA; 19296 MW; 5AAB33E39DC3C989 CRC64;
 Query Match 40.8%; Score 46.5; DB 2; Length 166;
 Best Local Similarity 52.9%; Pred. No. 42;
 Matches 9; Conservative 0; Mismatches 5; Indels 3; Gaps 1;
 Qy 1 GGCADPTLRWISFC 17
 Db 8 GSC---PTYGHWISLCG 21
 RESULT 24
 Q89HD8 PRELIMINARY; PRT; 426 AA.
 AC Q89HD8;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE B1r603 protein.
 GN OrderedNames=B1r603;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 CX NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE=2248498; PubMed=12597275;
 RX Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Iidesawa K., Iriuguchi M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimpo S., Tsunooka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110."
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005957; BAC51318.1; -
 DR HSP; P27017; 1Q00.
 KW Complete proteome.
 SQ SEQUENCE 426 AA; 47042 MW; AE20A1EC6CEB038 CRC64;
 Query Match 40.8%; Score 46.5; DB 2; Length 426;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;

Matches 8; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 GGCADGPTLRW 12
 |||||
 Db 416 GGCAG-PTFRW 426

RESULT 25

08FPC4 PRELIMINARY; PRT; 97 AA.

AC 08FPC4; 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, last sequence update)
 DE Hypothetical protein.
 GN OrderedlocusNames=CEI1858;
 OS Corynebacterium efficiens;
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=152794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YC-314;
 RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
 RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
 RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
 RT "Comparative complete genome sequence analysis of the amino acid
 RT replacements responsible for the thermostability of Corynebacterium
 RT efficiens.";
 RL Genome Res. 13:1572-1579 (2003).
 DR EMBL; AP005220; BAC18668.1; -
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 97 AA; 10632 MW; 6CPI1DA565B304C CRC64;

Query Match 40.4%; Score 46; DB 2; Length 97;
 Best Local Similarity 58.3%; Pred. No. 29;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCADGPTLRW 12
 |||||
 Db 77 GGALDGRTRW 88

RESULT 26

07MVA9 PRELIMINARY; PRT; 117 AA.

AC 07MVA9; 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, last sequence update)
 DE Hypothetical protein.
 GN OrderedlocusNames=PG1251;
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=W83;
 RX MEDLINE=22829867; PubMed=12949112;
 DOI=10.1128/JB.185.18.5591-5601.2003;
 RA Nelson K.E., Fleischman R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
 RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
 RA Hatte D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
 RA Dewhirst F.E., Fraser C.M.;
 RT "Complete genome sequence of the oral pathogenic bacterium
 RT Porphyromonas gingivalis strain W83.";
 RL J. Bacteriol. 185:5591-5601 (2003).
 DR EMBL; AB017176; AA066334.1; -
 RT TIGR; PG1251; -
 KM Complete proteome; Hypothetical protein.

SQ SEQUENCE 117 AA; 12589 MW; B4421EB01D18689 CRC64;

Query Match 40.4%; Score 46; DB 2; Length 117;
 Best Local Similarity 52.9%; Pred. No. 35;
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 GGCADGPTLRWISFCG 18
 |||||
 Db 17 GCYCVPVAVWIIIGAG 33

RESULT 27

08N852 PRELIMINARY; PRT; 159 AA.

AC 08N852; 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, last sequence update)
 DE Hypothetical protein FLJ40008.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Stomach;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Magatsuna M., Sugawara M.,
 RA Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Iwibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimura M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Horita T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara R., Tanase T., Nomura Y.,
 RA Musashino K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohnori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Maeno Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45 (2004).
 DR EMBL; AK097327; BAC04999.1; -
 SQ SEQUENCE 159 AA; 17782 MW; DF63A4A6D73129A8 CRC64;

Query Match 40.4%; Score 46; DB 2; Length 159;
 Best Local Similarity 52.6%; Pred. No. 48;
 Matches 10; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

QY 1 GGCA----DGPTLRWISF 15
 |||||
 Db 17 GGCGLVKHWTLRWNSF 35

RESULT 28

063KH8 PRELIMINARY; PRT; 162 AA.

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AC O63KH8;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=BPSS1383;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Tlball R.W., Peacock S.J., Cerdano-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bertley S.D., Sebailia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosser B., Davis P., Deshaizer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holtroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchaveest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
DR EMBL; BX571966; CAH38855.1; -.
KW Hypothetical protein.
SQ
SEQUENCE 162 AA; 17186 MW; 27CDFP4999112AB3 CRC64;

Query Match 40.4%; Score 46; DB 2; Length 162;
Best Local Similarity 88.9%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 GCADGPTLR 10
Db 93 GCADGPTLR 101

RESULT 29
Q7VWMS PRELIMINARY; PRT; 196 AA.
ID Q7VWMS;
AC Q7VWMS;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Putative lipoprotein.
GN OrderedLocustNames=BP2072;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=2827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Umwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40 (2003).
DR EMBL; BX640417; CAB2350.1; -.
KW Complete proteome; Lipoprotein.
SQ
SEQUENCE 196 AA; 21519 MW; FFE286B5EB968 CRC64;

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Query Match 40.4%; Score 46; DB 2; Length 196;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 GCADGPTLR 10
Db 18 GCADGPTLR 26

RESULT 30
Q7W9XL PRELIMINARY; PRT; 196 AA.
ID Q7W9XL;
AC Q7W9XL;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Putative lipoprotein.
GN OrderedLocustNames=BP1756;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Norbertczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutherford K., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Umwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40 (2003).
DR EMBL; BX640428; CAB37057.1; -.
KW Complete proteome; Lipoprotein.
SQ
SEQUENCE 196 AA; 21562 MW; D082FBA6A6C3A765 CRC64;

Query Match 40.4%; Score 46; DB 2; Length 196;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 GCADGPTLR 10
Db 18 GCADGPTLR 26

RESULT 31
Q8GVFS PRELIMINARY; PRT; 245 AA.
ID Q8GVFS;
AC Q8GVFS;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 26, Last annotation update)
DE Putative eukaryotic translation initiation factor 6.
GN Name=OU1340_C08.131;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC "Oryza sativa nippohare (GA3) genomic DNA, chromosome 7, BAC
RT clone=OU1340 C08."
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AP005292; BAC45212.1; -.
 DR HSSP; Q12522; 1G62.
 DR Gramene; O8GVF5; -.
 DR GO; GO:0003743; F:translation initiation factor activity; IEA.
 DR GO; GO:0006413; P:translational initiation; IEA.
 DR InterPro; IPR002769; eIF6.
 DR InterPro; IPR001912; eIF-6; 1.
 DR Pfam; PF01912; eIF-6; 1.
 DR ProDom; PD006880; eIF6; 1.
 DR SMART; SM00654; eIF6; 1.
 DR TIGRFAMs; TIGR00323; eIF-6; 1.
 KW Initiation factor.
 SQ SEQUENCE 245 AA; 2638 MM; EB526A7DD103291B CRC64;

Query Match 40.4%; Score 46; DB 2; Length 245;
 Best Local Similarity 50.0%; Pred. No. 73;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 ADGPTLRWISFCG 17
 DB 194 AAGWTVDWMTAFCG 207

RESULT 32
 O13090 PRELIMINARY; PRT; 275 AA.
 AC O13090;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE NCK-3.2.
 GN Name=PwNck-3.2;
 OS Pleurodeles waltlilii (Iberian ribbed newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
 OC Pleurodeles
 OX NCBI_TaxId=8319;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99255950; PubMed=10322640;
 RX DOI=10.1002/(SICI)1520-6408(1999)24:3/4<319::AID-DVG15>3.0.CO;2-#;
 RA Nicolas S., Caubit X., Massacrier A., Cau P., Le Parco Y.;
 RT "Two Nck-3-related genes are expressed in the adult and regenerating
 RT central nervous system of the urodele Pleurodeles waltlilii";
 RL Dev. Genet. 24:319-328(1999).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; U88714; AAC08704.1; -.
 DR HSSP; P22808; 1MK3.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR009057; Homeodomain like.
 DR InterPro; IPR000047; HTH_lambdarepressr.
 DR Pfam; PF00046; Homeobox_1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTHREPRESSR.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 275 AA; 30341 MM; 4519CD44E3348DE0 CRC64;

Query Match 40.4%; Score 46; DB 2; Length 275;
 Best Local Similarity 43.8%; Pred. No. 82;
 Matches 7; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFCG 18
 DB 32 CAEPACDWMRLCAG 47

RESULT 33

IMPL_MOUSE
 ID IMPL_MOUSE STANDARD; PRT; 277 AA.
 AC P70224;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Immunity-associated protein 1 (Immune associated protein 38) (IAP38).
 GN Name=Imap1; Synonyms=Imap38;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Ola, and C57BL/10; TISSUE=Spleen;
 RX MEDLINE=97148595; PubMed=9020038; DOI=10.1006/dbrc.1996.5876;
 RA Kruecken J., Schmitt-Wrede H.P., Markmann-Mullisch U., Wunderlich F.;
 RT "Novel gene expressed in spleen cells mediating acquired testosterone-
 RT resistant immunity to Plasmodium chabaudi malaria";
 RL Biochem. Biophys. Res. Commun. 230:167-170(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Ola, and C57BL/10; TISSUE=Spleen;
 RX MEDLINE=99377081; PubMed=10446218; DOI=10.1074/jbc.274.34.24383;
 RA Kruecken J., Stamm O., Schmitt-Wrede H.P., Mincheva A., Lichter P.,
 RA Wunderlich F.;
 RT "Spleen-specific expression of the malaria-inducible intronless mouse
 RT gene Imap38.";
 RL J. Biol. Chem. 274:24383-24391(1999).
 RN [3]
 RP IDENTIFICATION, SUBCELLULAR BINDING, AND GTP-BINDING.
 RC TISSUE=Spleen;
 RX MEDLINE=21673999; PubMed=11814688; DOI=10.1016/S0378-1119(01)00837-X;
 RA Stamm O., Kruecken J., Schmitt-Wrede H.-P., Benen W.P.M.,
 RA Wunderlich F.;
 RT "Human ortholog to mouse gene Imap38 encoding an ER-localizable G-
 RT protein belongs to a gene family clustered on chromosome 7q32-36.";
 RL Gene 282:159-167(2002).
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Endoplasmic
 CC reticulum.
 CC -1- SIMILARITY: Belongs to the GTP-binding IAN family.
 CC -1- CATION: Ref.1 and Ref.2 sequences were translated from the wrong
 CC open reading frame.

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 CC -----

DR EMBL; Y08026; CAA69283.2; ALT SEQ.
 DR EMBL; AJ131125; CAB53101.1; ALT_SEQ.
 DR PIR; A58583; A58583.
 DR MGI; MGI:109368; Imap38.
 DR InterPro; IPR006703; AIG1.
 DR Pfam; PF04548; AIG1; 1.
 KW Endoplasmic reticulum; GTP-binding; Transmembrane.
 FT DOMAIN 1 250 Cytoplasmic (Potential).
 FT TRANSMEM 251 266 Anchor for type IV membrane protein
 FT (Potential).
 FT DOMAIN 267 277 Extracellular (Potential).
 FT NP BIND 10 17 GTP (Potential).
 FT NP BIND 58 61 GTP (Potential).
 FT NP BIND 130 132 GTP (Potential).
 SQ SEQUENCE 277 AA; 30828 MM; F192E438A7579C5C CRC64;

Query Match 40.4%; Score 46; DB 1; Length 277;
 Best Local Similarity 41.2%; Pred. No. 82;
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFCGK 19

Db 144 CTDRALRDVAVCGGR 160

RESULT 34

Q9NDD0 PRELIMINARY; PRT; 312 AA.

AC Q9NDD0; 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 05-JUN-2004 (TREMBLrel. 27, Last annotation update)
 DE Casein kinase 1 homolog 1 (Casein kinase 1.1).
 GN Name=CKI.1;
 OS Trypanosoma cruzi.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 NC NCB1_TaxID=5693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Spadator C., Repetto Y., Robello C., Morello A., Castanys S.,
 RA Gamarro F.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22276527; PubMed=1387847; DOI=10.1016/S0166-6851(02)00156-1;
 RA Spadator C., Repetto Y., Torres C., Pino L., Robello C., Morello A.,
 RA Gamarro F., Castanys S.;
 RT "Two casein kinase 1 isoforms are differentially expressed in
 Trypanosoma cruzi."
 RL Mol. Biochem. Parasitol. 124:23-36 (2002).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AF164116; AAF80492.1; -;
 DR EMBL; AF274060; AAK58697.1; -;
 DR HSSP; Q06486; 1CKI.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase_1like.
 DR InterPro; IPR00719; Prot kinase.
 DR InterPro; IPR008271; Ser_Thr_kin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 312 AA; 35770 MW; 471E0BC2B0546321 CRC64;

Query Match 40.4%; Score 46; DB 2; Length 312;
 Best Local Similarity 57.1%; Pred. No. 93;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 GPTLRWISFCGK 19

Db 89 GPSLEDLFSFCGR 102

RESULT 35

Q7PP6 PRELIMINARY; PRT; 347 AA.

AC Q7PP6; 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE ENSANGP0000020769 (Fragment).
 GN Name=ENSANG0000018280;
 OS Anopheles gambiae str. PE8T.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.
 NC NCB1_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PE8T;

RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; AAA01008944; EAA10075.2; -;
 DR GO; GO:0008898; F:homocysteine S-methyltransferase activity; IEA.
 DR InterPro; IPR003726; S_methyl_trans.
 DR Pfam; PF02574; S-methyl_trans; 1.
 FT NON_TER
 SQ SEQUENCE 347 AA; 38585 MW; 66FF58A1000CDA4F CRC64;

Query Match 40.4%; Score 46; DB 2; Length 347;
 Best Local Similarity 61.5%; Pred. No. 1e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 CADGPTLRWISF 15

Db 201 CDEYPTVRFWISF 213

RESULT 36

Q88NU2 PRELIMINARY; PRT; 403 AA.

AC Q88NU2; 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=P1112;
 OS Pseudomonas putida (strain KT2440).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NC NCB1_TaxID=160488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22423060; PubMed=12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 RA Brinkac L.M., Beanan M.J., Deboy R.T., Daugherty S.C., Kolonay J.F.,
 RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
 RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
 RA Moazzar A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
 RA Wedler H., Luder J., Scjepandic D., Hohelsel J., Straetz M., Heim S.,
 RA Kiewitz C., Bisen J.A., Tilmias K.N., Duesterhoeft A., Tuenmler B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 metabolically versatile Pseudomonas putida KT2440."
 RL Environ. Microbiol. 4:799-806 (2002).
 DR EMBL; AE016778; AAN6737.1; -;
 DR TIGR; P1112; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 403 AA; 42380 MW; 4D71A1AF370C58A7 CRC64;

Query Match 40.4%; Score 46; DB 2; Length 403;
 Best Local Similarity 61.5%; Pred. No. 1.2e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GPTLRWISFCG 18

Db 149 GPTLRWLRDVCG 161

RESULT 37

Q9P858 PRELIMINARY; PRT; 443 AA.

AC Q9P858; 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Phaeosphaeria nodorum (Septoria nodorum).
 OC Plasmid plasmal.

```

OC Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
OX NCBI_TaxID=13684;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BS444;
RA Rawson J.M.;
RT "Transposable elements in the phytopathogenic fungus Stagonospora
nodorum.";
RL Thesis (2000), PhD thesis, University of Birmingham, UK.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BS444;
RA Rawson J.M.; Cutler S.B., Caten C.E.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ27966; CAB91876.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 443 AA; 4946 MW; 367E0762EB839568 CRC64;

Query Match 40.4%; Score 46; DB 2; Length 443;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 CADGPTLRWISPCGG 18
   ||| ||| |||
Db 170 CSENGTLEWITALQG 185

RESULT 38
ID Q6A1T0 PRELIMINARY; PRT; 482 AA.
AC Q6A1T0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=DP3021;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LSV54 / DSM 12343;
RX PubMed=15305914;
RA Rabus R., Ruepp A., Frickey T., Ratter T., Fartmann B., Stark M.,
  Bauer M., Zibat A., Lombardot T., Becker I., Amann K.,
  Tseling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
  Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
  from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL; CR522870; CAG37750.1; -.
DR InterPro; IPR003846; UPF0061.
DR Pfam; PF02696; UPF0061.1.
KW Complete proteome.
SQ SEQUENCE 482 AA; 54161 MW; 5F401BE29D89323D CRC64;

Query Match 40.4%; Score 46; DB 2; Length 482;
Best Local Similarity 69.2%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGCADGPTLRWMI 13
   ||| ||| |||
Db 120 GRCAVGPALRFT 132

RESULT 39
ID Q82L10 PRELIMINARY; PRT; 540 AA.
AC Q82L10;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative long chain-fatty acid CoA ligase.
GN OrderedLocustNames=SAV2030;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
  Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
  Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
  avermitilis: deducing the ability of producing secondary
  metabolites.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
  Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
  microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
  family.
DR EMBL; AP005029; BAC69741.1; -.
DR HSSP; P08659; ILCT.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00455; AMP BINDING; 1.
KW Complete proteome; Ligase.
SQ SEQUENCE 540 AA; 58879 MW; B3FBF500B20FFC64 CRC64;

Query Match 40.4%; Score 46; DB 2; Length 540;
Best Local Similarity 56.2%; Pred. No. 1.6e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 ADGPTLRWISPCGK 19
   ||| ||| |||
Db 485 ADGPTLRWISPCGK 500

RESULT 40
ID AAS5_HUMAN STANDARD; PRT; 926 AA.
AC Q9UDR5; O95462;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-aminoadipic semialdehyde synthase, mitochondrial precursor
  (LOR) [includes: lysine ketoglutarate reductase (EC 1.5.1.8) (LOR)
  (LKR); Saccharopine dehydrogenase (EC 1.5.1.9) (SDH)].
GN Name=AAS5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX PubMed=10775527;
RA Sacksteder K.A., Biery B.J., Morrell J.C., Goodman B.K.,
  Geisbrecht B.V., Cox R.P., Gould S.J., Geraghty M.T.;
RT "Identification of the alpha-aminoadipic semialdehyde synthase gene,
  which is defective in familial hyperlysinemia.";
RL Am. J. Hum. Genet. 66:1736-1743(2000).
RN [2]

```

RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Papes F., Kemper E.L., Cord-Neto G., Langone F., Arruda P.;
 RT "Cloning and expression analysis of the LKR/SDH gene in human
 tissues";
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
 RA Hillier L.M., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
 Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
 Ray J.K., Sekhon M., Becker M.C., Olafsholm M.D., Schaller M.E., Du H.,
 Rweil G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M.E., Du H.,
 Sun H., Edwards J., Bradshaw-Cordum H., All J., Andrews S., Isak A.,
 Vabnick P., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
 Ozerly P., Bielicki L., Scott K., Holmes A., Hartline R., Harris A.,
 Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
 Kozlowicz-Relly A., Leonard S., Rohlfing T., Rock S.M.,
 Tin-William A.-M., Abbott A., Mink P., Maupin R., Strommatt C.,
 Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
 Wendl M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
 Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
 Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
 Clifton W., Chissee S.L., Marra M.A., Raymond C., Haugen E.,
 Gillet W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
 Sims E., Levy R., Clendenning J., Kaul R., Kent W.J., Flurey T.S.,
 Baerbach R.A., Brent M.R., Keibler E., Flisek P., Bork P., Suyama M.,
 Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
 Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
 Waterston R.H., Wilson R.K.;
 RT "The DNA sequence of human chromosome 7";
 RL Nature 424:157-164(2003).
 CC -1- FUNCTION: A bifunctional enzyme that catalyzes the first two steps
 in lysine degradation. The N-terminal and the C-terminal contain
 lysine-ketoglutarate reductase and saccharopine dehydrogenase
 activity, respectively.
 CC -1- CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine +
 NADP(+) + H(2)O = L-lysine + 2-oxoglutarate + NADPH.
 CC -1- CATALYTIC ACTIVITY: N(6)-(L-1,3-dicarboxypropyl)-L-lysine + NMD(+) +
 H(2)O = L-glutamate + 2-aminoadipate 6-semialdehyde + NADH.
 CC -1- PATHWAY: Lysine degradation; Saccharopine pathway; first step.
 CC -1- PATHWAY: Lysine degradation; Saccharopine pathway; second step.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Mitochondrial (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed in all 16 tissues examined with
 highest expression in the liver.
 CC -1- INDUCTION: Induced by starvation (By similarity).
 CC -1- DISEASE: Defects in AAS are the cause of hyperlysinemia
 [MIM:238700]. Hyperlysinemia is an autosomal recessive condition
 characterized by hyperlysinemia lysinuria and variable
 saccharopinuria.
 CC -1- SIMILARITY: In the N-terminal section; belongs to the ALADH/PNT
 family.
 CC -1- SIMILARITY: In the C-terminal section; belongs to the saccharopine
 dehydrogenase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 or send an email to license@ebi.ac.uk).

DR InterPro: IPR005097; Saccharop-dh.
 DR Pfam: PF01262; Aladh_PNT_C; 1.
 DR Pfam: PF05222; Aladh_PNT_N; 1.
 DR Pfam: PF03435; Saccharop_dh; 1.
 KW Mitochondrion; Multifunctional enzyme; NAD; NADP; Oxidoreductase;
 KM Transit Peptide.
 FT TRANSIT 1 32 Mitochondrion (By similarity).
 FT CHAIN 33 926 Alpha-aminoacidic semialdehyde synthase.
 FT DOMAIN 33 455 Lysine-ketoglutarate reductase.
 FT DOMAIN 477 926 Saccharopine dehydrogenase.
 FT CONFLICT 589 589 S->C (in Ref. 2).
 SQ SEQUENCE 926 AA; 102131 MW; CB4194014351A18D CRC64;
 QY Query Match 40.4%; Score 46; DB 1; Length 926;
 DB Best Local Similarity 53.8%; Pred. No. 2.7e+02;
 Matches 7; Conservative 3; Mismatches 3; Gaps 0;
 6 GPTLRWISFPCGG 18
 623 GATIBSTITCGG 635
 RESULT 41
 ID Q9Y878 PRELIMINARY; PRT; 1902 AA.
 AC Q9Y878;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Glucan synthase.
 GN Name=FKS1;
 OS Coccidioides posadasii.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Oryziales; microsporitic Oryziales; Coccidioides.
 OX NCBI_TaxID=199306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Silveira;
 RA Siegel E.M., Orsborn K.I., Galgani J.N.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF159533; AAD45326.2; -
 DR GO: GO:000148; C:1,3-beta-glucan synthase complex; IEA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0003843; F:1,3-beta-glucan synthase activity; IEA.
 DR GO: GO:0006075; P:beta-1,3 glucan biosynthesis; IEA.
 DR InterPro: IPR003440; Glyco_trans_48.
 DR Pfam: PF02364; Glucan synthase; 1.
 SQ SEQUENCE 1902 AA; 217552 MW; 66FC3C60E725F2F CRC64;
 QY Query Match 40.4%; Score 46; DB 2; Length 1902;
 DB Best Local Similarity 46.7%; Pred. No. 5.5e+02;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 2 GCADGPTLRWISRC 16
 1381 GCADINPRDWMVQRC 1395
 RESULT 42
 ID Q8XZNS PRELIMINARY; PRT; 309 AA.
 AC Q8XZNS;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE PROBABLE TRANSCRIPTION REGULATOR PROTEIN.
 GN Name=RS04642; Order=edocNames=RS03360;
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.

```

RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Sallanoubat M., Gentil S., Artiguenave F., Gouzy J., Margenot S.,
RA Arlat M., Billault A., Brociter P., Camus J.C., Catolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Molan A., Robert C., Saurin W., Schlex T.,
RA Signier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
RU EMBL: A15497-502(2002).
DR HSP; G9KX7; I1XC.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR CO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR Pfam: PF00126; HTH_1; 1.
DR Pfam: PF03466; LysR_substrate; 1.
DR PROSITE; PS50931; HTH_LysR; 1.
KW complete proteome.
SQ SEQUENCE 309 AA; 33774 MW; 733551741CE83182 CRC64;

Query Match 39.9%; Score 45.5; DB 2; Length 309;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 1 GG---CADGPTLRW 12
DB 216 GGTMECTDGAVALRW 230

RESULT 43
Q8SC10 PRELIMINARY; PRT; 485 AA.
AC Q8SC10;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Orl6.
OS Propionibacterium phage phiB5.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=189836;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2186396; PubMed=1189111;
RX DOI=10.1128/JB.184.7.2030-2033.2002;
RA Chopin M.C., Rouault A., Ehrlich S.D., Gautier M.;
RT "Filamentous phage active on the gram-positive bacterium
RT Propionibacterium freudenreichii.";
RL U. Bacteriol. 184:2030-2033(2002).
DR EMBL: AF428260; AAL91699.1; -.
SQ SEQUENCE 485 AA; 48825 MW; 0B4F44ABE3DE91A4 CRC64;

Query Match 39.9%; Score 45.5; DB 2; Length 485;
Best Local Similarity 39.3%; Pred. No. 1.7e+02;
Matches 11; Conservative 4; Mismatches 4; Indels 9; Gaps 3;

QY 1 GG---CADGPTLR-----EW--ISFCGK 19
DB 418 GGAECGGGPTINLPAGAVSWRLPISWCGE 445

RESULT 44
Q7RUAS PRELIMINARY; PRT; 108 AA.
AC Q7RUAS;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein B24B19.30.
GN Name=NCU03933.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selltreinkoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kotle G.O., Ueda G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gierre S.,
RA Kamal M., Kamysellis M., Mauceli E., Bielke C., Rudd S., Fishman D.,
RA Kyrtsofva S., Raamsen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA Desonza C.C., Glass L., Orbach M.U., Berlund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebdole D.J., Freltag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
RU -1- CAUTION: the sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABX01000719; EAA28336.1; -.
KW Hypothetical protein.
SQ SEQUENCE 108 AA; 11994 MW; 093DC0D9617A252E CRC64;

Query Match 39.5%; Score 45; DB 2; Length 108;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 CADGPTLRWISFC 16
DB 70 CQCQPTLRWLSWC 83

RESULT 45
Q6ZTT4 PRELIMINARY; PRT; 146 AA.
AC Q6ZTT4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ44235.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA Tanai H., Watanabe S., Ishida S., Ono Y., Houta T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
RA Iishi S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsumoto K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Nagatsuna M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuno Y., Negai K., Isogai T.,
RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK126223; BAC86495.1; -.
SQ SEQUENCE 146 AA; 16475 MW; C0B7BBE49151B89B CRC64;

Query Match 39.5%; Score 45; DB 2; Length 146;
Best Local Similarity 69.2%; Pred. No. 63;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GCADGPTLRWIS 14
DB 28 GCADGCVLRGYIS 40

Search completed: September 1, 2005, 16:21:02
Job time : 71.6691 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:02 ; Search time 82.7482 Seconds
(without alignments)
84.131 Million cell updates/sec

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Title: US-10-083-768-9
Perfect score: 97
Sequence: 1 TIKGPTLRQWLKSRHTS 18
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 21056922

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
```

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Database :
1: A_Geneseq_16dec04.*
2: Geneseq1980s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003s.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	97	100.0	18	2	AAW09499	Aaw09499 Thrombopo
2	97	100.0	18	2	AAW09459	Aaw09459 Thrombopo
3	97	100.0	18	2	AAW36650	Aaw36650 Thrombopo
4	97	100.0	18	2	AAW35026	Aaw35026 Thrombopo
5	97	100.0	18	3	AAAB17024	Aab17024 TPO-mimete
6	97	100.0	18	4	AAU25869	Aau25869 Human chr
7	97	100.0	18	4	AAU25883	Aau25883 Human chr
8	97	100.0	18	5	ABB72910	Abb72910 TPO mimete
9	97	100.0	18	7	ADJ73062	Adj73062 TPO mimete
10	97	100.0	18	8	ADJ52697	Adj52697 CH1 delete
11	97	100.0	18	8	ADJ51658	Adj51658 CH1 delete
12	63	64.9	19	2	AAW09491	Aaw09491 Thrombopo
13	63	64.9	19	2	AAW35418	Aaw35418 Thrombopo
14	63	64.9	19	2	AAW36642	Aaw36642 Thrombopo
15	63	64.9	19	4	AAU25861	Aau25861 Human chr
16	63	64.9	19	4	AAU25998	Aau25998 Human chr
17	62	63.9	18	5	ABP51693	Abp51693 TPO mimete
18	62	63.9	18	5	ABP51691	Abp51691 TPO mimete
19	62	63.9	18	8	ADQ16625	Adq16625 TPO mimete
20	62	63.9	18	8	ADQ16629	Adq16629 TPO mimete
21	62	63.9	19	2	AAW09493	Aaw09493 Thrombopo
22	62	63.9	19	2	AAW36644	Aaw36644 Thrombopo
23	62	63.9	19	4	AAU25863	Aau25863 Human chr
24	62	63.9	144	6	ABG71748	Abg71748 Antibody
25	58	53.8	14	4	AAU26006	Aau26006 Human chr

26	58	59.8	18	2	AAW09460	AAW09460 Thrombopoietin
27	58	59.8	18	2	AAW09498	AAW09498 Thrombopoietin
28	58	59.8	18	2	AAW36649	AAW36649 Thrombopoietin
29	58	59.8	18	2	AAW33027	AAW33027 Thrombopoietin
30	58	59.8	18	2	AAW36652	AAW36652 Thrombopoietin
31	58	59.8	18	3	AAW17026	AAW17026 TPO-mimetic
32	58	59.8	18	4	AAW25868	AAW25868 Human thrombopoietin
33	58	59.8	18	4	AAW25824	AAW25824 Human thrombopoietin
34	58	59.8	18	4	AAW25871	AAW25871 Human thrombopoietin
35	58	59.8	18	5	AAW272912	AAW272912 TPO mimetic
36	58	59.8	18	7	AAW273064	AAW273064 TPO mimetic
37	58	59.8	18	7	AAW252699	AAW252699 CH1 delet
38	58	59.8	18	8	AAW15660	AAW15660 CH1 delet
39	58	59.8	18	8	AAW16705	AAW16705 Modified
40	58	59.8	128	8	AAW014705	AAW014705 Modified
41	57	58.8	13	2	AAW36779	AAW36779 Thrombopoietin
42	57	58.8	14	2	AAW09463	AAW09463 Thrombopoietin
43	57	58.8	14	2	AAW09468	AAW09468 Thrombopoietin
44	57	58.8	14	2	AAW33030	AAW33030 Thrombopoietin
45	57	58.8	14	2	AAW36774	AAW36774 Thrombopoietin
46	57	58.8	14	2	AAW124483	AAW124483 Thrombopoietin
47	57	58.8	14	2	AAW196515	AAW196515 Thrombopoietin
48	57	58.8	14	3	AAW196612	AAW196612 TPO-mimetic
49	57	58.8	14	3	AAW25827	AAW25827 Human thrombopoietin
50	57	58.8	14	4	AAW25837	AAW25837 Human thrombopoietin
51	57	58.8	14	4	AAW26037	AAW26037 Human thrombopoietin
52	57	58.8	14	4	AAW26004	AAW26004 Human thrombopoietin
53	57	58.8	14	5	AAW372853	AAW372853 TPO mimetic
54	57	58.8	14	5	AAW15669	AAW15669 Thrombopoietin
55	57	58.8	14	5	AAW18011	AAW18011 Human ligand
56	57	58.8	14	6	AAW17147	AAW17147 TPO receptor
57	57	58.8	14	7	AAW62907	AAW62907 Thrombopoietin
58	57	58.8	14	7	AAW33697	AAW33697 Erythropoietin
59	57	58.8	14	7	AAW39652	AAW39652 Thrombopoietin
60	57	58.8	14	8	AAW127293	AAW127293 Amino acid
61	57	58.8	14	8	AAW72503	AAW72503 TPO mimetic
62	57	58.8	14	8	AAW72483	AAW72483 TPO mimetic
63	57	58.8	14	8	AAW72487	AAW72487 TPO mimetic
64	57	58.8	14	8	AAW72487	AAW72487 TPO mimetic
65	57	58.8	14	8	AAW15684	AAW15684 Agonist T
66	57	58.8	15	2	AAW35416	AAW35416 Thrombopoietin
67	57	58.8	15	2	AAW36780	AAW36780 Thrombopoietin
68	57	58.8	15	2	AAW36776	AAW36776 Thrombopoietin
69	57	58.8	15	2	AAW68714	AAW68714 peptide c
70	57	58.8	15	2	AAW68712	AAW68712 peptide c
71	57	58.8	15	2	AAW66712	AAW66712 peptide c
72	57	58.8	15	3	AAW20684	AAW20684 Thrombopoietin
73	57	58.8	15	3	AAW25996	AAW25996 Human thrombopoietin
74	57	58.8	15	4	AAW26026	AAW26026 Human thrombopoietin
75	57	58.8	15	4	AAW26020	AAW26020 Human thrombopoietin
76	57	58.8	15	4	AAW25831	AAW25831 Human thrombopoietin
77	57	58.8	15	5	AAW26007	AAW26007 Human thrombopoietin
78	57	58.8	15	5	AAW51670	AAW51670 Human thrombopoietin
79	57	58.8	15	7	AAW62908	AAW62908 Thrombopoietin
80	57	58.8	15	8	AAW72485	AAW72485 TPO mimetic
81	57	58.8	15	8	AAW72479	AAW72479 TPO mimetic
82	57	58.8	15	8	AAW72502	AAW72502 TPO mimetic
83	57	58.8	15	8	AAW72492	AAW72492 TPO mimetic
84	57	58.8	15	8	AAW72478	AAW72478 TPO mimetic
85	57	58.8	15	8	AAW72533	AAW72533 TPO mimetic
86	57	58.8	15	8	AAW72490	AAW72490 TPO mimetic
87	57	58.8	15	8	AAW72486	AAW72486 TPO mimetic
88	57	58.8	15	8	AAW72491	AAW72491 TPO mimetic
89	57	58.8	15	8	AAW72522	AAW72522 TPO mimetic
90	57	58.8	15	8	AAW72523	AAW72523 TPO mimetic
91	57	58.8	15	8	AAW72493	AAW72493 TPO mimetic
92	57	58.8	15	8	AAW72482	AAW72482 TPO mimetic
93	57	58.8	15	8	AAW16585	AAW16585 TPO mimetic
94	57	58.8	16	2	AAW19534	AAW19534 Thrombopoietin
95	57	58.8	16	2	AAW33035	AAW33035 Thrombopoietin
96	57	58.8	16	2	AAW36775	AAW36775 Thrombopoietin
97	57	58.8	16	2	AAW36771	AAW36771 Thrombopoietin
98	57	58.8	16	2	AAW66709	AAW66709 peptide c

99 57 58.8 16 2 AAM66713 Peptide c
100 57 58.8 16 2 AAM66733 Peptide c

ALIGNMENTS

RESULT 1

AAM09499

AAM09499 standard; protein; 18 AA.

10-SEP-1997 (first entry)

Thrombopoietin receptor binding peptide.

Haematology; thrombocytopenia; TPO; TR; proliferation;
bone marrow transfusion; chemotherapy; radiation therapy.

Synthetic.

NO9640189-A1.

19-DEC-1996.

05-JUN-1996; 96MO-US008998.

07-JUN-1995; 95US-00472371.

07-JUN-1995; 95US-00473604.

07-JUN-1995; 95US-00476168.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00484090.

07-JUN-1995; 95US-00485301.

(GLAX) GLAXO GROUP LTD.

Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

WPI; 1997-051883/05.

Thrombopoietin receptor-binding/activating peptide(s) and peptide
mimetic(s) - useful in treatment of haematological disorders, esp.
thrombocytopenia resulting from chemotherapy, etc.

Disclosure; Page 27; 106pp; English.

The present sequence is a peptide which binds to thrombopoietin (TPO)

receptor (TR). The compound can be used for treating patients suffering

from haematological disorders and thrombocytopenia resulting from

chemotherapy, radiation therapy or bone marrow transfusions. The peptide

may also be used to maintain the proliferation and growth of TPO-

dependent cell lines and for use in biological research, for detecting

TPO receptors on living cells

Sequence 18 AA;

Query Match

Best Local Similarity 100.0%; Score 97; DB 2; Length 18;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TIKGPTLRQWLKSRHTS 18

1 TIKGPTLRQWLKSRHTS 18

10-SEP-1997 (first entry)
Thrombopoietin receptor binding compound peptide.
Haematology; thrombocytopenia; TPO; TR; proliferation;
bone marrow transfusion; chemotherapy; radiation therapy.

Synthetic.

Location/Qualifiers

Key

Misc-difference 1..18

Modified-site

Modified-site

Modified-site

Modified-site

Modified-site

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10-SEP-1997 (first entry)
Thrombopoietin receptor binding compound peptide.
Haematology; thrombocytopenia; TPO; TR; proliferation;
bone marrow transfusion; chemotherapy; radiation therapy.

Synthetic.

Location/Qualifiers

Key

Misc-difference 1..18

Modified-site

Modified-site

Modified-site

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Modified-site

Modified-site

Db 1 TIKGPTLRQWLKSRHTS 18

RESULT 3
AAW3650
ID AAW3650 standard; peptide; 18 AA.

XX AAW3650;

DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopaenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

XX Synthetic.

OS WO9640750-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009623.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

XX Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

PI Mattheakis LC, Schatz PJ, Magstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

XX Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX Disclosure; Page 27; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be

CC used to treat disorders which are susceptible to treatment with a

CC thrombopoietin agonist, preferably haematological disorders and

CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone

CC marrow transfusions. It can also be used diagnostically, e.g. to

CC investigate the mechanism of thrombopoietin signal transduction and

CC receptor activation, or to maintain the proliferation and growth of

CC thrombopoietin dependent cell lines

XX Sequence 18 AA;

XX Query Match 100.0%; Score 97; DB 2; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 1.7e-08;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 TIKGPTLRQWLKSRHTS 18

XX 1 TIKGPTLRQWLKSRHTS 18

KW Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopaenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

XX Synthetic.

XX WO9640750-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009623.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

XX Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

PI Mattheakis LC, Schatz PJ, Magstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

XX Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX Claim 19; Page 89; 106pp; English.

XX The present peptide binds the thrombopoietin receptor (TR), has a

CC molecular weight of less than 8000 Da and a TR binding affinity as

CC expressed by an IC50 of no more than about 100 microm, it can be used to

CC treat disorders which are susceptible to treatment with a thrombopoietin

CC agonist, preferably haematological disorders and thrombocytopaenia

CC resulting from chemotherapy, radiation therapy or bone marrow

CC transfusions. It can also be used diagnostically, e.g. to investigate the

CC mechanism of thrombopoietin signal transduction and receptor activation,

CC or to maintain the proliferation and growth of thrombopoietin dependent

CC cell lines

XX Sequence 18 AA;

XX Query Match 100.0%; Score 97; DB 2; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 1.7e-08;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 TIKGPTLRQWLKSRHTS 18

XX 1 TIKGPTLRQWLKSRHTS 18

XX RESULT 5

XX AAB17024

XX ID AAB17024 standard; peptide; 18 AA.

XX AAB17024;

XX 31-OCT-2000 (first entry)

XX TPO-mimetic peptide sequence SEQ ID NO:80.

XX Modified peptide; therapeutic agent; fusion; Fe domain; cancer;

XX autoimmune disease; cyclostatic; antileukemic; thrombolytic; VEGF;

XX immunosuppressive; BPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;

XX inhibitor; erythropoietin; thrombopoietin; interleukin 1;

XX cytotoxic T cell lymphocyte antigen 4; tumor necrosis factor;

XX vascular endothelial growth factor; matrix metalloproteinase; asthma;

XX thrombosis; pharmaceutical.

XX Synthetic.

XX WO200024782-A2.

PD 04-MAY-2000.
 XX
 XX 25-OCT-1999; 99WO-US025044.
 PF
 XX
 PR 23-OCT-1998; 98US-0105371P.
 PR 22-OCT-1999; 99US-00428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 DR WPI; 2000-350702/30.
 XX
 XX
 PT Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 XX
 PS Claim 19; Page 222; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)-a-F1-(X2)-b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)-C-P1, -(L1)-C-P1-(L2)-d-P2, -(L1)-C-P1-
 CC (L2)-d-P2-(L3)-e-P3, or -(L1)-C-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antitastmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AA69443 to AA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 100.0%; Score 97; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TIKGPTLRQWLKSRHTS 18
 Db 1 TIKGPTLRQWLKSRHTS 18
 XX
 RESULT 6
 AAU25869
 ID AAU25869 standard; peptide; 18 AA.
 XX
 AC AAU25869;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #55.
 XX
 KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX

PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 XX
 XX Dower WJ, Barrett RW, Cwila SE, Gates CM, Schatz PJ,
 PI Balasubramanian P, Wagerstrom CR, Hendren RW, DePrince RB, Podduturi S;
 PI Yin Q;
 DR WPI; 2001-564142/63.
 XX
 XX
 PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 PS Disclosure; Col 20; 128pp; English.
 XX
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 100.0%; Score 97; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TIKGPTLRQWLKSRHTS 18
 Db 1 TIKGPTLRQWLKSRHTS 18
 XX
 RESULT 7
 AAU25823
 ID AAU25823 standard; peptide; 18 AA.
 XX
 AC AAU25823;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #9.
 XX
 KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX

XX 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US0006623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RM, Cvrlia SE, Gates CM, Schatz PJ,
 PI Balaubramanian P, Wagstrom CR, Hendren RM, Deprince RB, Poddaturi S;
 PI Yin Q;
 DR WPI; 2001-564142/63.
 XX
 PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 PS
 PS Disclosure; Col 67-68; 128pp; English.
 XX
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent hematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 97; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TIKGPTLRQWLKSRHHTS 18
 1 TIKGPTLRQWLKSRHHTS 18
 DB
 RESULT 8
 ABB72910
 ID ABB72910 standard; peptide; 18 AA.
 XX
 AC ABB72910;
 XX
 DT 05-APR-2002 (first entry)
 XX
 DE TPO mimetic peptide SEQ ID NO:80.
 XX
 KW Modified peptide; mimetic; Pc domain; fusion; immunoglobulin G; IgG; EPO;
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
 KW TPO mimetic peptide; EPO mimetic peptide; BMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antineumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianemic; anorectic; antinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anemia;
 KW thrombocytopenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX
 PN W0200183525-A2.
 PD
 PD 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US014310.
 PR 03-MAY-2000; 2000US-00563286.
 XX
 XX (AMGEN-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheecham JC, Boone TC, Gudas JM;
 DR WPI; 2002-130313/17.
 XX
 PT Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 XX
 XX Claim 39; Page 44; 176pp; English.
 XX
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cyrostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianemic, anorectic, antinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 97; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 TIKGPTLRQWLKSRHHTS 18
 1 TIKGPTLRQWLKSRHHTS 18
 DB
 RESULT 9
 ADJ73062
 ID ADJ73062 standard; peptide; 18 AA.
 XX
 AC ADJ73062;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE TPO mimetic peptide sequence Seqid 516.
 XX
 KW mimetic; CDR mimetibody; gene therapy; transgenic; immune;
 KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
 KW immunomodulator; cardiac; antimicrobial; cytostatic; neuroprotective;
 KW TPO.
 XX
 OS Synthetic.

XX WO2003084477-A2.
 XX 16-OCT-2003.
 XX 24-MAR-2003; 2003WO-US009139.
 XX 29-MAR-2002; 2002US-0368791P.
 XX (CENZ) CENTOCOR INC.
 PA Heavner GA, Knight DM, Scallion BJ, Ghayeb J;
 PI WPI; 2003-804237/75.
 DR New CDR mimetibody comprising a portion of a heavy or light chain
 XX variable region comprising human framework or ligand binding region,
 PT useful for preparing a composition for treating e.g., immune,
 PT cardiovascular or neurologic disease.
 PS Disclosure; SEQ ID NO 516; 97pp; English.
 XX This invention relates to novel mammalian CDR mimetibodies, specific
 CC portions or variants thereof. Specifically, it refers to an antibody
 CC fragment where a protein has been inserted into, or replaces a portion
 CC of, one or more CDR regions, such that each CDR mimetibody comprises at
 CC least one portion of a heavy chain or light chain variable region, which
 CC itself comprises at least one human framework region and at least one
 CC ligand binding region (LBR). The present invention describes human
 CC CDR mimetibodies, including modified immunoglobulins and cleavage products
 CC that can be useful in gene therapy and the generation of transgenic
 CC plants and animals. Furthermore, the CDR mimetibody is useful for
 CC preparing compositions for modulating, treating or reducing the symptoms
 CC of immune, cardiovascular, infectious, malignant and/or neuromodulator,
 CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
 CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
 CC peptide sequence is a TPO mimetic peptide sequence used to make a
 CC mimetibody of the invention.
 SO Sequence 18 AA:
 QY 1 TIKGPTLRQWLKSRHNTS 18
 DB 1 TIKGPTLRQWLKSRHNTS 18
 Query Match 100.0%; Score 97; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 10
 ID ADJ52697 standard; peptide; 18 AA.
 AC ADJ52697;
 DT 06-MAY-2004 (first entry)
 DE CHI deleted mimetibody-related peptide SeqID516.
 XX CHI deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
 KW hypotensive; neuroprotective; nootropic; antibacterial; virucide;
 KW fungicide; gene therapy; immune disorder; cardiovascular disease;
 KW arrhythmia; hypertension; heart failure; neurodegenerative;
 KW multiple sclerosis; dementia; Alzheimer's disease; anaemia;
 KW cancerous condition; infectious disease; bacterial infection;
 KW viral infection; fungal infection.
 XX Unidentified.
 OS Synthetic.
 XX WO2004002417-A2.

PD 08-JUN-2004.
 XX 27-JUN-2003; 2003WO-US020347.
 XX 28-JUN-2002; 2002US-0392431P.
 XX (CENZ) CENTOCOR INC.
 PA Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
 PI Kutooski KA;
 DR WPI; 2004-082870/08.
 XX New CHI-deleted mimetibody polypeptides and nucleic acids, useful for
 PT modulating, treating, alleviating, preventing an immune, cardiovascular,
 PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
 PT diseases.
 PS Claim 2; SEQ ID NO 516; 129pp; English.
 XX This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an immunosuppressive,
 CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
 CC antibacterial, virucide or fungicide activity. In addition, the disclosed
 CC sequences may prove useful for gene therapy. The CHI-deleted mimetibody
 CC is useful for diagnosing or treating a disease condition in a cell,
 CC tissue, organ or animal, specifically for modulating, treating,
 CC alleviating, preventing the incidence or reducing the symptoms of an
 CC immune, cardiovascular (for example arrhythmia, hypertension or heart
 CC failure), or neurodegenerative (for example multiple sclerosis, dementia
 CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
 CC conditions, or infectious diseases (for example bacterial, viral or
 CC fungal infection). The present sequence is that of a peptide which may be
 CC used during the creation of a mimetibody of the invention.
 SO Sequence 18 AA:
 QY 1 TIKGPTLRQWLKSRHNTS 18
 DB 1 TIKGPTLRQWLKSRHNTS 18
 Query Match 100.0%; Score 97; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 11
 ID ADJ51658 standard; peptide; 18 AA.
 AC ADJ51658;
 DT 06-MAY-2004 (first entry)
 DE CHI deleted mimetibody-related peptide SeqID516.
 XX CHI deleted mimetibody; osteopathic; cardiovascular-Gen;
 KW dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
 KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KW anti-allergic; muscular-Gen; cytostatic; anti-inflammatory; neuroleptic;
 KW ophthalmological; nephroretropic; respiratory-Gen; tumour necrosis factor;
 KW TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KW dental disorder; oral disorder; dermatological disorder; ear disorder;
 KW nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KW gastrointestinal disorder; gynaecological disorder; hepatic disorder;
 KW obstetric disorder; hematologic disorder; immunologic disorder;
 KW allergic disorder; infectious disorder; musculoskeletal disorder;
 KW oncological disorder; neurological disorder; nutritional disorder;
 KW ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KW renal disorder; pulmonary disorder.
 XX Unidentified.
 OS

OS Synthetic.
 XX
 PN WO2004002424-A2.
 XX
 PD 08-JAN-2004.
 XX
 PF 30-JUN-2003; 2003WO-US020495.
 XX
 PR 28-JUN-2002; 2002US-0392431P.
 PR 19-SEP-2002; 2002US-0412144P.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Heavner GA, Knight DM, Ghrayeb J, Scallion BJ, Neseppor TC,
 PI Kutolowski KA;
 XX
 DR WPI; 2004-082872/08.
 XX
 PT New CHI deleted mimetibody polypeptide and nucleic acid, useful for
 PT diagnosing, preventing or treating cardiovascular, dermatologic,
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
 PT nutritional disorders.
 XX
 PS Claim 15; SEQ ID NO 516; 123pp; English.
 XX
 CC This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an osteopathic,
 CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
 CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
 CC immunomodulatory, antiallergic, muscular-Gen, cytostatic,
 CC antiinflammatory, neuroleptic, ophthalmological, nephrotropic or
 CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
 CC modulator or cytokine-agonist. The methods and compositions of the
 CC present invention are useful for the diagnosis, prevention and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the CHI deleted mimetibody, such as a bone or joint,
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
 CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
 CC obstetric, haematologic, immunological, allergic, infectious,
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
 CC pediatric, psychiatric, renal or pulmonary disorders. The present
 CC sequence is that of a peptide which may be used during the creation of a
 CC mimetibody of the invention.
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 100.0%; Score 97; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 TIKGPTLRQWLKSRHTS 18
 |||||
 DB 1 TIKGPTLRQWLKSRHTS 18
 |||||
 RESULT 12
 AAM09491
 ID AAM09491 standard; protein; 19 AA.
 XX
 AC AAM09491;
 XX
 DT 10-SEP-1997 (first entry)
 XX
 DE Thrombopoietin receptor binding peptide.
 XX
 KW Haematology; thrombocytopenia; TPO; TR; proliferation;
 KW bone marrow transfusion; chemotherapy; radiation therapy.
 XX
 OS Synthetic.
 XX
 PN WO9640189-A1.
 XX

PD 19-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US008998.
 XX
 PR 07-JUN-1995; 95US-00472371.
 PR 07-JUN-1995; 95US-00473604.
 PR 07-JUN-1995; 95US-00476168.
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00484090.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX
 DR WPI; 1997-051883/05.
 XX
 PT Thrombopoietin receptor-binding/activating peptide(s) and peptide
 PT mimetic(s) - useful in treatment of haematological disorders, esp.
 PT thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Disclosure; Page 26; 106pp; English.
 XX
 CC The present sequence is a peptide which binds to thrombopoietin (TPO)
 CC receptor (TR). The compound can be used for treating patients suffering
 CC from haematological disorders or thrombocytopenia resulting from
 CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide
 CC may also be used to maintain the proliferation and growth of TPO-
 CC dependent cell lines and for use in biological research, for detecting
 CC TPO receptors on living cells
 XX
 SQ Sequence 19 AA;
 XX
 Query Match 64.9%; Score 63; DB 2; Length 19;
 Best Local Similarity 73.3%; Pred. No. 0.0052;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 4 GPTLRQWLKSRHTS 18
 |||||
 DB 5 GPTLRQWLKSRHTS 19
 |||||
 RESULT 13
 AAM35418
 ID AAM35418 standard; peptide; 19 AA.
 XX
 AC AAM35418;
 XX
 DT 11-MAR-1998 (first entry)
 XX
 DE Thrombopoietin receptor binding peptide.
 XX
 KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Cross-links 3
 FT /note= "linked via disulfide bond to Cys3 of identical
 FT peptide"
 FT Modified-site 19
 FT /note= "NH2-Ser"
 XX
 PN WO9640750-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009623.
 XX

PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower MJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 DR WPI; 1997-052226/05.
 XX
 PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Example 9; Page 73; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 XX
 SQ Sequence 19 AA;
 XX
 Query Match 64.9%; Score 63; DB 2; Length 19;
 Best Local Similarity 73.3%; Pred. No. 0.0052;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 4 GPTLRQWLKSRHNTS 18
 DB 5 GPTLRQWLARNHLS 19
 XX
 RESULT 14
 AAW36642
 ID AAW36642 standard; peptide; 19 AA.
 XX
 AC AAW36642;
 XX
 DT 11-MAR-1998 (first entry)
 XX
 DE Thrombopoietin receptor binding peptide.
 XX
 KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 PN WO9640750-A1.
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009623.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower MJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 DR WPI; 1997-052226/05.
 XX
 PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX

PS Disclosure; Page 26; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 XX
 SQ Sequence 19 AA;
 XX
 Query Match 64.9%; Score 63; DB 2; Length 19;
 Best Local Similarity 73.3%; Pred. No. 0.0052;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 4 GPTLRQWLKSRHNTS 18
 DB 5 GPTLRQWLARNHLS 19
 XX
 RESULT 15
 AAU25861
 ID AAU25861 standard; peptide; 19 AA.
 XX
 AC AAU25861;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #47.
 XX
 KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower MJ, Barrett RW, Cwirla SE, Gates CM, Schatz PJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Depirince RB, Poddaturi S;
 PI Yin Q;
 DR WPI; 2001-564142/63.
 XX
 PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hemtological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 PS Disclosure; Col 20; 128pp; English.
 XX
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The

CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines

Query Match 64.9%; Score 63; DB 4; Length 19;
 Best Local Similarity 73.3%; Pred. No. 0.0052;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 GPTLRQWLKSRHNTS 18
 |||||
 DB 5 GPTLRQWLAAARNHLS 19

RESULT 16
 AAU25998
 ID AAU25998 standard; peptide; 19 AA.

AC AAU25998;

DT 17-DEC-2001 (first entry)

DE Human thrombopoietin receptor (TPO-R) activator peptide #184.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lact gene.

OS Homo sapiens.

PN US6251864-B1.

PD 26-JUN-2001.

PF 01-MAR-2000; 2000US-00516704.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PR 07-JUN-1996; 96WO-US009623.

PR 15-AUG-1996; 96US-00699027.

PA (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ,
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Depince RB, Podduturi S;
 PI Yin Q;

DR WPI; 2001-564142/63.

PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.

PS Disclosure: Col 143-144; 128pp; English.

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow

CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines

Query Match 64.9%; Score 63; DB 4; Length 19;
 Best Local Similarity 73.3%; Pred. No. 0.0052;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 GPTLRQWLKSRHNTS 18
 |||||
 DB 5 GPTLRQWLAAARNHLS 19

RESULT 17
 ABP51693
 ID ABP51693 standard; peptide; 18 AA.

AC ABP51693;

DT 01-OCT-2002 (first entry)

DE TPO mimetic peptide SEQ ID NO:49.

XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 KW complementarily determining region; immunoglobulin; antianemic;
 KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

OS Homo sapiens.

PN WO200246238-A2.

PD 13-JUN-2002.

PF 05-DEC-2001; 2001WO-US047656.

PR 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

PA (ALEXION PHARM INC.

PI Bowdish KS, Barbac-Frederickson S, Renshaw M;

DR WPI; 2002-566610/60.

DR N-PSDB; ABQ73371.

PT A novel immunogen molecule comprising a region in which amino acid
 PT residues corresponding to at least a portion of the complementary
 PT determining region are replaced or fused with an erythropoietin or
 PT thrombopoietin mimetic.

PS Claim 20; Fig 5; 113pp; English.

XX The present invention describes an immunoglobulin molecule or its fragment
 CC (1) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (1) has
 CC antianemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of

CC haematopoietic cells, and a stimulator of haematopoiesis. (1) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (1) is contacted with
 CC promegakaryocytes or megakaryocytes, which results in increased platelet
 CC production. (1) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (1) is contacted with haematopoietic
 CC stem cells or their progenitors. (1) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP5169 to ABP51696 represent sequences used in
 CC the exemplification of the present invention

XX
 SO Sequence 18 AA;

Query Match 63.9%; Score 62; DB 5; Length 18;
 Best Local Similarity 78.6%; Pred. No. 0.007;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TIKGPTLRQWLKSR 14
 ||:|||||||:|
 Db 2 TIKGPTLRQWLAKR 15

RESULT 18

ABP51691
 ID ABP51691 standard; peptide; 18 AA.

AC ABP51691;

DT 01-OCT-2002 (first entry)

XX TPO mimetic peptide SEQ ID NO:45.

DE TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;

KW complementarity determining region; immunoglobulin; antiaemic;

KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX Homo sapiens.

OS Synthetic.

XX WO200246238-A2.

PN 13-JUN-2002.

PD 05-DEC-2001; 2001WO-US047656.

PF 05-DEC-2001; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288899P.

PR 29-MAY-2001; 2001US-0294068P.

XX (ALEX-) ALEXION PHARM INC.

PA Bowdish KS, Barbas-Fredrickson S, Renshaw M;

PI WPI; 2002-566610/60.

DR N-PSDB; ABQ73369.

XX A novel immunogen molecule comprising a region in which amino acid

PT residues corresponding to at least a portion of the complementary

PT determining region are replaced or fused with an erythropoietin or

PT thrombopoietin mimetic.

XX Claim 20; Fig 5; 113pp; English.

XX The present invention describes an immunoglobulin molecule or its fragment

CC (1) comprising a region where amino acid residues corresponding to at

CC least a portion of the complementary determining region (CDR) are

CC replaced or fused with biologically active peptides e.g. a peptide

CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,

CC that is flanked with proline at its carboxy terminus. (1) has

CC antiaemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (1) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (1) is contacted with
 CC promegakaryocytes or megakaryocytes, which results in increased platelet
 CC production. (1) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (1) is contacted with haematopoietic
 CC stem cells or their progenitors. (1) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP5169 to ABP51696 represent sequences used in
 CC the exemplification of the present invention

XX
 SO Sequence 18 AA;

Query Match 63.9%; Score 62; DB 5; Length 18;
 Best Local Similarity 78.6%; Pred. No. 0.007;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TIKGPTLRQWLKSR 14
 ||:|||||||:|
 Db 2 TIKGPTLRQWLAKR 15

RESULT 19

ADQ16625
 ID ADQ16625 standard; peptide; 18 AA.

AC ADQ16625;

DT 09-SEP-2004 (first entry)

XX TPO mimetic peptide with random flanking residues SEQ ID NO:45.

DE immunoglobulin; complementarity determining region; CDR; peptide mimetic;

KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;

KW immunotherapy; thrombocytopenia.

XX Unidentified.

XX WO2004050017-A2.

PN 17-JUN-2004.

PD 17-NOV-2003; 2003WO-US036894.

PF 02-DEC-2002; 2002US-00307724.

PR (ALEX-) ALEXION PHARM INC.

PA Bowdish KS, Fredrickson S, Renshaw M;

PI WPI; 2004-460973/43.

DR N-PSDB; ADQ16626.

XX New immunoglobulin molecule comprising a region, where two

PT complementarity determining regions (CDRs) are replaced with EPO mimetic

PT or a TPO mimetic, useful for treating thrombocytopenia.

PT Example 1; SEQ ID NO 45; 107pp; English.

XX The invention relates to a novel immunoglobulin molecule or its fragment

CC comprising a region where amino acid residues corresponding to at least a

CC portion of a two complementarity determining regions (CDRs) are replaced

CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and

CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the

CC invention has immunosuppressive activity, and may have a use in

CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or

CC treating thrombocytopenia as a result of chemotherapy, bone marrow

CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide with flanking residues.
 CC
 XX
 SQ Sequence 18 AA;

Query Match 63.9%; Score 62; DB 8; Length 18;
 Best Local Similarity 78.6%; Pred. No. 0.007;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 TIKGPTLRQWLKSR 14
 ||:|||||:
 Db 2 TIEGPTLRQWLAR 15

RESULT 20

ADQ16629
 ID ADQ16629 standard; peptide; 18 AA.

XX AC ADQ16629;

XX DT 09-SEP-2004 (first entry)

XX DE TPO mimetic peptide with random flanking residues SEQ ID NO:49.

XX KW immunoglobulin; complementarily determining region; CDR; peptide mimetic;
 KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 XX immunotherapy; thrombocytopenia.

XX OS Unidentified.

XX PN WO2004050017-A2.

XX PD 17-JUN-2004.

XX PF 17-NOV-2003; 2003WO-US036894.

XX PR 02-DEC-2002; 2002US-00307724.

XX PA (ALEX-) ALEXION PHARM INC.

XX PI Bowdish KS, Frederickson S, Renshaw M;

XX DX WPI; 2004-460973/43.

XX DR N-PSDB; ADQ16630.

XX PT New immunoglobulin molecule comprising a region, where two
 PT complementarily determining regions (CDRs) are replaced with EPO mimetic
 PT or a TPO mimetic, useful for treating thrombocytopenia.

XX PS Example 1; SEQ ID NO 49; 107pp; English.

XX CC The invention relates to a novel immunoglobulin molecule or its fragment
 CC comprising a region where amino acid residues corresponding to at least a
 CC portion of a two complementarily determining regions (CDRs) are replaced
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 CC invention has immunosuppressive activity, and may have a use in
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow
 CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide with flanking
 CC residues.

XX SQ Sequence 18 AA;

Query Match 63.9%; Score 62; DB 8; Length 18;
 Best Local Similarity 78.6%; Pred. No. 0.007;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 TIKGPTLRQWLKSR 14
 ||:|||||:
 Db 2 TIEGPTLRQWLAR 15

RESULT 21

AAW09493
 ID AAW09493 standard; protein; 19 AA.

XX AC AAW09493;

XX DT 10-SEP-1997 (first entry)

XX DE Thrombopoietin receptor binding peptide.

XX KW Haematology; thrombocytopenia; TPO; TR; proliferation;
 KW bone marrow transfusion; chemotherapy; radiation therapy.

XX OS Synthetic.

XX PN WO9640189-A1.

XX PD 19-DEC-1996.

XX PF 05-JUN-1996; 96WO-US008998.

XX PR 07-JUN-1995; 95US-00472371.

XX PR 07-JUN-1995; 95US-00473604.

XX PR 07-JUN-1995; 95US-00476168.

XX PR 07-JUN-1995; 95US-00478128.

XX PR 07-JUN-1995; 95US-00484090.

XX PR 07-JUN-1995; 95US-00485301.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Dower WJ, Barrett RW, Cwirja SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX DR WPI; 1997-051883/05.

XX PT Thrombopoietin receptor-binding/activating peptide(s) and peptide
 PT mimetic(s) - useful in treatment of haematological disorders, esp.
 PT thrombocytopenia resulting from chemotherapy, etc.

XX PS Disclosure; Page 26; 106pp; English.

XX CC The present sequence is a peptide which binds to thrombopoietin (TPO)
 CC receptor (TR). The compound can be used for treating patients suffering
 CC from haematological disorders and thrombocytopenia resulting from
 CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide
 CC may also be used to maintain the proliferation and growth of TPO-
 CC dependent cell lines and for use in biological research, for detecting
 CC TPO receptors on living cells

XX SQ Sequence 19 AA;

Query Match 63.9%; Score 62; DB 2; Length 19;
 Best Local Similarity 73.3%; Pred. No. 0.0075;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 GPTLRQWLKSRHTS 18
 |||||||:
 Db 5 GPTLRQWLKARHTLS 19

RESULT 22

AAW36644
 ID AAW36644 standard; peptide; 19 AA.

XX AC AAW36644;

XX DT 11-MAR-1998 (first entry)

XX DE Thrombopoietin receptor binding peptide.

XX KW Thrombopoietin receptor; binding peptide; treatment; agonist;

KM haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 PN W09640750-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009623.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RM, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 DR WPI; 1997-052226/05.
 XX
 PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Disclosure; Page 26; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 XX
 SQ Sequence 19 AA;
 XX

Query Match 63.9%; Score 62; DB 2; Length 19;
 Best Local Similarity 73.3%; Pred. No. 0.0075;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 GPTLRQWLKSRHETS 18
 ||||| : |||
 Db 5 GPTLRQWLARTHLS 19

RESULT 23
 AAU25863
 ID AAU25863 standard; peptide; 19 AA.
 XX
 AC AAU25863;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #49.
 XX
 KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haematologic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX

PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RM, Cwirla SE, Gates CM, Schatz PJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprience RB, Poddaturi S;
 PI Yin Q;
 DR WPI; 2001-564142/63.
 XX
 PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 PS Disclosure; Col 20; 128pp; English.
 XX
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX
 SQ Sequence 19 AA;
 XX

Query Match 63.9%; Score 62; DB 4; Length 19;
 Best Local Similarity 73.3%; Pred. No. 0.0075;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 GPTLRQWLKSRHETS 18
 ||||| : |||
 Db 5 GPTLRQWLARTHLS 19

RESULT 24
 ABG71748
 ID ABG71748 standard; protein; 144 AA.
 XX
 AC ABG71748;
 XX
 DT 20-JAN-2003 (first entry)
 XX
 DE Antibody CDR containing MPL-TPO binding sequence, TPOVHCDR1.
 XX
 KW Agonist; immunoglobulin; Ig; variable domain; heavy chain; light chain;
 KW complementarity determining region; CDR; antigenic; thrombopoietin; TPO;
 KW thrombopoietin receptor; MPL; cytotoxic T-lymphocyte; CTL; epitope;
 KW T-helper cell; B-helper cell; synthebody; pharmaceutical; vaccine;
 KW proliferation; growth; differentiation; haematopoietic cell; antibody;
 KW platelet progenitor cell; immune disorder; thrombocytopenia;
 KW disseminated intravascular coagulation; stem cell; transplantation;
 KW gene therapy; diagnostic; haematologic; immunomodulator; anticoagulant;
 KW consensus variable heavy chain domain; CONVH.
 XX
 OS Synthetic.
 OS Unidentified.
 XX
 FH Key Location/Qualifiers


```

OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 1.18
FT /note="Preferably linkages are selected from: -
FT CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-; -C(O)NR6
FT ; -NHC(O)NH; where R is hydrogen or lower alkyl and R6 is
FT lower alkyl"
FT Modified-site
FT 1
FT /note="Preferably N-terminus is selected from: -NRR1; -
FT NRC(O)R; -NRC(O)R; -NRC(O)2R; -NRC(O)NR; succinimide;
FT benzylloxycarbonyl-NH; benzylloxycarbonyl-NH with 1-3
FT substitutions on the phenyl ring selected from lower
FT alkyl, lower alkoxy, chloro, bromo; where R and R1 are
FT independently selected from hydrogen and lower alkyl"
FT Modified-site
FT 18
FT /note="Preferably C-terminus is -C(O)R2 where R2 is
FT selected from hydroxy, lower alkoxy, and -NR3R4, where R3
FT and R4 are independently selected from hydrogen and lower
FT alkyl, and where the nitrogen atom of the -NR3R4 group
FT can optionally be the amine group of the N-terminus of
FT the peptide forming a cyclic peptide"
XX
XX W09640189-A1.
XX
XX 19-DEC-1996.
XX
XX 05-JUN-1996; 96WO-US008998.
XX
XX 07-JUN-1995; 95US-00472371.
XX 07-JUN-1995; 95US-00473604.
XX 07-JUN-1995; 95US-00476168.
XX 07-JUN-1995; 95US-00478128.
XX 07-JUN-1995; 95US-00484090.
XX 07-JUN-1995; 95US-00485301.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
XX Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX WPI; 1997-051883/05.
XX
XX Thrombopoietin receptor-binding/activating peptide(s) and peptide
XX mimetic(s) - useful in treatment of haematological disorders, esp.
XX thrombocytopenia resulting from chemotherapy, etc.
XX
XX Claim 18; Page 89; 106pp; English.
XX
XX The present sequence is a compound which binds to thrombopoietin (TPO)
XX receptor (TR). It has a molecular weight of < 8000 Da, and a binding
XX affinity to TR as expressed by an IC50 of no more than about 100 nm. The
XX compound (especially if modified, see features table) can be used for
XX treating patients suffering from haematological disorders and
XX thrombocytopenia resulting from chemotherapy, radiation therapy or bone
XX marrow transfusions. The peptide may also be used to maintain the
XX proliferation and growth of TPO-dependent cell lines and for use in
XX biological research, for detecting TPO receptors on living cells
XX
XX Sequence 18 AA;
XX
XX Query Match 59.8%; Score 58; DB 2; Length 18;
XX Best Local Similarity 71.4%; Pred. No. 0.031;
XX Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 TIKPTLRQWLKSR 14
XX :|:|||||:|
XX 1 SIEGPTLRWLTJR 14
XX
XX RESULT 27
XX AAW09498
XX ID AAW09498 standard; procein; 18 AA.

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XX
XX AAW09498;
XX
XX 10-SEP-1997 (first entry)
XX
XX Thrombopoietin receptor binding peptide.
XX
XX Haematology; thrombocytopenia; TPO; TR; proliferation;
XX bone marrow transfusion; chemotherapy; radiation therapy.
XX
XX Synthetic.
XX
XX W09640189-A1.
XX
XX 19-DEC-1996.
XX
XX 05-JUN-1996; 96WO-US008998.
XX
XX 07-JUN-1995; 95US-00472371.
XX 07-JUN-1995; 95US-00473604.
XX 07-JUN-1995; 95US-00476168.
XX 07-JUN-1995; 95US-00478128.
XX 07-JUN-1995; 95US-00484090.
XX 07-JUN-1995; 95US-00485301.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
XX Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX WPI; 1997-051883/05.
XX
XX Thrombopoietin receptor-binding/activating peptide(s) and peptide
XX mimetic(s) - useful in treatment of haematological disorders, esp.
XX thrombocytopenia resulting from chemotherapy, etc.
XX
XX Disclosure; Page 27; 106pp; English.
XX
XX The present sequence is a peptide which binds to thrombopoietin (TPO)
XX receptor (TR). The compound can be used for treating patients suffering
XX from haematological disorders and thrombocytopenia resulting from
XX chemotherapy, radiation therapy or bone marrow transfusions. The peptide
XX may also be used to maintain the proliferation and growth of TPO-
XX dependent cell lines and for use in biological research, for detecting
XX TPO receptors on living cells
XX
XX Sequence 18 AA;
XX
XX Query Match 59.8%; Score 58; DB 2; Length 18;
XX Best Local Similarity 71.4%; Pred. No. 0.031;
XX Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 TIKPTLRQWLKSR 14
XX :|:|||||:|
XX 1 SIEGPTLRWLTJR 14
XX
XX RESULT 28
XX AAW36649
XX ID AAW36649 standard; peptide; 18 AA.
XX
XX AAW36649;
XX
XX 11-MAR-1998 (first entry)
XX
XX Thrombopoietin receptor binding peptide.
XX
XX Thrombopoietin receptor; binding peptide; treatment; agonist;
XX haematological disorder; thrombocytopenia; chemotherapy;
XX radiation therapy; bone marrow transfusion; diagnosis;
XX signal transduction; receptor activation; cell culture.
XX
XX Synthetic.
XX

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XX PN WO9640750-A1.
XX PD 19-DEC-1996.
XX PF 07-JUN-1996; 96WO-US009623.
XX PR 07-JUN-1995; 95US-00478128.
XX PR 07-JUN-1995; 95US-00485301.
XX PA (GLAX ) GLAXO GROUP LTD.
XX PI Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
XX PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX DR WPI; 1997-052226/05.
XX PT Peptides and peptide mimetics which bind to and activate the
XX PT thrombopoietin receptor - useful in treatment of haematological
XX PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX PS Disclosure; Page 27; 106pp; English.
XX CC The present peptide, which binds the thrombopoietin receptor (TR), can be
XX CC used to treat disorders which are susceptible to treatment with a
XX CC thrombopoietin agonist, preferably haematological disorders and
XX CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
XX CC marrow transfusions. It can also be used diagnostically, e.g. to
XX CC investigate the mechanism of thrombopoietin signal transduction and
XX CC receptor activation, or to maintain the proliferation and growth of
XX CC thrombopoietin dependent cell lines
XX SQ Sequence 18 AA;

Query Match 59.8%; Score 58; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 0.031;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TIKGPTLRQWLKSR 14
   :|:|||||:|
Db 1 SIEGPTLRWLTSR 14

RESULT 29
AAW33027
ID AAW33027 standard; peptide; 18 AA.
XX
XX AC AAW33027;
XX DT 11-MAR-1998 (first entry)
XX DE Thrombopoietin receptor binding peptide.
XX KW Thrombopoietin receptor; binding peptide; treatment; agonist;
XX KW haematological disorder; thrombocytopenia; chemotherapy;
XX KW radiation therapy; bone marrow transfusion; diagnosis;
XX KW signal transduction; receptor activation; cell culture.
XX OS Synthetic.
XX PN WO9640750-A1.
XX PD 19-DEC-1996.
XX PF 07-JUN-1996; 96WO-US009623.
XX PR 07-JUN-1995; 95US-00478128.
XX PR 07-JUN-1995; 95US-00485301.
XX PA (GLAX ) GLAXO GROUP LTD.
XX PI Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
XX PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

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XX DR WPI; 1997-052226/05.
XX PT Peptides and peptide mimetics which bind to and activate the
XX PT thrombopoietin receptor - useful in treatment of haematological
XX PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX PS Claim 19; Page 89; 106pp; English.
XX CC The present peptide binds the thrombopoietin receptor (TR), has a
XX CC molecular weight of less than 8000 Da and a TR binding affinity as
XX CC expressed by an IC50 of no more than about 100 microm. It can be used to
XX CC treat disorders which are susceptible to treatment with a thrombopoietin
XX CC agonist, preferably haematological disorders and thrombocytopenia
XX CC resulting from chemotherapy, radiation therapy or bone marrow
XX CC transfusions. It can also be used diagnostically, e.g. to investigate the
XX CC mechanism of thrombopoietin signal transduction and receptor activation,
XX CC or to maintain the proliferation and growth of thrombopoietin dependent
XX CC cell lines
XX SQ Sequence 18 AA;

Query Match 59.8%; Score 58; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 0.031;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TIKGPTLRQWLKSR 14
   :|:|||||:|
Db 1 SIEGPTLRWLTSR 14

RESULT 30
AAW3652
ID AAW3652 standard; peptide; 18 AA.
XX
XX AC AAW3652;
XX DT 11-MAR-1998 (first entry)
XX DE Thrombopoietin receptor binding peptide.
XX KW Thrombopoietin receptor; binding peptide; treatment; agonist;
XX KW haematological disorder; thrombocytopenia; chemotherapy;
XX KW radiation therapy; bone marrow transfusion; diagnosis;
XX KW signal transduction; receptor activation; cell culture.
XX OS Synthetic.
XX PN WO9640750-A1.
XX PD 19-DEC-1996.
XX PF 07-JUN-1996; 96WO-US009623.
XX PR 07-JUN-1995; 95US-00478128.
XX PR 07-JUN-1995; 95US-00485301.
XX PA (GLAX ) GLAXO GROUP LTD.
XX PI Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
XX PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX DR WPI; 1997-052226/05.
XX PT Peptides and peptide mimetics which bind to and activate the
XX PT thrombopoietin receptor - useful in treatment of haematological
XX PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX PS Disclosure; Page 27; 106pp; English.
XX CC The present peptide, which binds the thrombopoietin receptor (TR), can be
XX CC used to treat disorders which are susceptible to treatment with a
XX CC thrombopoietin agonist, preferably haematological disorders and

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CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

CC Sequence 18 AA;

Query Match 59.8%; Score 58; DB 2; Length 18;

Best Local Similarity 71.4%; Pred. No. 0.031;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TIKGPTLRQMLKSR 14

Db 1 SIEGPTLRRLWTSR 14

RESULT 31

AAB17026 standard; peptide; 18 AA.

AC AAB17026;

DT 31-OCT-2000 (first entry)

DE TPO-mimetic peptide sequence SEQ ID NO:82.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;

KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;

KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;

KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;

KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;

KW vascular endothelial growth factor; matrix metalloproteinase; asthma;

XX thrombosis; pharmaceutical.

OS Synthetic.

XX WO200024782-A2.

XX 04-MAY-2000.

XX 25-OCT-1999; 99WO-US025044.

XX 23-OCT-1998; 98US-0105371P.

XX 22-OCT-1999; 99US-00428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and pharmacologically

PT active peptides, useful for treating cancer and autoimmune diseases.

XX Claim 19; Page 222; 608pp; English.

XX The present invention describes composition of matter (I) comprising an

CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

CC (X1)-a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

CC independently selected from -(L1)-c-P1, -(L1)-c-P1-(L2)d-P2, -(L1)-c-P1-

CC (L2)d-P2-(L3)e-P3, or -(L1)-c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,

CC P3, and P4 = are each independently sequences of pharmacologically active

CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,

CC c, d, e, and f = are each independently 0 or 1, provided that at least 1

CC AAB18003 represent nucleotide and amino acid sequences used in the

CC exemplification of the present invention

XX

XX Sequence 18 AA;

Query Match 59.8%; Score 58; DB 3; Length 18;

Best Local Similarity 71.4%; Pred. No. 0.031;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TIKGPTLRQMLKSR 14

Db 1 SIEGPTLRRLWTSR 14

RESULT 32

AAU25868 standard; peptide; 18 AA.

AC AAU25868;

DT 17-DEC-2001 (first entry)

DE Human thrombopoietin receptor (TPO-R) activator peptide #54.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;

KW bone marrow transplantation; haematological disorder; platelet disorder;

KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;

KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;

KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.

XX Homo sapiens.

OS US6251864-B1.

XX 26-JUN-2001.

XX 01-MAR-2000; 2000US-00516704.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

XX 15-AUG-1996; 96US-00699027.

XX (GLAXO) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;

XX Balasubramanian P, Wagstrom CR, Hendren RW, Deprience RB, Poddaturi S;

XX WPI; 2001-564142/63.

XX Activating thrombopoietin receptors in cells, used to treat

PT thrombocytopenia and hematological disorders, comprises contacting cells

PT with peptides and peptide mimetics attached to hydrophilic polymers.

XX Disclosure, Col 20; 128pp; English.

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that

CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods

CC of activating thrombopoietin receptors in cells comprise contacting the

CC cells with effective amounts of peptides and peptide mimetics attached to

CC hydrophilic polymers. The methods are used to treat thrombocytopenia such

CC as that due to chemotherapy, radiation therapy or bone-marrow

CC transplantation and to prevent thrombocytopenia in patients at risk. The

CC sequences are used to treat and prevent hematological disorders

CC including thrombocytopenia and platelet disorders. They are used in vitro

CC as unique tools for understanding the biological role of thrombopoietin

CC (TPO) and to develop other compounds that bind to and activate the TPO

CC receptor. The peptides can be used to detect TPO receptors on living

CC cells and fixed cells, in biological fluids, in tissue homogenates, and

CC in purified or natural biological materials. They may also be used for in

CC situ staining, fluorescence-activated cell sorting, Western blotting and

CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
CC be used for in vitro expansion of megakaryocytes and their committed
CC progenitors alone or in conjunction with additional cytokines
XX
SQ Sequence 18 AA;

CC situ staining, fluorescence-activated cell sorting, Western blotting and
CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
CC be used for *in vitro* expansion of megakaryocytes and their committed
CC progenitors alone or in conjunction with additional cytokines
XX
CC Sentence 18 aa.

		59.8%;	Score 58;	DB 4;	Length 18;
Query Match		Pred.	No. 0.031;		
Best Local Similarity		71.4%;			
Matches	10; Conservative	3;	Mismatches	1;	Indels
				0;	Gaps
QY	1 TIKGPTLRWLKSR	14			
	: :: ::				
Db	1 SIEGPFLREWLTSR	14			

Query Match	59.8%	Score 58	DB 4	Length 18
Best Local Similarity	71.4%	Pred. No. 0.031		
Matches	10	Conservative	3	Mismatches 1
				Indels 0
				Gaps 0
Qy	1	TIRGPTLRQWLRKR	14	
	:	:		
Db	1	SIEGPTUREWLRKR	14	

RESULT 33
AAU25824
ID AAU25824 standard; peptide; 18 AA

RESULT 34
AAU25871
ID AAU25871 standard; peptide; 18 AA

DT 17-DEC-2001 (first entry)

DT 17-DEC-2001 (first entry)

Human thrombopoietin receptor (TPO-R) activator peptide #10.

DE Human thrombopoietin receptor (TPO-R) activator peptide #57.

KM Peptidylimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KM haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KM bone marrow transplantation; haematological disorder; platelet disorder;
 KM enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KM tissue homogenate; fluorescence-activated cell sorting; Western blotting
 KM in vitro expansion; megakaryocyte Headpiece Dimer gene; lact gene.

KM Peptide iminetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
KM haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
KM bone marrow transplantation; haematological disorder; platelet disorder;
KM enzyme-linked immunosorbent assay; in situ staining; biological fluid;
KM tissue homogenate; fluorescence-activated cell sorting; Western blotting
KM in vitro expansion; megakaryocyte; headpiece dimer gene; lacI gene.

Homo sapiens.

05 Homo sapiens.

PN US6251864-B1.

PN US6251864-B1.

PD 26-JUN-2001.

PD 26-JUN-2001.

PF 01-MAR-2000; 2000US-00516704.

PF 01-MAR-2000; 2000US-00516704.

PR 07-JUN-1995; 95US-00478128
ED 07 JUN 1995 0600Z 00485301

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1996; 96WO-US009623

PR 07-JUN-1996; 96WO-US009623.

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PI Balasubramanian P, Wager
PI Vignani O.

PI Balasubramanian P, Wages

Pl
xx
xx

pl yln Q;
yy

DK WFL; 2001-564142/63
XX

DR WPI; 2001-564142/63.

PT Activating thrombopoietin receptors in cells, used to treat thrombocytopenia and hematological disorders, comprises contacting cells with peptides and peptide mimetics attached to hydrophilic polymers.

PT Activating thrombopoietin receptors in cells, used to treat
PT thrombocytopenia and hematological disorders, comprises contacting cells
PT with peptides and peptide mimetics attached to hydrophilic polymers.

PS Disclosure; Col 67-68; 128pp; English

PS Disclosure; Col 20; 128pp; English.

CC Sequences ANU25815-ANU26049 represent peptides and peptide mimetics that
CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
CC of activating thrombopoietin receptors in cells comprise contacting the
CC cells with effective amounts of peptides and peptide mimetics attached to
CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
CC as that due to chemotherapy, radiation therapy or bone-marrow
CC transplantation and to prevent thrombocytopenia in patients at risk. The
CC sequences are used to treat and prevent haematological disorders
CC including thrombocytopenia and platelet disorders. They are used in vitro
CC as unique tools for understanding the biological role of thrombopoietin
CC (TPO) and to develop other compounds that bind to and activate the TPO
CC receptor. The peptides can be used to detect TPO receptors on living
CC cells and fixed cells, in biological fluids, in tissue homogenates, and
CC in purified or natural biological materials. They may also be used for in

CC Sequence ANU25815-ANU26049 represent peptides and peptide mimetics that
CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
CC of activating thrombopoietin receptors in cells comprise contacting the
CC cells with effective amounts of peptides and peptide mimetics attached to
CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
CC as that due to chemotherapy, radiation therapy or bone-marrow
CC transplantation and to prevent thrombocytopenia in patients at risk. The
CC sequences are used to treat and prevent haematological disorders
CC including thrombocytopenia and platelet disorders. They are used in vitro
CC as unique tools for understanding the biological role of thrombopoietin
CC (TPO) and to develop other compounds that bind to and activate the TPO
CC receptor. The peptides can be used to detect TPO receptors on living
CC cells and fixed cells, in biological fluids, in tissue homogenates, and

CC in purified or natural biological materials. They may also be used for in
CC situ staining, fluorescence-activated cell sorting, western blotting and
CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
CC be used for in vitro expansion of megakaryocytes and their committed
CC progenitors alone or in conjunction with additional cytokines
SQ Sequence 18 AA;

Query Match 59.8%; Score 58; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 0.031;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TIKGPTLRQWLKSR 14
:|:|||||:|
Db 1 SIEGPTLRWLTSR 14

RESULT 35
ID ABB72912 standard; peptide; 18 AA.
XX ABB72912;
AC ABB72912;

DT 05-APR-2002 (first entry)

DE TPO mimetic peptide SEQ ID NO:82.

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KM erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KM TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KM TPO mimetic peptide; EPO mimetic peptide; BMP; VEGF antagonist;
KM MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KM cyclostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KM antineoplastic; anorectic; antifertility; haemostatic; dermatological;
KM neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KM cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KM sleep disorder; neurological degenerative disease; anaemia;
KM thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
XX Fanconi's syndrome.

OS Homo sapiens.
OS Synthetic.

XX WO200183525-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014310.

XX 03-MAY-2000; 2000US-00563286.

XX (AMGEN-) AMGEN INC.

XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX WPI; 2002-130313/17.

PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.

XX Claim 39; Page 44; 176pp; English.

XX The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cyclostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antiaanaemic, anorectic, antifertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC proteins of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful

CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, EPO-
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABB35695 to ABB35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention

SQ Sequence 18 AA;
Query Match 59.8%; Score 58; DB 5; Length 18;
Best Local Similarity 71.4%; Pred. No. 0.031;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TIKGPTLRQWLKSR 14
:|:|||||:|
Db 1 SIEGPTLRWLTSR 14

RESULT 36
ADJ73064 standard; peptide; 18 AA.
ID ADJ73064;
XX ADJ73064;

DT 06-MAY-2004 (first entry)

DE TPO mimetic peptide sequence SeqID 518.

XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KM cardiovascular; infectious; malignant; neurologic disease; anaemia;
KM immunomodulator; cardiant; antimicrobial; cyclostatic; neuroprotective;
KM TPO.

OS Synthetic.

XX WO2003084477-A2.

XX 16-OCT-2003.

XX 24-MAR-2003; 2003WO-US009139.

XX 29-MAR-2002; 2002US-0368791P.

XX (CENTZ) CENTOCOR INC.

XX Heavner GA, Knight DW, Scallion BJ, Ghayeb J;

XX WPI; 2003-804237/75.

PT New CDR mimetibody comprising a portion of a heavy or light chain
PT variable region comprising human framework or ligand binding region,
PT useful for preparing a composition for treating e.g., immune,
PT cardiovascular or neurologic disease.

XX Disclosure; SEQ ID NO 518; 97pp; English.

XX This invention relates to novel mammalian CDR mimetibodies, specific
CC portions or variants thereof. Specifically, it refers to an antibody
CC fragment where a protein has been inserted into, or replaces a portion
CC of, one or more CDR regions, such that each CDR mimetibody comprises at
CC least one portion of a heavy chain or light chain variable region, which
CC itself comprises at least one human framework region and at least one
CC ligand binding region (LBR). The present invention describes human
CC mimetibodies, including modified immunoglobulins and cleavage products
CC that can be useful in gene therapy and the generation of transgenic
CC plants and animals. Furthermore, the CDR mimetibody is useful for
CC preparing compositions for modulating, treating or reducing the symptoms

CC of immune, cardiovascular, infectious, malignant and/ or neurologic
 CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
 CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
 CC peptide sequence is a TPO mimetic peptide sequence used to make a
 CC mimetibody of the invention.

XX Sequence 18 AA;

Query Match 59.8%; Score 58; DB 7; Length 18;
 Best Local Similarity 71.4%; Pred. No. 0.031;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TIKGPTLRQWLKSR 14
 : : : : : : : : : : : : : : : : : :
 Db 1 SIEGPTLRWLTSTR 14

RESULT 37

ADJ52699
 ID ADJ52699 standard; peptide; 18 AA.

XX ADJ52699;

XX 06-MAY-2004 (first entry)

DE CHI deleted mimetibody-related peptide SeqID518.

XX CHI deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
 KW hyponotensive; neuroprotective; nootropic; antibacterial; virucide;
 KW fungicide; gene therapy; immune disorder; cardiovascular disease;
 KW arrhythmia; hypertension; heart failure; neurodegenerative;
 KW multiple sclerosis; dementia; Alzheimer's disease; anaemia;
 KW cancerous condition; infectious disease; bacterial infection;
 KW viral infection; fungal infection.

XX Unidentified.
 OS Synthetic.

PN WO2004002417-A2.

PD 08-JAN-2004.

PF 27-JUN-2003; 2003WO-US020347.

XX 28-JUN-2002; 2002US-0392431P.

XX (CENZ) CENTOCOR INC.

XX Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
 PI Kuroloski KA;

XX WPI; 2004-082870/08.

PT New CHI-deleted mimetibody polypeptides and nucleic acids, useful for
 PT modulating, treating, alleviating, preventing an immune, cardiovascular,
 PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
 PT diseases.

XX Claim 2; SEQ ID NO 518; 123pp; English.

XX This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an immunosuppressive,
 CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
 CC antibacterial, virucide or fungicide activity. In addition, the disclosed
 CC sequences may prove useful for gene therapy. The CHI-deleted mimetibody
 CC is useful for diagnosing or treating a disease condition in a cell,
 CC tissue, organ or animal, specifically for modulating, treating,
 CC alleviating, preventing the incidence or reducing the symptoms of an
 CC immune, cardiovascular (for example arrhythmia, hypertension or heart
 CC failure), or neurodegenerative (for example multiple sclerosis, dementia
 CC or Alzheimer's disease) diseases or disorders, anemia, cancerous
 CC conditions, or infectious diseases (for example bacterial, viral or

CC fungal infection). The present sequence is that of a peptide which may be
 CC used during the creation of a mimetibody of the invention.

XX Sequence 18 AA;

Query Match 59.8%; Score 58; DB 8; Length 18;
 Best Local Similarity 71.4%; Pred. No. 0.031;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TIKGPTLRQWLKSR 14
 : : : : : : : : : : : : : : : : : :
 Db 1 SIEGPTLRWLTSTR 14

RESULT 38

ADJ51660
 ID ADJ51660 standard; peptide; 18 AA.

XX ADJ51660;

XX 06-MAY-2004 (first entry)

DE CHI deleted mimetibody-related peptide SeqID518.

XX CHI deleted mimetibody; osteopathic; cardiovascular-Gen;
 KW dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
 KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KW antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
 KW ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
 KW TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KW dental disorder; oral disorder; dermatological disorder; ear disorder;
 KW nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KW gastrointestinal disorder; gynaecological disorder; hepatic disorder;
 KW obstructive disorder; haematologic disorder; immunologic disorder;
 KW allergic disorder; infectious disorder; musculoskeletal disorder;
 KW oncological disorder; neurological disorder; nutritional disorder;
 KW ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KW renal disorder; pulmonary disorder.

XX Unidentified.
 OS Synthetic.

PN WO2004002424-A2.

PD 08-JAN-2004.

PF 30-JUN-2003; 2003WO-US020495.

XX 28-JUN-2002; 2002US-0392431P.

XX 19-SEP-2002; 2002US-0412144P.

XX (CENZ) CENTOCOR INC.

XX Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
 PI Kuroloski KA;

XX WPI; 2004-082872/08.

PT New CHI deleted mimetibody polypeptide and nucleic acid, useful for
 PT diagnosing, preventing or treating cardiovascular, dermatologic,
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
 PT nutritional disorders.

XX Claim 15; SEQ ID NO 518; 123pp; English.

XX This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an osteopathic,
 CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
 CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
 CC immunomodulator, antiallergic, muscular-Gen, cytostatic,
 CC antiinflammatory, neuroleptic, ophthalmological, nephrotropic or
 CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-

modulator or cytokine-agonist. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the CHI deleted mimetobody, such as a bone or joint, cardiovascular, dental or oral, dermatological, ear, nose or throat, endocrine, metabolic, gastrointestinal, allergic, infectious, obstetric, haematologic, immunological, nutritional, ophthalmologic, musculoskeletal, oncological, neurological, renal or pulmonary disorders. The present sequence is that of a peptide which may be used during the creation of a mimetobody of the invention.

Sequence 18 AA;

Query Match 59.8%; Score 58; DB 8; Length 18;
Best Local Similarity 71.4%; Pred. No. 0.031;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TIKPTLRQWLKSR 14
:|||||:|
Db 1 SIEGPTLRWLTSR 14

RESULT 39
ADQ16705
ID ADQ16705 standard; protein; 128 AA.
XX
AC ADQ16705;
XX
DT 09-SEP-2004 (first entry)
XX
DE Modified immunoglobulin clone 116 HC variable region SEQ ID NO:125.
XX
XX immunoglobulin; complementarity determining region; CDR; peptide mimetic;
KM erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
KW immunotherapy; thrombocytopenia.
XX
OS Synthetic.
XX
PN WO2004050017-A2.
XX
PD 17-JUN-2004.
XX
PF 17-NOV-2003; 2003WO-US036894.
XX
PR 02-DEC-2002; 2002US-00307724.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Frederickson S, Renshaw M,
XX
DR WPI; 2004-460973/43.
XX
PT New immunoglobulin molecule comprising a region, where two
PT complementarity determining regions (CDRs) are replaced with EPO mimetic
PT or a TPO mimetic, useful for treating thrombocytopenia.
XX
PS Claim 9; SEQ ID NO 125; 107pp; English.
XX
XX The invention relates to a novel immunoglobulin molecule or its fragment
CC comprising a region where amino acid residues corresponding to at least a
CC portion of a two complementarity determining regions (CDRs) are replaced
CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC invention has immunosuppressive activity, and may have a use in
CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC treating thrombocytopenia as a result of chemotherapy, bone marrow
CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC The present sequence represents immunoglobulin clone 116 heavy chain
CC variable region.
XX
SQ Sequence 128 AA;

Query Match 59.8%; Score 58; DB 8; Length 128;
Best Local Similarity 62.5%; Pred. No. 0.29;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKGPTLRQWLKSRHT 17
:|||||:|
Db 52 IEGPTLRQWLARANS 67

RESULT 40
ADQ16704
ID ADQ16704 standard; protein; 225 AA.
XX
AC ADQ16704;
XX
DT 09-SEP-2004 (first entry)
XX
DE Modified immunoglobulin clone 116 heavy chain SEQ ID NO:124.
XX
XX immunoglobulin; complementarity determining region; CDR; peptide mimetic;
KM erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
KW immunotherapy; thrombocytopenia.
XX
OS Synthetic.
XX
PN WO2004050017-A2.
XX
PD 17-JUN-2004.
XX
PF 17-NOV-2003; 2003WO-US036894.
XX
PR 02-DEC-2002; 2002US-00307724.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Frederickson S, Renshaw M,
XX
DR WPI; 2004-460973/43.
XX
PT New immunoglobulin molecule comprising a region, where two
PT complementarity determining regions (CDRs) are replaced with EPO mimetic
PT or a TPO mimetic, useful for treating thrombocytopenia.
XX
PS Example 8; SEQ ID NO 124; 107pp; English.
XX
XX The invention relates to a novel immunoglobulin molecule or its fragment
CC comprising a region where amino acid residues corresponding to at least a
CC portion of a two complementarity determining regions (CDRs) are replaced
CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC invention has immunosuppressive activity, and may have a use in
CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC treating thrombocytopenia as a result of chemotherapy, bone marrow
CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC The present sequence represents immunoglobulin clone 116 heavy chain.
XX
SQ Sequence 225 AA;

Query Match 59.8%; Score 58; DB 8; Length 225;
Best Local Similarity 62.5%; Pred. No. 0.56;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKGPTLRQWLKSRHT 17
:|||||:|
Db 52 IEGPTLRQWLARANS 67

RESULT 41
AAW36779
ID AAW36779 standard; peptide; 13 AA.
XX
AC AAW36779;
XX

DT	11-MAR-1998	(first entry)	
XX	Thrombopoietin receptor binding peptide.		
DE	Thrombopoietin receptor; binding peptide; treatment; agonist;		
XX	Thrombopoietin receptor; binding peptide; treatment; agonist;		
KW	haematological disorder; thrombocytopenia; chemotherapy;		
KW	radiation therapy; bone marrow transfusion; diagnosis;		
KW	signal transduction; receptor activation; cell culture.		
XX	Synthetic.		
OS			
XX	Key	Location/Qualifiers	
FT	Cross-Links	13	
FT		/note="terminal carboxy group linked to epsilon amino	
FT		group of Lys15 in AAM36780"	
XX			
PN	MO9640750-A1.		
XX			
PD	19-DEC-1996.		
XX			
PF	07-JUN-1996;	96WO-US009623.	
XX			
PR	07-JUN-1995;	95US-00478128.	
XX			
PR	07-JUN-1995;	95US-00485301.	
XX			
PA	(GLAX) GLAXO GROUP LTD.		
XX			
PI	Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;		
PI	Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;		
XX	WPI, 1997-052226/05.		
XX			
PT	Peptides and peptide mimetics which bind to and activate the		
PT	thrombopoietin receptor - useful in treatment of haematological		
PT	disorders, esp. thrombocytopenia resulting from chemotherapy, etc.		
XX			
PS	Example 9; Page 78; 106pp; English.		
XX			
CC	The present peptide, which binds the thrombopoietin receptor (TR), can be		
CC	used to treat disorders which are susceptible to treatment with a		
CC	thrombopoietin agonist, preferably haematological disorders and		
CC	thrombocytopenia resulting from chemotherapy, radiation therapy or bone		
CC	marrow transfusions. It can also be used diagnostically, e.g. to		
CC	investigate the mechanism of thrombopoietin signal transduction and		
CC	receptor activation, or to maintain the proliferation and growth of		
CC	thrombopoietin dependent cell lines		
XX			
XX	Sequence 13 AA;		
XX			
XX	Query Match	58.8%;	Score 57; DB 2; Length 13;
XX	Best Local Similarity	76.9%;	Pred. No. 0.031;
XX	Matches	10; Conservative	2; Mismatches
XX			1; Indels
XX			0; Gaps
XX			0
XX			
XX	2 IKGPTLRQWLKSR	14	
XX	: :		
XX	: :		
XX	1 IEGPLRQWLAR	13	
XX			
XX	RESULT 42		
XX	AAM09463		
XX	AAM09463 standard; protein; 14 AA.		
XX			
XX	AAM09463;		
XX			
XX	10-SEP-1997	(first entry)	
XX			
XX	Thrombopoietin receptor binding compound peptide.		
XX			
XX	Haematology; thrombocytopenia; TPO; TR; proliferation;		
XX	bone marrow transfusion; chemotherapy; radiation therapy.		
XX			
XX	Synthetic.		
XX			

HH	Key	Location/Qualifiers
FT	Misc-difference	1. 14
FT		/note= "Preferably linkages are selected from: -
FT		CH2OC(O)NR-; phosphonate, -CH2S(O)2NR-; -CH2NR-; -C(O)NR6
FT		; -NHC(O)NH; where R is hydrogen or lower alkyl and R6 is
FT		lower alkyl"
FT	Modified-site	1
FT		/note= "Preferably N-terminus is selected from: -NR(R1), -
FT		NR(O)R; -NR(O)OR; -NRS(O)2R; -NHC(O)NHR; succinimide;
FT		benzylloxycarbonyl-NH; benzylloxycarbonyl-NH with 1-3
FT		substitutions on the phenyl ring selected from lower
FT		alkyl, lower alkoxy, chloro, bromo; where R and R1 are
FT		independently selected from hydrogen and lower alkyl"
FT	Modified-site	14
FT		/note= "Preferably C-terminus is -C(O)R2 where R2 is
FT		selected from hydroxy, lower alkoxy, and -NR3R4, where R3
FT		and R4 are independently selected from hydrogen and lower
FT		alkyl, and where the nitrogen atom of the -NR3R4 group
FT		can optionally be the amine group of the N-terminus of
FT		the peptide forming a cyclic peptide"
XX		WO9640189-A1.
XX		19-DEC-1996.
XX		05-JUN-1996; 96WO-US008998.
XX		07-JUN-1995; 95US-00472371.
XX		07-JUN-1995; 95US-00473604.
XX		07-JUN-1995; 95US-00476168.
XX		07-JUN-1995; 95US-00478128.
XX		07-JUN-1995; 95US-00484090.
XX		07-JUN-1995; 95US-00485301.
XX		(GLAX) GLAXO GROUP LTD.
XX		Dower MJ, Barrett RM, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
XX		Mattheakis LC, Schatz PJ, Magstrom CR, Wrighton NC;
XX		WPI; 1997-051883/05.
XX		Thrombopoietin receptor-binding/activating peptide(s) and peptide
XX		mimetic(s) - useful in treatment of haematological disorders, esp.
XX		thrombocytopenia resulting from chemotherapy, etc.
XX		Claim 18; Page 89; 106pp; English.
XX		The present sequence is a compound which binds to thrombopoietin (TPO)
XX		receptor (TR). It has a molecular weight of < 8000 Da, and a binding
XX		affinity to TR as expressed by an IC50 of no more than about 100 nM. The
XX		compound (especially if modified, see features table) can be used for
XX		treating patients suffering from haematological disorders and
XX		thrombocytopenia resulting from chemotherapy, radiation therapy or bone
XX		marrow transfusions. The peptide may also be used to maintain the
XX		proliferation and growth of TPO-dependent cell lines and for use in
XX		biological research, for detecting TPO receptors on living cells
XX		Sequence 14 AA;
XX		Query Match 58.8%; Score 57; DB 2; Length 14;
XX		Best Local Similarity 76.9%; Pred. No. 0.033; Mismatches 1; Indels 0; Gaps 0;
XX		Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX		2 IKGPTLRQWLKSR 14
XX		1 IEGPTLRQWLKSR 13
XX		RESULT 43
XX		AAW09468
XX		AAW09468 standard; protein; 14 AA.
XX		AAW09468;


```

XX 07-JUN-1996; 96WO-US009623.
PF
XX
PR 07-JUN-1995; 95US-00478128.
PR 07-JUN-1995; 95US-00485301.
XX
PA (GLAXO ) GLAXO GROUP LTD.
XX
PI Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Mattheakis LC, Schatz PJ, Weststrom CR, Wrighton NC;
XX
DR WPI; 1997-052226/05.
XX
PT Peptides and peptide mimetics which bind to and activate the
PT thrombopoietin receptor - useful in treatment of haematological
PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX
XX
PS Claim 30; Page 91; 106pp; English.
XX
CC The present peptide binds the thrombopoietin receptor (TR), has a
CC molecular weight of less than 8000 Da and a TR binding affinity as
CC expressed by an IC50 of no more than about 100 microm. It can be used to
CC treat disorders which are susceptible to treatment with a thrombopoietin
CC agonist, preferably haematological disorders and thrombocytopaenia
CC resulting from chemotherapy, radiation therapy or bone marrow
CC transfusions. It can also be used diagnostically, e.g. to investigate the
CC mechanism of thrombopoietin signal transduction and receptor activation,
CC or to maintain the proliferation and growth of thrombopoietin dependent
CC cell lines
XX
SQ Sequence 14 AA;

```

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Query Match 58.8%; Score 57; DB 2; Length 14;
Best Local Similarity 76.9%; Pred. No. 0.033;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2 IKGPTLRQWLKSR 14
   |:|||||:|
Db 1 IEGPTLRQWLAAAR 13

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Search completed: September 1, 2005, 16:12:12
 Job time : 84.7482 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:57:33 ; Search time 13.7266 Seconds
(without alignments)
126.171 Million cell updates/sec

Title: US-10-083-768-9

Perfect score: 97

Sequence: 1 TTKGPTLRQWLKSRHETS 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	50.5	122	2 A10380	conserved hypothet
2	47	48.5	327	2 B71900	hypothetical prote
3	45	46.4	186	2 A90167	adenylate cyclase,
4	44	45.4	161	2 T06826	beta-fructofuranos
5	44	45.4	1019	2 T11560	pol polypeptide -
6	44	45.4	1058	2 S08436	pol polypeptide -
7	43	44.3	63	2 T30614	hypothetical prote
8	43	44.3	216	2 S35151	photosystem I chai
9	43	44.3	217	2 S46354	pol polypeptide -
10	43	44.3	233	2 A83862	initiation of chro
11	43	44.3	241	2 S07740	hypothetical prote
12	43	44.3	269	2 S73999	hypothetical prote
13	43	44.3	656	2 S30484	pol polypeptide -
14	43	44.3	656	2 S30483	pol polypeptide -
15	43	44.3	1583	2 S59644	slister chromatid c
16	42.5	43.8	275	2 AC0189	probable exported
17	42	43.3	114	2 E71171	hypothetical prote
18	42	43.3	171	2 T20567	hypothetical prote
19	42	43.3	416	2 D72456	probable glutamyl-
20	42	43.3	438	2 S71157	cytochrome c bioge
21	42	43.3	519	2 C86160	hypothetical prote
22	42	43.3	581	2 T12095	beta-fructofuranos
23	42	43.3	617	2 S75447	proline-CRNA ligas
24	42	43.3	1061	1 GNLJG4	HIV-1 retropepsin
25	42	43.3	2108	1 H70819	probable polyketid
26	41.5	42.8	877	2 T03098	p97 protein - Toxo
27	41	42.3	70	2 T06920	ribosomal protein
28	41	42.3	153	2 A87524	hypothetical prote
29	41	42.3	178	2 A82743	hypothetical prote

30	41	42.3	188	2 C82863	recombinase Xfa001
31	41	42.3	203	2 T40206	hypothetical prote
32	41	42.3	228	2 S76936	hypothetical prote
33	41	42.3	257	2 E70429	tRNA guanine-N1 me
34	41	42.3	264	2 AG2095	hypothetical prote
35	41	42.3	306	2 D70601	UTP-glucose-1-phos
36	41	42.3	380	2 B47029	methylase LlaPI -
37	41	42.3	397	2 G69449	tryptophan synthas
38	41	42.3	419	1 S29127	carboxypeptidase A
39	41	42.3	422	2 F70876	probable pap3 pro
40	41	42.3	622	2 S35122	site-specific DNA-
41	41	42.3	1039	2 S46347	pol polypeptide -
42	41	42.3	1123	2 TS1517	telomerase reverse
43	41	42.3	1140	2 S73786	hypothetical prote
44	41	42.3	1191	2 T31081	hypothetical prote
45	41	42.3	1345	2 T13423	hypothetical prote
46	40	41.2	158	2 D72305	hypothetical prote
47	40	41.2	185	2 T49611	hypothetical prote
48	40	41.2	200	2 T23485	probable glutathio
49	40	41.2	207	2 T37464	dihydropteridine r
50	40	41.2	236	1 T24385	hypothetical prote
51	40	41.2	242	2 C70895	ABC transporter, A
52	40	41.2	249	2 E87575	probable transcrip
53	40	41.2	262	2 B83126	UTP-glucose-1-phos
54	40	41.2	306	2 T45453	hypothetical prote
55	40	41.2	336	2 E72389	hypothetical prote
56	40	41.2	344	2 E84377	protein export (im
57	40	41.2	349	2 B97912	UDP-glucose 4,6-de
58	40	41.2	395	2 S40171	phosphoprotein pho
59	40	41.2	419	1 CPRTA	carboxypeptidase A
60	40	41.2	505	2 T19971	hypothetical prote
61	40	41.2	506	2 T19973	hypothetical prote
62	40	41.2	521	2 T01923	hypothetical prote
63	40	41.2	527	2 B64653	glucan 1,4-alpha-g
64	40	41.2	612	2 JQ1346	conserved hypothet
65	40	41.2	978	2 B89971	pol polypeptide -
66	40	41.2	1009	2 S28081	pol polypeptide -
67	40	41.2	1009	2 S44621	C50C3.2 protein -
68	40	41.2	1034	1 GNLJCA	HIV-1 retropepsin
69	40	41.2	1035	1 GNLJG6	HIV-1 retropepsin
70	40	41.2	1036	1 GNLJG2	HIV-1 retropepsin
71	40	41.2	1040	2 T08190	hypothetical prote
72	40	41.2	1054	1 GNLJG5	HIV-1 retropepsin
73	40	41.2	1055	1 GNLJST	HIV-1 retropepsin
74	40	41.2	1055	1 S53092	pol polypeptide -
75	40	41.2	1056	1 GNLJG3	collagen alpha 2(I
76	40	41.2	1712	1 CGHU2B	probable transport
77	40	41.2	2609	2 T40399	probable soluble 1
78	39.5	40.7	642	2 A83258	probable G2-specif
79	39.5	40.7	722	2 T37970	hypothetical prote
80	39.5	40.7	1758	2 T34393	probable nicotinam
81	39	40.2	195	2 T36141	probable nicotinam
82	39	40.2	220	2 AC0318	uracil DNA glycosy
83	39	40.2	240	2 S73922	phosphoribosylform
84	39	40.2	240	2 AE1145	hypothetical prote
85	39	40.2	314	2 H90638	nitrate reductase
86	39	40.2	318	2 S17197	hypothetical prote
87	39	40.2	320	2 H85489	probable transposa
88	39	40.2	327	2 E82277	glyoxaldehyde-3-P
89	39	40.2	331	2 B48445	short-chain alchoh
90	39	40.2	336	2 A47542	UDP-glucose 4,6-d
91	39	40.2	349	2 F86649	probable activator
92	39	40.2	373	2 D64729	hypothetical prote
93	39	40.2	410	2 H86290	hypothetical prote
94	39	40.2	533	2 C83658	adhesin Ape5-1 pre
95	39	40.2	567	2 S69778	DNA43 protein - ye
96	39	40.2	571	2 S48384	hypothetical prote
97	39	40.2	615	2 T15575	E1 protein - human
98	39	40.2	644	1 W1LW58	erythrocyte membra
99	39	40.2	721	2 A39707	microtubule-associ
100	39	40.2	721	2 A33319	

ALIGNMENTS

RESULT 1

AI0380 conserved hypothetical protein YP03137 [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_rev1sion 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AI0380
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tiliwall, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; M01D:21470413; PMID:11586360
A/Accession: AI0380

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-122 <KUR>
A/Cross-references: UNIPROT:Q8ZC84; GB:AL590842; PIDN:CAC92372.1; PID:G15981075; GSPDB:C
C/Genetics:
A/Gene: YP03137
C/Superfamily: Escherichia coli ybaJ protein

Query Match 50.5%; Score 49; DB 2; Length 122;
Best Local Similarity 53.3%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IKGPTLRQWLKSRH 16
DB 92 INDELRWQKTEH 106

RESULT 2

B71900 hypothetical protein jhp0682 - Helicobacter pylori (strain J99)

C/Species: Helicobacter pylori
A/Variety: strain J99
C/Date: 12-Feb-1999 #sequence_rev1sion 12-Feb-1999 #text_change 09-Jul-2004
C/Accession: B71900
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; ives, C.; Gibson, R.; Weiberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovle, G.F.; Nature 397, 176-180, 1999
A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A/Reference number: A71800; M01D:99120557; PMID:9923682
A/Accession: B71900

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-327 <ARN>
A/Cross-references: UNIPROT:Q9ZL98; GB:AE001500; GB:AE001439; NID:G4155238; PIDN:AAD0627
A/Experimental source: strain J99
C/Genetics:
A/Gene: jhp0682

C/Superfamily: conserved hypothetical protein HI0176

Query Match 48.5%; Score 47; DB 2; Length 327;
Best Local Similarity 50.0%; Pred. No. 8;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 TIKGPTLRQWLKSRH 16
DB 103 SVKEPTLVDMTKSQNY 118

RESULT 3

A90167 adenylate cyclase, cyab-type, probable (cyab) [imported] - Sulfolobus solfataricus

C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_rev1sion 24-May-2001 #text_change 16-Aug-2004
C/Accession: A90167
R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Adayez, M.U.; Chan- 1, J.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R
artelt, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A/Description: Sulfolobus solfataricus complete genome.

A/Reference number: A99139
A/Accession: A90167
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-186 <KUR>
A/Cross-references: UNIPROT:Q980N7; GB:AE006641; NID:G13813390; PIDN:AAK40592.1; GSPDB:C
C/Genetics:
A/Gene: cyab
C/Superfamily: Thermophilic adenylate cyclase, Cyab type

Query Match 46.4%; Score 45; DB 2; Length 186;
Best Local Similarity 55.6%; Pred. No. 9;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 TIKGPTLRQWLKSRH 18
DB 65 TYKGPTLRHSSLKARBSIS 82

RESULT 4

T06826 beta-fructofuranosidase (FC 3.2.1.26) II - garden pea (fragment)

N/Alternate names: cell wall invertase II
C/Species: Pisum sativum (garden pea)
C/Date: 30-Apr-1999 #sequence_rev1sion 30-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06826
R:Buchner, P.
submitted to the EMBL Data Library, December 1996
A/Reference number: Z15838
A/Accession: T06826
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-161 <BUC>
A/Cross-references: UNIPROT:P93490; EMBL:Z83339; PIDN:CAB05954.1
C/Superfamily: beta-fructofuranosidase
C/Keywords: glycosidase; hydrolase

Query Match 45.4%; Score 44; DB 2; Length 161;
Best Local Similarity 46.7%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 IKGPTLRQWLKSRH 16
DB 76 VSDPFLREWKSPEN 90

RESULT 5

T11560 pol polyprotein - simian immunodeficiency virus HIVm (strain E543) (fragment)

C/Species: simian immunodeficiency virus HIVm
A/Variety: strain E543
C/Date: 16-Jul-1999 #sequence_rev1sion 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T11560
R:Hirsch, V.M.; Adger-Johnson, D.; Gambell, B.; Goldstein, S.; Brown, C.; Elkins, W.R.; 1, J. Virol. 71, 1608-1620, 1997
A/Title: A molecularly cloned, pathogenic, neutralization-resistant simian immunodefici
A/Reference number: Z17285; M01D:97151152; PMID:8995688
A/Accession: T11560

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1019 <HIR>
A/Cross-references: UNIPROT:P89154; EMBL:U72748; NID:G1695908; PIDN:AA056559.1; PID:G16
C/Genetics:
A/Gene: pol
C/Superfamily: pol polyprotein
C/Keywords: AIDS; immunodeficiency

Query Match 45.4%; Score 44; DB 2; Length 1019;
Best Local Similarity 61.5%; Pred. No. 82;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 KGPTRLQWLKRSRE 15
 :|||:|:|:
 Db 184 EGPRLQWPLSKSRE 196

RESULT 6

S08436
 pol polyprotein - human immunodeficiency virus type 2 D205 (fragment)
 C:Species: human immunodeficiency virus type 2 D205, HIV-2 D205
 C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C:Accession: S08436
 R:Detrich, U.; Adamaki, M.; Kreuz, R.; Seipp, A.; Kuehn, H.; Ruesamen-Waismann, H.
 Nature 342, 948-950, 1989
 A:Title: A highly divergent HIV-2-related isolate.
 A:Reference number: S08434; MUID:90081881; PMID:2594088
 A:Accession: S08436
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1058 <DIE>
 A:Cross-references: UNIPROT:P15833; EMBL:X16109
 A>Note: this sequence was submitted to the EMBL Data Library, Aug-1989
 C:Genetics:
 A:Gene: pol
 C:Superfamily: pol polyprotein
 C:Keywords: polyprotein

Query Match 45.4%; Score 44; DB 2; Length 1058;
 Best Local Similarity 66.7%; Pred. No. 86;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 GPTLRQWLKRSRE 15
 ||:|:|:|:
 Db 222 GPKLRQWPLSKSRE 233

RESULT 7

T30614
 hypothetical protein 12L - Molluscum contagiosum virus 1
 N:Alternate names: MC0012L
 C:Species: Molluscum contagiosum virus 1
 C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
 C:Accession: T30614
 R:Senkevich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
 Science 279, 813-816, 1996
 A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
 A:Reference number: 220876; MUID:96325459; PMID:8670425
 A:Accession: T30614
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-63 <SEN>
 A:Cross-references: UNIPROT:Q98183; EMBL:U60315; PIDN:AAC55140.1
 C:Genetics:
 A>Note: MC012L

Query Match 44.3%; Score 43; DB 2; Length 63;
 Best Local Similarity 41.2%; Pred. No. 5.8;
 Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 IKGPTRLQWLKRSREHTS 18
 :|||:|:|:|:
 Db 41 VLGETLRWRSKRNTA 57

RESULT 8

S35151
 photosystem I chain XI precursor - spinach
 C:Species: Spinacia oleracea (spinach)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S35151; S14446
 R:Flieger, K.; Oelmueller, R.; Hermann, R.G.
 Plant Mol. Biol. 22, 703-709, 1993
 A:Title: Isolation and characterization of cDNA clones encoding a 18.8 kDa polypeptide,
 A:Reference number: S35151; MUID:93344519; PMID:8343606

A:Accession: S35151
 A:Molecule type: mRNA
 A:Residues: 1-216 <FRI>
 A:Cross-references: UNIPROT:Q41385; EMBL:X64445; NID:G396274; PIDN:CAA45775.1; PID:G396
 A:Experimental source: seed
 R:Keuchl, M.; Inoue, Y.
 FEBS Lett. 280, 332-334, 1991

A:Title: Two new components of 9 and 14 kDa from spinach photosystem I complex.
 A:Reference number: S14316; MUID:91192162; PMID:2013332
 A:Accession: S14446
 A:Molecule type: protein
 A:Residues: 158-175, 'X', 177-178 <IKS>
 C:Genetics:
 A:Gene: psal
 A:Function:
 C:Description: this protein is a component of photosystem I which catalyzes the light-
 C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid; transmembrane protein
 F:1-47/Domain: transit peptide (chloroplast) #status predicted <TMP>
 F:48-216/Product: photosystem I chain XI #status predicted <MAT>
 F:131-153/Domain: transmembrane #status predicted <TM2>
 F:187-209/Domain: transmembrane #status predicted <TM2>

Query Match 44.3%; Score 43; DB 2; Length 216;
 Best Local Similarity 52.9%; Pred. No. 22;
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 IKGPTRLQWLKRSREHTS 18
 |||:|:|:|:
 Db 27 ISGPALRGFSPRRHTS 43

RESULT 9

S46354
 pol polyprotein - simian immunodeficiency virus SIVagm (isolate SABD37) (fragment)
 C:Species: simian immunodeficiency virus SIVagm
 A:Variety: isolate SABD37
 C>Date: 25-Dec-1994 #sequence_revision 14-Feb-1997 #text_change 26-Aug-1999
 C:Accession: S46354
 R:Jin, M.J.; Hui, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V.M.,
 EMBO J. 13, 2935-2947, 1994
 A:Title: Mosaic genome structure of simian immunodeficiency virus from West African grc
 A:Reference number: S46355; MUID:94298785; PMID:8026477
 A:Accession: S46354
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-217 <JIN>
 A:Cross-references: EMBL:U04018; NID:G466250; PIDN:AAA21512.1; PID:G466251
 A:Experimental source: isolate SABD37; babaeus monkey
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
 C:Genetics:
 A:Gene: pol
 C:Superfamily: pol polyprotein
 C:Keywords: polyprotein

Query Match 44.3%; Score 43; DB 2; Length 217;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 GPTLRQWLKRSRE 15
 |||:|:|:|:
 Db 87 GPKLRQWPLSKSRE 98

RESULT 10

A83862
 initiation of chromosome replication dnaB [imported] - Bacillus halodurans (strain C-12
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: A83862
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hi
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83860; MUID:20512582; PMID:11058132

A/Accession: A83862
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-233 <STO>
A/Cross-references: UNIPROT:Q9KCT7; GB:AP001512; GB:BA000004; NID:G10174030; PIDN:BA054
A/Experimental source: strain C-125
C/Genetics:
A/Gene: dhad

Query Match 44.3%; Score 43; DB 2; Length 233;
Best Local Similarity 43.8%; Pred. No. 24;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 IKGPTLRQWLKSRREHT 17
Db 144 IEGETLSMWIDQOQHT 159

RESULT 11

S07740
hypothetical protein 8 - Paramaecium tetraurelia mitochondrion
C/Species: mitochondrion Paramaecium tetraurelia
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C/Accession: S07740
R/Pitchard, A.E.; Seilhamer, J.J.; Mahalingam, R.; Sable, C.L.; Venuti, S.E.; Cummings, N.; Pitchard, A.E.; 18, 173-180, 1990
A/Title: Nucleotide sequence of the mitochondrial genome of Paramaecium.
A/Reference number: S07725; MUID:90174913; PMID:2308823
A/Accession: S07740
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-241 <PRI>
A/Cross-references: UNIPROT:P15609; EMBL:X15917; NID:G13256; PID:9578757
C/Genetics:
A/Gene: mitochondrion
A/Genetic code: SGC6
A/Start codon: ATT
C/Superfamily: mitochondrial ribosomal protein S18, paramaecium type
C/Keywords: mitochondrion

Query Match 44.3%; Score 43; DB 2; Length 241;
Best Local Similarity 41.2%; Pred. No. 25;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 IKGPTLRQWLKSRREHTS 18
Db 26 VKGPTTEKFLKRFYNA 42

RESULT 12

S73999
hypothetical protein yaac homolog VXpSPT7_orf269 - Mycoplasma pneumoniae (strain ATCC 29
N/Alternate names: Hypothetical protein VXpSPT7_orf269
C/Species: Mycoplasma pneumoniae
A/Variety: ATCC 29342
C/Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: S73999
R/Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A/Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A/Reference number: S73327; MUID:97105885; PMID:8948633
A/Accession: S73999
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-269 <HIM>
A/Cross-references: UNIPROT:P75587; EMBL:AE000062; GB:U00089; NID:G1674373; PIDN:AAB9632
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C/Genetics:
A/Genetic code: SGC3
C/Superfamily: uncharacterized conserved protein HI0963

Query Match 44.3%; Score 43; DB 2; Length 269;
Best Local Similarity 58.3%; Pred. No. 28;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TIKGPTLRQWLK 12
Db 124 TLSSSTRQWLK 135

RESULT 13

S30484
pol polyprotein - human immunodeficiency virus type 2
C/Species: human immunodeficiency virus type 2, HIV-2
C/Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 23-Mar-2001
C/Accession: S30484
R/Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
submitted to the EMBL Data Library, December 1992
A/Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa.
A/Reference number: S30460
A/Accession: S30484
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-656 <GAO>
A/Cross-references: EMBL:M87114
C/Superfamily: pol polyprotein

Query Match 44.3%; Score 43; DB 2; Length 656;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 GPTLRQWLKSRRE 15
Db 31 GPTLRQWLKSRRE 42

RESULT 14

S30483
pol polyprotein - human immunodeficiency virus type 2
C/Species: human immunodeficiency virus type 2, HIV-2
C/Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 23-Mar-2001
C/Accession: S30483
R/Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
submitted to the EMBL Data Library, December 1992
A/Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa
A/Reference number: S30460
A/Accession: S30483
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-656 <GAO>
A/Cross-references: EMBL:M87111
C/Superfamily: pol polyprotein

Query Match 44.3%; Score 43; DB 2; Length 656;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 GPTLRQWLKSRRE 15
Db 31 GPTLRQWLKSRRE 42

RESULT 15

S59644
sister chromatid cohesion molecule Mis4p - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 14-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C/Accession: T38603; T43392; S59644
R/Devlin, K.; Churcher, C.M.; Barrell, B.G.; Raiaudream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, July 1995
A/Reference number: Z21731
A/Accession: T38603
A/Status: preliminary; translated from GB/EMBL/DDBO
A/Molecule type: DNA
A/Residues: 1-1583 <DE2>

Query Match 44.3%; Score 43; DB 2; Length 1583;
Best Local Similarity 58.3%; Pred. No. 28;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

A;Experimental source: strain 972b-; cosmid c31a2
R;Rutya, K.; Takahashi, K.; Yanagida, M.
submitted to the EMBL Data Library, August 1998
A;Description: Faithful anaphase is ensured by Mts4, a sister chromatid cohesion molecule
A;Reference number: 222478
A;Accession: T43392
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1583 <FUR>
A;Cross-references: EMBL:AB016866; PIDN:CAB19489.1
C;Genetics:
A;Gene: mts4; SPAC31A2.05c
A;Map position: 1
A;introns: 33/1; 98/2; 543/3; 699/3; 1294/2; 1339/3; 1558/3
Query Match 44.3%; Score 43; DB 2; Length 1583;
Best Local Similarity 46.2%; Pred. No. 1.9e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 4 GPTLRQWLKSRREH 16
|||:|:|:|:
Db 1483 GPTTGMKKLDH 1495
RESULT 16
AC0189
probably exported protein YP01551 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
A;Accession: AC0189
R;Perkhill, J.; Wren, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0189
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-275 <KUR>
A;Cross-references: UNIPROT:Q8ZFX2; GB:AL590842; PIDN:CAC90374.1; PID:G15979594; GSPDB:C
C;Genetics:
A;Gene: YP01551
Query Match 43.8%; Score 42.5; DB 2; Length 275;
Best Local Similarity 47.6%; Pred. No. 34;
Matches 10; Conservative 1; Mismatches 7; Indels 3; Gaps 1;
QY 1 TIKGPT--LQWLKSRREHTS 18
|:|:|:|:|:|:
Db 133 TVAGKTMLAEQWLHQLPHTS 153
RESULT 17
E71171
hypothetical protein PH0569 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
A;Accession: E71171
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekit
M.; Ohnuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: E71171
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-114 <KAW>
A;Cross-references: UNIPROT:O58304; GB:AP000002; NID:G3236129; PIDN:BAA29658.1; PID:G325
A;Experimental source: strain OT3
C;Genetics:
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
A;Gene: PH0569

Query Match 43.3%; Score 42; DB 2; Length 114;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 IKGPTLRQWLK 12
:|:|:|:|:
Db 47 VKGDTLKVWLK 57
RESULT 18
T20567
hypothetical protein F08A10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A;Accession: T20567
R;Kershaw, J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19293
A;Accession: T20567
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-171 <WIL>
A;Cross-references: UNIPROT:Q19186; EMBL:Z75534; PIDN:CAA9825.1; GSPDB:GN00019; CESP:
C;Genetics:
A;Experimental source: clone F08A10
A;Gene: CESP:F08A10.1
A;Map position: 1
A;introns: 26/3; 64/1; 91/3; 118/3
Query Match 43.3%; Score 42; DB 2; Length 171;
Best Local Similarity 57.1%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 GPTLRQWLKSRREHT 17
|||:|:|:|:
Db 103 GPSLRPFLNSGNHT 116
RESULT 19
D72456
probable glutamyl-tRNA reductase APE2296 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
A;Accession: D72456
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Take
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: D72456
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-416 <KAW>
A;Cross-references: UNIPROT:Q9Y9J2; DDBJ:AP000064; NID:G5105945; PIDN:BAA81308.1; PID:
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE2296
A;Superfamily: glutamyl-tRNA reductase
Query Match 43.3%; Score 42; DB 2; Length 416;
Best Local Similarity 57.1%; Pred. No. 65;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2 IKGPTLRQWLKSRRE 15
:|:|:|:|:
Db 105 VLGQVRRAWLKSRRE 118
RESULT 20
S71157
cytochrome c biogenesis protein 454 - evening primrose mitochondrion
C;Species: mitochondrion Oenothera lutea (evening primrose)

C>Date: 28-Oct-1996 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
C/Accession: S71157; SS5283; S42984
R/Gruska, I.; Jekabsons, W.; Schuster, W.
Mol. Gen. Genet. 247, 529-536, 1995
A>Title: Oenothera mitochondrial orf454, a gene involved in cytochrome c biogenesis core
A/Reference number: SS5283; MUID:95327048; PMID:7603411
A/Accession: S71157
A/Molecule type: mRNA
A/Residues: 1-438 <GRU>
A/Cross-references: UNIPROT:Q35213; EMBL:X78036
A>Note: differences are due to RNA editing; premature stop codon is due to RNA editing
A/Accession: SS5283
A/Molecule type: DNA
A/Residues: 1-16, 'PR', 19-34, 'P', 36-39, 'SS', 42-48, 'P', 50, 'PS', 53, 'P', 55-108, 'U', 110-130, '
A/Cross-references: EMBL:X78036; NID:9459536; PIDN:CAAS4966.1; PID:9459537
C/Genetics:
A/Genome: mitochondrion
A/Introns: 256/2
C/Keywords: mitochondrion; RNA editing

Query Match 43.3%; Score 42; DB 2; Length 438;
Best Local Similarity 50.0%; Pred. No. 68;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 7 LRQWLKSRHETS 18
| : | : | : | : | :
Db 342 LHRVWKNRHHNN 353

RESULT 21
C86160
hypothetical protein F22D16.3 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: C86160
R/Rheologis, A.; Eckert, J.R.; Palm, C.U.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chn., C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Matti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: AB6141; MUID:21016719; PMID:11130712
A/Accession: C86160
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-519 <STO>
A/Cross-references: UNIPROT:Q9SKY9; GB:AE005172; NID:96056405; PIDN:AAFO2869.1; GSPDB:GN
C/Genetics:
A/Map position: 1

Query Match 43.3%; Score 42; DB 2; Length 519;
Best Local Similarity 40.0%; Pred. No. 82;
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 2 IKGPTLRQWLKSRH 16
| : | : | : | : | :
Db 498 IRGHTEWMLAKON 512

RESULT 22
T12095
beta-fructofuranosidase (EC 3.2.1.26), cell wall - fava bean
N/Alternate names: cell wall invertase II
C/Species: Vicia faba (fava bean)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T12095
R/Weder, H.; Borstjuk, L.; Heim, U.; Buchner, P.; Mobus, U.
Plant Cell 7, 1833-1846, 1995
A>Title: Seed coat-associated invertases of fava bean control both unloading and storage

A:Reference number: Z17416; MUID:96093423; PMID:8535137
A:Accession: T12095
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: T12095
A:Molecule type: mRNA
A:Residues: 1-581 <WEB>
A:Cross-references: UNIPROT:Q43856; EMBL:Z35163; NID:9861156; PIDN:CA04527.1; PID:9861156
A:Experimental source: strain minor; cultivar Fibro; seed coat; clone VECWINV2
C:Genetic8:
A:Gene: CWINV2
C:Function:
A:Description: hydrolyzes terminal non-reducing beta-D-fructofuranoside residues in bet
C:Superfamily: beta-fructofuranosidase
C:Keywords: cell wall, glycoprotein; glycosidase; hydrolase

Query Match 43.3%; Score 42; DB 2; Length 581;
Best Local Similarity 58.3%; Pred. No. 93;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 PTLRWLKSREH 16
Db 160 PFLRWIKSPEN 171

RESULT 23
S75447
proline-tRNA ligase - Synechocystis sp. (strain PCC 6803)
N:Alternate names: protein sll1425
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75447
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
S.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75447
A:Status: nucleic acid sequence not shown; translation not shown
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-617 <KAN>
A:Cross-references: UNIPROT:P73942; EMBL:D90911; GB:AB001339; NID:91653083; PIDN:BA180
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: pros
A:Start codon: GTG
C:Superfamily: proline-tRNA ligase

Query Match 43.3%; Score 42; DB 2; Length 617;
Best Local Similarity 50.0%; Pred. No. 99;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 PTLRWLKSREH 18
Db 604 PTLRWLKSREH 617

RESULT 24
GNLJG4
HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green monkey
N:Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA pol
C:Species: simian immunodeficiency virus, SIV
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 03-Jun-2002
C:Accession: B30045
R:Fukusawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kitamura
Nature 333, 457-461, 1989
A:Title: Sequence of simian immunodeficiency virus from African green monkey, a new mem
A:Reference number: A30045; MUID:86232906; PMID:3374586
A:Accession: B30045
A:Molecule type: DNA
A:Residues: 1-1061 <PUK>
A:Cross-references: EMBL:X07805; NID:961748; PID:91335593
C:Comment: Specific enzymatic cleavages may yield mature proteins including protease, r

C:Genetics:
 A:Gene: pol
 C:Superfamily: pol polypeptide
 C:Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase; polypeptide; reverse
 F:11-210/Product: retropepsin #status predicted <RTP>
 F:134/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 43.3%; Score 42; DB 1; Length 1061;
 Best Local Similarity 53.8%; Pred. No. 1.8e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 3 KGPTRLQWLKSRH 15
 Db 229 RGPVTRQWLKSRH 241

RESULT 25

H70819
 Probable polyketide synthase - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: H70819

R:Cole, S.T.; Broch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulstrom, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: H70819
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-2108 <COL>

A:Cross-references: UNIPROT:O53901; GB:AL022000; GB:AL123456; NID:g3261541; PIDN:CAA1759
 A:Experimental source: strain H37RV
 C:Genetics:

A:Gene: pks5
 C:Superfamily: mycocerosic acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I h
 C:Keywords: carrier protein
 C:Keywords: carrier protein
 F:36-434/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
 F:546-826/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
 F:1444-1733/Domain: long-chain alcohol dehydrogenase homology <LADH>
 F:1765-1945/Domain: short-chain alcohol dehydrogenase homology <SDH>
 F:2029-2094/Domain: acyl carrier protein homology <ACP>

Query Match 43.3%; Score 42; DB 2; Length 2108;
 Best Local Similarity 46.7%; Pred. No. 3.8e+02;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy 2 IKGPTRLQWLKSRH 16
 Db 1047 VDGAEEVRQWLKSRH 1061

RESULT 26

T03098

P97 protein - Toxoplasma gondii

C:Species: Toxoplasma gondii

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C:Accession: T03098

R:Matsumura, T.; Kasper, L.

Mol. Biochem. Parasitol. 90, 403-413, 1997

A:Title: Molecular analysis and characterization of a protein involved in the replicatio
 A:Reference number: Z14838; MUID:98135655; PMID:9476788

A:Accession: T03098
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-877 <MAT>

A:Cross-references: UNIPROT:O15644; EMBL:AF005059; NID:g2581824; PIDN:AACT47857.1; PID:g2

A:Experimental source: strain RH

C:Function:
 A:Description: involved in replication of intracellular Toxoplasma gondii

C:Superfamily: Toxoplasma gondii p97 protein

Query Match 42.8%; Score 41.5; DB 2; Length 877;
 Best Local Similarity 50.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Oy 4 GP---TLQWLKSRH 16
 Db 72 GPEVTRQWLQONEH 87

RESULT 27

T06920

ribosomal protein L28 - Cyanophora paradoxa cyanelle

C:Species: cyanelle Cyanophora paradoxa

C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T06920

R:Stewart, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.

submitted to the EMBL Data Library, July 1995

A:Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.

A:Reference number: Z15840

A:Accession: T06920

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-70 <ST>

A:Cross-references: UNIPROT:P48129; EMBL:U30821; NID:g1016083; PIDN:AAA81263.1; PID:g10

A:Experimental source: strain Pflingsheim LB555

C:Genetics:

A:Gene: rpl28

C:Superfamily: Escherichia coli ribosomal protein L28

C:Keywords: cyanelle; ribosome

Query Match 42.3%; Score 41; DB 2; Length 70;
 Best Local Similarity 50.0%; Pred. No. 13;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy 2 IKGPTRLQWLKSRH 17
 Db 38 IWSEPTLQWLKSRH 53

RESULT 28

A97524

hypothetical protein AGR_C_2500 [imported] - Agrobacterium tumefaciens (strain C58, Cer

C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C:Accession: A97524

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium t

A:Reference number: A97524; MUID:21608551; PMID:11743194

A:Accession: A97524

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-153 <AGR>

A:Cross-references: UNIPROT:Q8UPF3; GB:AB007869; PIDN:AAK87146.1; PID:g15156416; GSPDB

C:Genetics:

A:Gene: AGR_C_2500

A:Map position: circular chromosome

C:Superfamily: 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase; 2-a

Query Match 42.3%; Score 41; DB 2; Length 153;
 Best Local Similarity 37.5%; Pred. No. 32;
 Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 2 IKGPTRLQWLKSRH 17
 Db 119 VKGPRVQWLQOADR 134

RESULT 29

AB2743
 hypothetical protein foik [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C/Accession: AB2743
 R/Wood, D.W.; Secubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McNeill
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A/Reference number: AB2577; MUID:2168550; PMID:11743193
 A/Accession: AB2743
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-178 <KUR>
 A/Cross-references: UNIPROT:Q8UPF3; GB:AE008688; PIDD:RAL42360.1; PID:G17739767; GSPDB:C
 A/Experimental source: strain C58 (Dupont)
 C/Genetics:
 A/Gene: foik
 A/Map position: circular chromosome
 C/Superfamily: 2-amino-4-hydroxy-6-hydroxymethylidihydroperidine pyrophosphokinase; 2-am

Query Match 42.3%; Score 41; DB 2; Length 178;
 Best Local Similarity 37.5%; Pred. No. 37;
 Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IKGPTLRWLKSRHNT 17
 Db 144 VKGAPVQWLOQADRS 159

RESULT 30
 C82863
 recombinase xfa019 [imported] - Xylella fastidiosa (strain 9a5c)
 C/Species: Xylella fastidiosa
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C/Accession: C82863
 C/Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A/Reference number: A82515; MUID:20365717; PMID:10910347
 A/Note: for a complete list of authors see reference number A59328 below
 A/Accession: C82863
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-188 <SIM>
 A/Cross-references: UNIPROT:Q9PH16; GB:AE003851; NID:g9112238; PIDD:JAF85588.1; GSPDB:GN
 A/Experimental source: strain 9a5c
 R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Agencio, M.; Alvarenga, R.; A
 Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to Genbank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 U.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kurame, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, B
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Mizocca, R.C.; Miyaki, C.Y.;
 ; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, E.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsubako, M.H.; Vailada, H.; Van Sluys, W.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A/Reference number: A59328
 A/Contents: annotation
 C/Genetics:
 A/Gene: Xfa0019
 A/Genome: plasmid
 A/Note: Plasmid pXf5.1
 C/Superfamily: transposase repressor

Query Match 42.3%; Score 41; DB 2; Length 188;
 Best Local Similarity 53.8%; Pred. No. 39;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PTLRQWLKSRHNT 17
 Db 176 PTLRQWLKSRHNT 188

RESULT 31
 T40206
 hypothetical protein SPBC31F10.03 - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T40206
 R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Pohl, T.
 submitted to the EMBL Data Library, August 1997
 A/Reference number: Z21913
 A/Accession: T40206
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-203 <WOO>
 A/Cross-references: UNIPROT:P87305; EMBL:Z97204; PIDD:CAE10080.1; GSPDB:GN00067; SPDB:S
 A/Experimental source: strain 972h-; cosmid c31f10
 C/Genetics:
 A/Gene: SPDB:SPBC31F10.03
 A/Map position: 2
 C/Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC31F10.03

Query Match 42.3%; Score 41; DB 2; Length 203;
 Best Local Similarity 46.7%; Pred. No. 43;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IKGPTLRWLKSRHNT 16
 Db 34 IKGYRRFWRSSEDH 48

RESULT 32
 S76936
 hypothetical protein - Synecocystis sp. (strain PCC 6803)
 C/Species: Synecocystis sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: S76936
 R/Kaneko, T.; Sato, S.; Kori, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
 o, K.; Okumura, S.; Shino, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
 DNA Res. 3, 109-136, 1996
 A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocysti
 S.
 A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S76936
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-238 <KAN>
 A/Cross-references: UNIPROT:P74728; EMBL:D90917; GB:AB001339; NID:g1653836; PIDD:BA1188
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 42.3%; Score 41; DB 2; Length 238;
 Best Local Similarity 50.0%; Pred. No. 51;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IKGPTLRWLKSRHNT 17
 Db 13 ILAPLRWLKSRHNT 28

RESULT 33
 E70429
 tRNA guanine-N1 methyltransferase - Aquifex aeolicus
 C/Species: Aquifex aeolicus
 C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
 C/Accession: E70429
 R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; C
 V.
 Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: E70429
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-257 <ACF>
A:Cross-references: UNIPROT:O67463; GB:AEO00742; NID:g2983858; PIDN:AAO07418.1; PID:g2983858
A:Experimental source: strain VFS
C:Genetics:
A:Gene: lrmD
C:Superfamily: crna (guanine-N1) methyltransferase

Query Match 42.3%; Score 41; DB 2; Length 257;
Best Local Similarity 33.3%; Pred. No. 55;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

2 IKGPTLRQWLKSRHH 16
:|:|:|:|:|:|:
241 LSGKSPKMKLKKH 255

RESULT 34
AG2095
Hypothetical protein all2318 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Saamoto, S.; Watanabe, A.; Iriyuchihara, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; Nakazaki, N.; Shimo, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2095
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <KUR>
A:Cross-references: UNIPROT:O8YTM2; GB:BA000019; PIDN:BA074017.1; PID:g17131410; GSPDB:C:G17131410
C:Genetics:
A:Gene: all2318

Query Match 42.3%; Score 41; DB 2; Length 264;
Best Local Similarity 38.5%; Pred. No. 57;
Matches 5; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

5 PTLRQWLKSRHH 17
|:|:|:|:|:|:
95 PALKQWLQKQIS 107

RESULT 35
D70601
UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) galU [similarity] - Mycobacterium tuberculosis
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
A:Accession: D70601
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70601
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-306 <COL>
A:Cross-references: UNIPROT:O05576; GB:Z94752; GB:AL123456; NID:g3261731; PIDN:CAB08153
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: galU
C:Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase

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C:Keywords: nucleotidyltransferase

Query Match      42.3%; Score 41; DB 2; Length 306;
Best Local Similarity 63.6%; Pred. No. 67;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 GPTLRQWLKSR 14
      |||||:
DB      290 GPDLRQWLVAR 300

RESULT 36
B47029
methylesterase 1 - phage nck202.50 (ph1 50) (fragment)
C:Species: phage nck202.50 (ph1 50)
C:Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 16-Aug-2004
C:Accession: B47029
R:Hall, C.; Miller, L.A.; Klaenhammer, T.R.
J. Bacteriol. 173, 4363-4370, 1991
A:Title: In vitro genetic exchange of a functional domain from a type II A methylase bet
A:Reference number: A47029; MUID:91294179; PMID:11906061
A:Contents: Lactococcus lactis
A:Accession: B47029
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <HIL>
A:Note: sequence inconsistent with the nucleotide translation
C:Superfamily: Modification methylase (adenine-specific), NlaIII type

Query Match      42.3%; Score 41; DB 2; Length 380;
Best Local Similarity 57.1%; Pred. No. 85;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      4 GPTLRQWLKSR 17
      |||||:
DB      81 GKTPEQWLNREY 94

RESULT 37
G69449
tryptophan synthase (EC 4.2.1.20) beta chain - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: G69449
R:Klank, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirsch, B.F.
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Attlich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: G69449
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-397 <KLE>
A:Cross-references: UNIPROT:O28672; GB:AE000992; GB:AE000782; NID:92689315; PIDN:AAB996
C:Genetics:
A:Gene: trpB-2
C:Function:
A:Description: catalyzes conversion of indoleglycerol phosphate and serine to tryptophan
A:Pathway: tryptophan biosynthesis
A:Note: cofactor pyridoxal phosphate; last step in pathway
C:Superfamily: tryptophan synthase beta chain; tryptophan synthase beta chain homology
C:Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein; pyridoxal phosphate; tryp
F:193/Domain: tryptophan synthase beta chain homology <TRPB>
F:193/Active site: His #status predicted
F:194/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match      42.3%; Score 41; DB 2; Length 397;
Best Local Similarity 63.6%; Pred. No. 89;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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OY 7 LRQWLSREHT 17
 Db 181 LRDMVESFEHT 191

RESULT 38

S29127
 carboxypeptidase A (EC 3.4.17.1) CPA1 precursor - human
 N/Alternate names: pancreatic carboxypeptidase A1
 C/Species: Homo sapiens (man)
 C/Date: 25-Feb-1994 #sequence revision 19-Jan-1996 #text change 09-Jul-2004
 C/Accession: S29127; A34205; S08253; S02810; S71394; S02811
 R/Catalysis: L.; Villlegas, V.; Pascual, R.; Aviles, F.X.; Wicker-Planquart, C.; Puigserver
 Biochem. J. 287, 299-303, 1992
 A/Title: cDNA cloning and sequence analysis of human pancreatic procarboxypeptidase A1.
 A/Reference number: S29127; MUID:93038569; PMID:1417781
 A/Accession: S29127
 A/Molecule type: mRNA
 A/Residues: 1-419 <CMT>
 A/Cross-references: UNIPROT:P15085; EMBL:X67318; NID:935329; PIDN:CAA47732.1; PID:935330
 R/Stewart, E.A.; Craik, C.S.; Hake, L.; Bowcock, A.M.
 Am. J. Hum. Genet. 46, 795-800, 1990
 A/Title: Human carboxypeptidase A identifies a BgIII RFLP and maps to 7q31-qter.
 A/Reference number: A34205; MUID:90196012; PMID:1969228
 A/Accession: A34205
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 330-396 <STE>
 A/Note: the authors translated the codon CTG for residue 391 as Val
 R/Moulard, M.; Michon, T.; Kerfelec, B.; Chapuis, C.
 FEBS Lett. 261, 179-183, 1990
 A/Title: Further studies on the human pancreatic binary complexes involving procarboxypeptidase A
 A/Reference number: S08253; MUID:90169111; PMID:2307232
 A/Accession: S08253
 A/Molecule type: protein
 A/Residues: 17-43; XXX', 114-135 <MOU>
 R/Pascual, R.; Burgos, F.J.; Salva, M.; Soriano, F.; Mendez, E.; Aviles, F.X.
 Eur. J. Biochem. 179, 609-616, 1989
 A/Title: Purification and properties of five different forms of human procarboxypeptidase A
 A/Reference number: S02809; MUID:89150596; PMID:2920728
 A/Accession: S02810
 A/Molecule type: protein
 A/Residues: 17-42 <PAS>
 R/Laethem, R.M.; Blumentopf, T.A.; Cory, M.; Elwell, L.; Moxham, C.P.; Ray, P.H.; Walton
 Arch. Biochem. Biophys. 332, 8-18, 1996
 A/Title: Biochemical and characterization of human pancreatic procarboxypeptidase A1
 A/Reference number: S71394; MUID:96400327; PMID:8806703
 A/Accession: S71394
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-419 <LAB>
 C/Genetics:
 A/Genes: GDB:CPA1; CPA
 A/Cross-references: GDB:120597; OMTM:114850
 A/Map position: 7q32-7qter
 C/Superfamily: carboxypeptidase
 C/Keywords: hydrolase; metallo-carboxypeptidase; metalloprotein; protein digestion; zinc
 F.1-16/Domain: signal sequence #status predicted <SIG>
 F.11-110/Domain: activation peptide #status predicted <ACP>
 F.111-419/Product: carboxypeptidase A isozyme 1 #status predicted <MAT>
 F.119,182,306/Binding site: zinc (His, Glu, His) #status predicted
 F.248-271/Disulfide bonds: #status predicted
 F.358,380/Active site: Tyr, Glu #status predicted

Query Match 42.3%; Score 41; DB 1; Length 419;
 Best Local Similarity 53.8%; Pred. No. 94;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 6 LRQWLSREHTS 18
 Db 232 TNRWKRKRSHTA 244

RESULT 39

F70876
 probable papA3 protein - Mycobacterium tuberculosis (strain H37RV)
 C/Species: Mycobacterium tuberculosis
 C/Date: 17-Jul-1998 #sequence revision 17-Jul-1998 #text change 09-Jul-2004
 C/Accession: F70876
 R/Cole, S.T.; Broesch, R.; Parthill, J.; Garnier, T.; Churcher, C.; Harrie, D.; Gordon, J.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentile, S.; Hamlin, N.; Holroyd, S.; Rajadream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.
 Nature 393, 537-544, 1998
 A/Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A/Reference number: A70500; MUID:98295987; PMID:9634230
 A/Accession: F70876
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-472 <COL>
 A/Cross-references: UNIPROT:O50438; GB:AL010186; GB:AL123456; NID:93261493; PIDN:CAA158
 A/Experimental source: strain H37RV
 C/Genetics:
 A/Genes: papA3

Query Match 42.3%; Score 41; DB 2; Length 472;
 Best Local Similarity 38.9%; Pred. No. 1,1e+02;
 Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 TTKPTLRQWLSREHTS 18
 Db 224 TVESPQVRAWTKFAEGTN 241

RESULT 40

S35122
 site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) LlaI - Lactococcus
 N/Alternate names: type II modification methylase LlaI
 C/Species: Lactococcus lactis
 C/Date: 16-Apr-1997 #sequence revision 09-May-1997 #text change 09-Jul-2004
 C/Accession: S35122; S77702; A47029
 R/Hill, C.; Miller, L.A.; Klaenhammer, T.R.
 J. Bacteriol. 173, 4363-4370, 1991
 A/Title: In vivo genetic exchange of a functional domain from a type II A methylase bet
 A/Reference number: A47029; MUID:91294179; PMID:1906061
 A/Accession: S35122
 A/Molecule type: DNA
 A/Residues: 1-622 <HIL>
 A/Cross-references: UNIPROT:P3516; EMBL:M77136
 A/Experimental source: bacteriophage resistance plasmid pTR2030
 A/Note: the sequence of residues 469 and 470 is interchanged in the authors' translation
 A/Note: sequence extracted from NCBI backbone (NCBIN:41635, NCBI:P41636)
 R/Klaenhammer, T.R.
 submitted to the EMBL Data Library, November 1994
 A/Reference number: S77702
 A/Accession: S77702
 A/Molecule type: DNA
 A/Residues: 1-248; G', 250-622 <KLA>
 A/Cross-references: EMBL:U17233; NID:9639886; PIDN:AAA65073.1; PID:9639892
 C/Genetics:
 A/Genes: LlaI
 A/Genome: plasmid
 C/Keywords: methyltransferase; restriction modification system; S-adenosylmethionine

Query Match 42.3%; Score 41; DB 2; Length 622;
 Best Local Similarity 57.1%; Pred. No. 1,4e+02;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 4 GPTLRQWLSREHT 17
 Db 81 GKTPQWLNREHTT 94

RESULT 41

S46347

pol polyprotein - simian immunodeficiency virus SIVagm (isolate SAB-1)
C:Species: simian immunodeficiency virus SIVagm
A:Variety: isolate SAB-1
C:Date: 25-Dec-1994 #sequence_revision 14-Feb-1997 #text_change 26-Aug-1999
C:Accession: S46347
R:Jin, M.J.; Hui, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V.M.;
EMBO J. 13, 2935-2947, 1994
A:Title: Mosaic genome structure of simian immunodeficiency virus from West African green
A:Reference number: S46345; MUID:94298785; PMID:8026477
A:Accession: S46347
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1039 <JIN>
A:Cross-references: EMBL:U04005; NID:9466229; PIDN:AAA21505.1; PID:9466231
A:Experimental source: isolate SAB-1; Sabaeus monkey
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
C:Genetics:
A:Gene: pol
C:Superfamily: pol polyprotein

Query Match 42.3%; Score 41; DB 2; Length 1039;
Best Local Similarity 58.3%; Pred. No. 2.5e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

4 GPTLRQWLKSRRE 15
|||:|||||:
Db 205 GPRIRQWPLSKRE 216

RESULT 42
T51517
telomerase reverse transcriptase - Arabidopsis thaliana
N:Alternate names: protein F5E19_190
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: T51517
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew
submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25394
A:Accession: T51517
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1123 <SAT>
A:Cross-references: UNIPROT:Q9SPU7; EMBL:AL391147
A:Experimental source: cultivar Columbia; BAC clone F5E19
C:Genetics:
A:Map position: 5
A:Insertions: 100/3; 125/3; 147/3; 185/1; 300/3; 325/1; 369/2; 414/3; 765/3; 942/2; 1033/2
A:Notes: F5E19_190

Query Match 42.3%; Score 41; DB 2; Length 1123;
Best Local Similarity 58.3%; Pred. No. 2.7e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

2 IKGPTLRQWLKS 13
:|||:|||||:
Db 200 VQPTKRWLSS 211

RESULT 43
S73786
hypochemical protein A19, orf1140 - Mycoplasma pneumoniae (strain ATCC 29342)
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C:Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S73786
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327; MUID:9710585; PMID:8948633
A:Accession: S73786
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-1140 <HIM>
A:Cross-references: UNIPROT:P75405; EMBL:AE000045; GB:U00089; NID:g1674145; PIDN:AA8961
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Genetic code: SGC3

Query Match 42.3%; Score 41; DB 2; Length 1140;
Best Local Similarity 53.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

4 GPTLRQWLKSRRE 16
|||:|||||:
Db 1116 GVTLHRWKRKRKH 1128

RESULT 44
T31091
hypochemical protein wdbk [imported] - Serratia marcescens
C:Species: Serratia marcescens
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31091
R:Saigi, F.; Climent, N.; Pique, N.; Sanchez, C.; Merino, S.; Rubires, X.; Aguilar, A.;
J. Bacteriol. 181, 1883-1891, 1999
A:Title: Genetic analysis of the Serratia marcescens N28b O4 antigen gene cluster.
A:Reference number: Z20974; MUID:99173913; PMID:10074083
A:Accession: T31091
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1191 <SAI>
A:Cross-references: UNIPROT:O52484; EMBL:AF038816; NID:g2828669; PID:g2828673; PIDN:AAC
C:Genetics:
A:Gene: wdbk

Query Match 42.3%; Score 41; DB 2; Length 1191;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

5 PTLRQWLKSRREHTS 18
|||:|||||:
Db 491 PELTQWLREARFETA 504

RESULT 45
T13423
hypochemical protein 3088.4 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13423
R:Murphy, D.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17668
A:Accession: T13423
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3345 <MUR>
A:Cross-references: UNIPROT:O46074; EMBL:AL009195; NID:e1355203; PID:e1248585; PIDN:CAA
C:Genetics:
A:Map position: X
A:Insertions: 51/3; 159/1; 476/1; 526/1; 1465/1; 1826/3; 1947/3; 2081/1; 2196/3; 3007/3
A:Notes: EG:3088.4

Query Match 42.3%; Score 41; DB 2; Length 3345;
Best Local Similarity 58.3%; Pred. No. 9e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

2 IKGPTLRQWLKS 13
:|||:|||||:
Db 2203 VKNPKLRQWLAS 2214

Fri Sep 2 09:00:11 2005

us-10-083-768-9.rpt

Page 12

Search completed: September 1, 2005, 16:22:54
Job time : 16.7266 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:37 ; Search time 66.9496 Seconds
(without alignments)
137.677 Million cell updates/sec

Title: US-10-083-768-9

Perfect score: 97

Sequence: 1 TIKPTLRQMIKREHTS 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

Query Match

Length

DB ID

Description

1	49	50.5	122	2	Q66DR4	Q66dr4 yersinia ps
2	49	50.5	122	2	Q82C84	Q82c84 yersinia pe
3	48	49.5	326	2	P95613	P95613 rhizobium g
4	47	48.5	327	1	Y745 HELPU	Q92198 helicobacte
5	47	48.5	327	2	Q750V6	Q750v6 ashdvya goss
6	46.5	47.9	332	1	GPD2 MYCPA	P61744 mycobacteri
7	46	47.4	126	2	Q6TUC3	Q6Tuc3 oryza sativ
8	46	47.4	365	2	Q6C114	Q6c114 yarrowia li
9	46	47.4	941	2	Q82R87	Q82r87 streptomyc
10	46	47.4	941	2	Q82R87	Q82r87 streptomyc
11	45	46.4	186	2	Q980N7	Q980n7 sulfolobus
12	45	46.4	243	2	Q8XR40	Q8xr40 ralsstonia s
13	45	46.4	286	2	Q8T462	Q8t462 drosophila
14	45	46.4	302	2	Q742B3	Q742b3 mycobacteri
15	45	46.4	351	2	Q7V126	Q7v126 helicobacte
16	45	46.4	789	2	Q6N3B8	Q6n3b8 rhodospheo
17	45	46.4	1715	2	Q7PS78	Q7ps78 rhodospheo
18	44	45.4	161	2	P93490	P93490 plasmu sativ
19	44	45.4	313	2	P90433	P90433 chimpanzee
20	44	45.4	347	2	Q8G7M6	Q8g7m6 bifidobacte
21	44	45.4	377	2	Q82PK5	Q82pk5 streptomyc
22	44	45.4	500	2	Q6AKH3	Q6akh3 desulfotale
23	44	45.4	648	2	Q9P888	Q9p888 gibberella
24	44	45.4	1017	2	Q6VGA0	Q6vg40 chimpanzee
25	44	45.4	1019	1	POL_STVSA	P15502 simian immu
26	44	45.4	1019	2	P89154	P89154 chimpanzee
27	44	45.4	1019	2	Q7ZBR5	Q7zbr5 chimpanzee
28	44	45.4	1019	2	Q7ZBR7	Q7zbr7 chimpanzee
29	44	45.4	1058	1	POL_HVZD2	P15833 human immun
30	44	45.4	1928	2	Q8D674	Q8d674 vibrio vuln
31	43.5	44.8	561	2	Q6MDL6	Q6mdl6 paracniamyd

32	43.5	44.8	657	2	Q88L07	Q88l07 pseudomonas
33	43	44.3	63	2	Q981B3	Q981b3 molluscum c
34	43	44.3	113	2	Q8VL09	Q8vl09 uncultured
35	43	44.3	124	2	Q48532	Q48532 leptochrix
36	43	44.3	215	2	Q6AM22	Q6am22 desulfotale
37	43	44.3	216	2	PSAL_SPIOL	Q41385 spinacia ol
38	43	44.3	217	2	Q87115	Q87115 chimpanzee
39	43	44.3	233	2	Q9KC77	Q9kc77 bacillus ha
40	43	44.3	237	1	PYRC_GLOVI	Q7hk22 gloeobacter
41	43	44.3	238	2	Q8XSK8	Q8xsk8 ralsstonia s
42	43	44.3	241	1	YMO8_PARTB	P15609 parametium
43	43	44.3	269	1	RIBF_MYCPN	P75587 mycoplasma
44	43	44.3	340	2	Q8UN03	Q8un03 chimpanzee
45	43	44.3	340	2	Q8UN04	Q8un04 chimpanzee
46	43	44.3	349	2	Q7SKX8	Q7skx8 human immun
47	43	44.3	349	2	Q7SKX9	Q7skx9 human immun
48	43	44.3	352	1	ID12_PYRAE	Q8zyf6 pyrobaculum
49	43	44.3	369	2	Q830B7	Q830b7 enterococcu
50	43	44.3	396	2	Q90PU1	Q90pu1 chimpanzee
51	43	44.3	450	2	Q9XHE9	Q9xhe9 prunus arme
52	43	44.3	454	2	Q897U6	Q897u6 clostridium
53	43	44.3	472	2	Q9WH29	Q9wh29 human immun
54	43	44.3	527	2	TP6B_PYRAE	Q8zyw2 pyrobaculum
55	43	44.3	536	2	Q8VYF2	Q8vfy2 arabidopsis
56	43	44.3	537	2	Q946D4	Q946d4 arabidopsis
57	43	44.3	609	2	Q856X8	Q856x8 mycobacteris
58	43	44.3	900	2	Q8GHS7	Q8ghs7 pseudomonas
59	43	44.3	986	2	Q57059	Q57059 chimpanzee
60	43	44.3	1005	2	Q6Y8X5	Q6y8x5 human immun
61	43	44.3	1022	1	POL_STVSP	P19505 simian immu
62	43	44.3	1022	2	Q90317	Q90317 chimpanzee
63	43	44.3	1022	2	Q87956	Q87956 chimpanzee
64	43	44.3	1022	2	Q87965	Q87965 chimpanzee
65	43	44.3	1022	2	Q88135	Q88135 chimpanzee
66	43	44.3	1022	2	Q89620	Q89620 chimpanzee
67	43	44.3	1056	2	Q04097	Q04097 chimpanzee
68	43	44.3	1057	1	POL_STVAI	Q02836 simian immu
69	43	44.3	1150	2	P90246	P90246 feline immu
70	43	44.3	1150	2	Q64F60	Q64f60 feline immu
71	43	44.3	1226	2	Q6H0K6	Q6h0k6 human immun
72	43	44.3	1583	1	MIS4_SCHPO	Q09723 schizosacch
73	43	44.3	1896	1	VITI_PERAM	Q9u8m0 periplaneta
74	42.5	43.8	88	2	Q6Y8T5	Q6y8t5 oryza sativ
75	42.5	43.8	275	2	Q66C47	Q66c47 yersinia ps
76	42.5	43.8	275	2	Q82FX2	Q82fx2 yersinia pe
77	42.5	43.8	307	2	Q761R3	Q761r3 sulfolobus
78	42.5	43.8	595	2	Q6N169	Q6n169 cornebacte
79	42.5	43.8	2281	2	Q68RX2	Q68rx2 gibberella
80	42	43.3	114	2	Q58304	Q58304 pyrococcus
81	42	43.3	173	2	Q8D9X7	Q8d9x7 vibrio vuln
82	42	43.3	189	2	Q9MFE1	Q9mfe1 beta vulgar
83	42	43.3	226	2	Q8KFP8	Q8kfp8 chlorobium
84	42	43.3	238	2	Q835J7	Q835j7 enterococcu
85	42	43.3	244	2	Q8BPV5	Q8bpv5 xanthomonas
86	42	43.3	266	2	Q81D70	Q81d70 bacillus ce
87	42	43.3	296	2	Q7V459	Q7v459 prochloroc
88	42	43.3	315	2	Q6H135	Q6h135 bacillus th
89	42	43.3	319	2	Q9RKM5	Q9rkm5 streptomyc
90	42	43.3	379	2	Q8PRC6	Q8prc6 xanthomonas
91	42	43.3	386	1	ERR2_CANTR	Q8wzm2 candida tro
92	42	43.3	386	1	Q6U0H2	Q6u0h2 oryza sativ
93	42	43.3	391	2	Q6U0H2	Q6u0h2 oryza sativ
94	42	43.3	416	1	HEM1_AERPE	Q9y9j2 aeropyrum p
95	42	43.3	438	2	Q9MFE2	Q9mfe2 beta vulgar
96	42	43.3	443	2	Q89FY2	Q89fy2 bradyrhizob
97	42	43.3	454	2	Q35213	Q35213 oenothera b
98	42	43.3	519	2	Q9SR19	Q9sr19 arabidopsis
99	42	43.3	580	2	Q89RH2	Q89rh2 bradyrhizob
100	42	43.3	581	2	Q43856	Q43856 vicia faba

ALIGNMENTS

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RESULT 1
Q66DR4 PRELIMINARY; PRT; 122 AA.
AC Q66DR4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=YPTB0979;
OS Yersinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OC NCBI_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lemerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinebusch B.J., Marceau M., Medigue C.,
RA Sismont M., Chenaï-François V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the genome evolution of Yersinia pestis through whole
RT genome comparison with Yersinia pseudotuberculosis."
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL; BX936398; CAH20219.1; -.
KM Hypothetical protein.
SQ SEQUENCE 122 AA; 14215 MW; 7C49F0A1E8BC157 CRC64;

Query Match 50.5%; Score 49; DB 2; Length 122;
Best Local Similarity 53.3%; Pred. No. 4.5;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IKGPTLRQWLKSRH 16
DB 92 INDELRRQKTKH 106

RESULT 2
Q8ZC84 PRELIMINARY; PRT; 122 AA.
AC Q8ZC84; Q74WQ2; Q7CK17;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein YPO3137 (Hypothetical protein Y1047).
GN OrderedLocustNames=YPO794, YPO3137, Y1047;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OC NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=2147043; PubMed=1156360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titchell R.W., Holden M.T.G.,
RA Penrice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holtroyd S., Jagers K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1126/STB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,

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RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=1001 / Biovar Mediaevalis;
RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
RA Yang R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ414155; CAC92372.1; -.
DR EMBL; AE013708; AAM84628.1; -.
DR EMBL; AE017129; AAS61059.1; -.
DR PIR; A10380; A10380.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 122 AA; 14215 MW; 7C49F0A1E8BC157 CRC64;

Query Match 50.5%; Score 49; DB 2; Length 122;
Best Local Similarity 53.3%; Pred. No. 4.5;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IKGPTLRQWLKSRH 16
DB 92 INDELRRQKTKH 106

RESULT 3
P95613 PRELIMINARY; PRT; 326 AA.
AC P95613;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NodD2 protein.
GN Name=nodD2;
OS Rhizobium galegae.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OC NCBI_TaxID=399;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HAMBT;
RA Suominen L., Roos C., Paulin L., Kaijalainen S., Lindstrom K.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
DR EMBL; Y08963; CAA70157.1; -.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PRO0039; HTHLYSR.
DR PROSITE; PS50931; HTH_LysR; 1.
KW DNA-binding; Transcription; Transcription regulation.
SQ SEQUENCE 326 AA; 36373 MW; BFE9C32F6719E28B CRC64;

Query Match 49.5%; Score 48; DB 2; Length 326;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KGPTLRQWLKSR 14
DB 204 KGRSLQWLSSQ 215

RESULT 4
Y745_HELPJ STANDARD; PRT; 327 AA.
ID Y745_HELPJ
AC Q9ZL58;

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DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Hypothetical pseudouridine synthase JHP0682 (EC 4.2.1.70)
DB Pseudouridylate synthase (Uracil hydrolyase).
GN OrderedLocustNames=JHP0682;
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummato P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -1- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
CC 5'-phosphate + H(2)O.
CC -1- SIMILARITY: Belongs to the pseudouridine synthase rluA family.
CC -1- SIMILARITY: Contains 1 S4 RNA-binding domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE001500; AAD06270.1; -.
DR PIR: B71900; B71900.
DR InterPro: IPR006225; Pseud_synth_RLud.
DR InterPro: IPR006145; Pseudou synth.
DR InterPro: IPR006224; Rlu_synth.
DR InterPro: IPR002942; S4_synth.
DR Pfam: PF00849; Pseudou_synth_2; 1.
DR Pfam: PF01479; S4; 1.
DR ProDom: PD001819; Pseudou_synth; 1.
DR SMART: SM00363; S4; 1.
DR TIGRFAMs: TIGR00005; rluD subfam; 1.
DR PROSITE: PS01129; PSI_RLU; 1.
DR PROSITE: PSS0889; S4; 1.
KW Complete proteome; Hypothetical protein; Lyase; RNA-binding.
FT ACT SITE 12 79 S4 RNA-binding.
FT ACT SITE 136 136 By similarity.
SQ SEQUENCE 327 AA; 37722 MW; 7EDC7F6840D818BD CRC64;

Query Match 48.5%; Score 47; DB 1; Length 327;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TIKPTLRQWLKSRH 16
Db 103 SVKEPTLVDMKSNY 118

RESULT 5
Q750V6 PRELIMINARY; PRT; 727 AA.
AC Q750V6.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE AG1.67CD.
GN ORFNames=AG1.67C;
OS Asbya goesypii (yeast) (Eremothecium goesypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.

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OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 10895;
RA Lerch A., Brachat S., Voegel S.E., Gaffney T., Philippsen P.,
RA Dietrich F.S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB016820; AAS54324.1; -.
DR AG1.67C; -.
SQ SEQUENCE 727 AA; 82748 MW; 58A66322705F6767 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 727;
Best Local Similarity 56.2%; Pred. No. 70;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 3 KGPTLRQWLKSRH 18
Db 92 RGETGRSWRDRHGS 107

RESULT 6
GP2 MYCPA STANDARD; PRT; 332 AA.
ID GP2 MYCPA.
AC P61744;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Glycerol-3-phosphate dehydrogenase 2 [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-
DE dependent glycerol-3-phosphate dehydrogenase 2).
GN Name=gp2; OrderedLocustNames=MAP4061c;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Sn-glycerol 3-phosphate + NAD(P) (+) =
CC glycerone phosphate + NAD(P)H.
CC -1- PATHWAY: De novo phospholipid biosynthesis; glycerol-3 phosphate
CC formation.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: Belongs to the NAD-dependent glycerol-3-phosphate
CC dehydrogenase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE017241; AAS06611.1; -.
DR HAMAP: MF_00394; -; 1.
DR ProDom: PD001278; NAD_G3PD_C; 1.
DR PROSITE: PS00957; NAD_G3PDH; FALSE NEG.
KW Complete proteome; NAD; Oxidoreductase; Phospholipid biosynthesis.
SQ SEQUENCE 332 AA; 35220 MW; B149RF540B13DB3 CRC64;

Query Match 47.9%; Score 46.5; DB 1; Length 332;
Best Local Similarity 49.2%; Pred. No. 35;
Matches 9; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 3 KGPTLRQWLKSR 15
Db 29 RGPRL-QWVRSRE 40

RESULT 7
Q6YUC3

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ID Q6YUC3 PRELIMINARY; PRT; 126 AA.
AC Q6YUC3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein B116H04.2 (Hypothetical protein
DE B116H04.2).
GN Name=B116H04.2; Synonyms=B111C03.14;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005871; BAD10677.1; -.
DR EMBL; AP005405; BAD10301.1; -.
KW Hypothetical protein.
SQ
SEQUENCE 126 AA; 12558 MW; F316174EC475BAC6 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 126;
Best Local Similarity 46.7%; Pred. No. 14;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 TIRGPTLRQWLKSRRE 15
Db 66 TAAAGPATRRWVVKTRQ 80

RESULT 8
Q6C114 PRELIMINARY; PRT; 365 AA.
ID Q6C114;
AC Q6C114;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to tr|O93968 Candida boidinii Formate dehydrogenase.
GN ORFNames=YAI10F15983g;
OS Varrovia lillopolylifica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Varrovia.
OC NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckertich J.M., Beyne E., Bleykasten C.,
RA Boismere A., Boyer J., Cattoiello L., Confiantolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreuve F., Hennequin C., Janniaux N., Joyet P., Kachouri R.,
RA Kerres A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicard J.M., Nikolaki M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenon-Meyer M., Zivanovic I., Bolocin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Soucieu J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=CLIB99;
RG Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

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CC -1- SIMILARITY: Belongs to the D-isomer specific 2-hydroxyacid
CC dehydrogenase family.
DR EMBL; CR82132; CAG78287.1; -.
DR GO; GO:001616; P-oxidoreductase activity, acting on the CH-O. .; IEA.
DR GO; GO:0006564; P.L-serine biosynthesis; IEA.
DR InterPro; IPR006139; 2-Hacid DH.
DR InterPro; IPR006140; 2-Hacid_DH_C.
DR Pfam; PF00389; 2-Hacid_dh; 1.
DR Pfam; PF02826; 2-Hacid_dh_C; 1.
DR PROSITE; PS00065; D_2_HYDROXYACID_DH_1; 1.
DR PROSITE; PS00670; D_2_HYDROXYACID_DH_2; 1.
DR PROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.
KW Oxidoreductase.
SQ
SEQUENCE 365 AA; 40172 MW; 8AAC7FE8785139E0 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 365;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 LRQWLKSRREHT 17
Db 30 LRQWLKSRREHT 40

RESULT 9
Q82R87 PRELIMINARY; PRT; 402 AA.
ID Q82R87;
AC Q82R87;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transposase.
GN OrderedLocNames=SAV256;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OC NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sasaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sasaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
DR EMBL; AP005021; BAC67965.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004803; F:transposase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR InterPro; IPR002559; Transposase_11.
DR Pfam; PF01609; Transposase_11; 1.
KW Complete proteome.
SQ
SEQUENCE 402 AA; 43379 MW; 71EC0A91143451BE CRC64;

Query Match 47.4%; Score 46; DB 2; Length 402;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 10; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 2 IRG--PTLRQWLK 13
Db 234 IRG--PTLRQWLK 247

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RESULT 10
O8QU6 PRELIMINARY; PRT; 941 AA.
ID O8QU6;
AC O8QU6;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE ORF14L.
OS Infectious spleen and kidney necrosis virus.
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae;
OC unclassified Iridoviridae.
OX NCBI_TaxID=180170;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21874810; PubMed=11878882; DOI=10.1006/viro.2001.1208;
RA He J.G., Deng M., Weng S.P., Li Z., Zhou S.Y., Long Q.X., Wang X.Z.,
  Chan S.M.;
RT "Complete genome analysis of the mandarin fish infectious spleen and
  kidney necrosis Iridovirus.";
RL Virology 291:126-139 (2001).
DR EMBL: AF371960; AAL98838.1; -.
SQ SEQUENCE 941 AA; 106703 MW; EB66398C7F6C83 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 941;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 IKGPTLRQWLKSRHT 17
   ||||| |||
Db 581 VQGPTLAQWICSTAF 596

RESULT 11
O980N7 PRELIMINARY; PRT; 186 AA.
ID O980N7;
AC O980N7;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Adenylate cyclase, cyab-type, putative (Cyab) (EC 4.6.1.1).
GN Name=Cyab; OrderedLocustNames=SS00253;
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
  She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
  Aweyer M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
  De Moers A., Erasmo G., Fletcher C., Gordon P.M.K., Medina N., Peng X.,
  Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Theriault C., Tolstrup N.,
  Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
  Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840 (2001).
DR EMBL: AE006661; AAK0592.1; -.
DR PIR: A90167; A90167.
DR GO: GO:0004016; F:adenylate cyclase activity; IEA.
DR GO: GO:0016829; F:lyase activity; IEA.
DR GO: GO:0006171; P:cAMP biosynthesis; IEA.
DR InterPro: IPR008172; Adenylate_cyc.
DR InterPro: IPR008173; Cyab.
DR Pfam: PF01928; CYTH; 1.
DR ProDom: PD009560; Cyab; 1.
DR TIGRFAMs: TIGR00318; cyab; 1.
KW Complete proteome; lyase.
SQ SEQUENCE 186 AA; 21820 MW; 1B47C630B438C868 CRC64;

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Query Match 46.4%; Score 45; DB 2; Length 186;
Best Local Similarity 55.6%; Pred. No. 33;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 TIKGPTLRQWLKSRHTS 18
   ||||| |||
Db 65 TYKGPRLHSSLKAREIS 82

RESULT 12
O8XR40 PRELIMINARY; PRT; 243 AA.
ID O8XR40;
AC O8XR40;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein Rsp1028.
GN Name=RS02365; OrderedLocustNames=Rsp1028;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GM1000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Guzy J., Mengent S.,
  Ariat M., Billault A., Broctier P., Camus J.C., Catolico L.,
  Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
  Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
  Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
  Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502 (2002).
DR EMBL: AL646082; CAD18179.1; -.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 243 AA; 27220 MW; 2B941BEADAF832 CRC64;

Query Match 46.4%; Score 45; DB 2; Length 243;
Best Local Similarity 61.5%; Pred. No. 44;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 5 PTLRQWLKSRHT 17
   ||||| |||
Db 149 PGLRNLWLSRROT 161

RESULT 13
O8T462 PRELIMINARY; PRT; 286 AA.
ID O8T462;
AC O8T462;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE AT14183p.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STAPLETON M., Brokstein P., Hong L., Agbayani A., Carlson J.,
  Champe M., Chavez C., Dorett V., Dresnek D., Farfan D., Frise E.,
  George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
  Miranda A., Mungell C.J., Munoo J., Pacleb J., Paragas V., Park S.,
  Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
  Ceilikier S.;
RL submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY089335; AAL90073.1; -.
DR FlyBase: FBgn0063731; BGDNA:AT14183.
SQ SEQUENCE 286 AA; 30787 MW; 99374B2615D88594 CRC64;

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OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
   EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
   preliminary data.
CC EMBL: AAB010884; EAA06040.2; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR InterPro: IPR001395; Aido/ket_red.
DR InterPro: IPR007735; Pecanex_C.
DR Pfam: PF05041; Pecanex_C; 1.
DR PROSITE: PS00063; ALDOXETO_REDUCTASE_3; UNKNOWN_1.
FT NON TER 1715 1715
SQ SEQUENCE 1715 AA; 189675 MW; ADP294494F2B236A CRC64;

Query Match 46.4%; Score 45; DB 2; Length 1715;
Best Local Similarity 37.5%; Pred. No. 3.9e+02;
Matches 9; Conservative 5; Mismatches 4; Indels 6; Gaps 1;

OY 1 TIKGPTLRQWLKSR-----HTS 18
   ||| ||| ||| |||
   ||| ||| ||| |||
DB 1128 TLRSPLKMSWLSQALIBALHHTT 1151

RESULT 18
P93490 PRELIMINARY; PRT; 161 AA.
AC P93490;
DT 01-MAY-1997 (TREMBlrel. 03; Created)
DT 01-MAY-1997 (TREMBlrel. 03; Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24; Last annotation update)
DE Cell wall invertase II (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=var. final; TISSUE=seed coat;
RA Buchner P.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 32 of glycosyl hydrolases.
CC EMBL: Z83339; CAB05954.1; -.
DR PIR: T06826; T06826.
DR GO: GO:0004553; F: hydrolase activity, hydrolyzing O-glycosyl . . ; IEA.
DR GO: GO:0005975; P: carbohydrate metabolism; IEA.
DR InterPro: IPR001362; Glyco_hydro_32.
DR InterPro: IPR011040; Stalidase.
DR Pfam: PF00251; Glyco_hydro_32; 1.
DR SMART: SM00640; Glyco_32; 1.
DR Glycosidase; Hydrolase.
FT NON TER 1 1
FT NON TER 161 161
SQ SEQUENCE 161 AA; 18033 MW; 32E6B0767F4ABD6 CRC64;

Query Match 45.4%; Score 44; DB 2; Length 161;
Best Local Similarity 46.7%; Pred. No. 41;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 2 IKGPTLRQWLKSRHH 16
   ||| ||| ||| |||
   ||| ||| ||| |||
DB 76 VSDPFLREMIKSPEN 90

RESULT 19
P90433 PRELIMINARY; PRT; 313 AA.
AC P90433;

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DT 01-MAY-1997 (TREMBlrel. 03; Created)
DT 01-MAY-1997 (TREMBlrel. 03; Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
DE Truncated reverse transcriptase (Fragment).
GN Name=pol;
OS Chimpanzee immunodeficiency virus (SIV/cpz) (CIV).
OC Viruses; Retroid viruses; Retroviridae; Lentiviruses.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith J.M., Krauselburd E.N., Torres J.V.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family A2.
CC EMBL: U83413; AAB41428.1; -.
DR HSP; Q07387; ITCW.
DR MEROPS; A02.002; -.
DR GO: GO:0004190; F: aspartic-type endopeptidase activity; IEA.
DR GO: GO:0008233; F: peptidase activity; IEA.
DR GO: GO:0003723; F: RNA binding; IEA.
DR GO: GO:0003964; F: RNA-directed DNA polymerase activity; IEA.
DR GO: GO:0016740; F: transferase activity; IEA.
DR GO: GO:0006508; P: proteolysis and peptidolysis; IEA.
DR GO: GO:0006278; P: RNA-dependent DNA replication; IEA.
DR InterPro: IPR001995; Peptidase A2.
DR InterPro: IPR009007; Pept_Aspartic.
DR InterPro: IPR001969; Pept_Asp_AS.
DR InterPro: IPR00477; RVTse.
DR Pfam; PF00077; RVP; 1.
DR Pfam; PF00078; RVT_1; 1.
DR PROSITE; PS00141; ASP_PROT_RETROV; 1.
DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
RW Aspartyl protease; Hydrolase; Protease; RNA-directed DNA polymerase;
KW transferase.
FT NON TER 1 1
SQ SEQUENCE 313 AA; 34674 MW; 5A0BB016783FC8A6 CRC64;

Query Match 45.4%; Score 44; DB 2; Length 313;
Best Local Similarity 61.5%; Pred. No. 85;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 KGPTRQWLKSRRE 15
   ||| ||| ||| |||
   ||| ||| ||| |||
DB 184 EGPTRQWLKSRRE 196

RESULT 20
O8G7M6 PRELIMINARY; PRT; 347 AA.
ID O8G7M6;
AC O8G7M6;
DT 01-MAR-2003 (TREMBlrel. 23; Created)
DT 01-MAR-2003 (TREMBlrel. 23; Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
DE DTP-glucose 4,6-dehydratase enzyme involved in rhamnose
DE biosynthesis.
GN Name=rmlB1; Ordered locus Names=BL0229;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=NCC 2705;
RC MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schnell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Peesi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
   to the human gastrointestinal tract."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -1- SIMILARITY: Belongs to the sugar epimerase family.
CC EMBL: AE014641; AAN24075.1; -.
DR HSP; P95780; IKEP.
DR GO: GO:0003824; F: catalytic activity; IEA.

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DR GO; GO:0008460; F:dtDP-glucose 4,6-dehydratase activity; IEA.
 DR GO; GO:0009225; P:nucleotide-sugar metabolism; IEA.
 DR InterPro; IPR005888; dtDP_gluC_dehyd.
 DR InterPro; IPR001509; Epimerase_Dh.
 DR Pfam; PF01370; Epimerase; 1.
 DR TIGRfam; TIGR01181; dtDP_gluC_dehyd; 1.
 DR Complete proteome; NAD.
 KW SEQUENCE 347 AA; 39388 MW; 34852801FD1334FD CRC64;

Query Match 45.4%; Score 44; DB 2; Length 347;
 Best Local Similarity 37.5%; Pred. No. 96;
 Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 3 KGPTRLQWLKSRHTS 18
 Db 222 KGENVRDWMHTEDHSS 237

RESULT 21

Q82PX5 PRELIMINARY; PRT; 377 AA.
 AC Q82PX5;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=SAV747;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Shimura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinoue M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites.";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinoue M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis.";
 RT Nat. Biotechnol. 21:526-531(2003).
 DR EMBL; AP005023; BAC68457.1; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 377 AA; 41307 MW; 0253176AAABE6253 CRC64;

Query Match 45.4%; Score 44; DB 2; Length 377;
 Best Local Similarity 46.7%; Pred. No. 1e+02;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IKGPTLRQWLKSRHTS 16
 Db 168 MEGPDRLAWLPNRRY 182

RESULT 22

Q6AKH3 PRELIMINARY; PRT; 500 AA.
 AC Q6AKH3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Related to penicillin-binding protein (Pbpa).
 GN OrderedLocustNames=DP2423;

OS Desulfotalea psychrophila.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
 OC Desulfobulbaceae; Desulfotalea.
 OX NCBI_TaxID=84980;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LSv54 / DSM 12343;
 RX PubMed=15305914;
 RA Rabus R., Ruepp A., Frickey T., Ralte T., Fartmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;

RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 RT from permanently cold Arctic sediments.";
 RL Environ. Microbiol. 6:987-902(2004).
 DR EMBL; CR522870; CAG37152.1; -;
 DR GO; GO:0008658; P:penicillin binding; IEA.
 DR GO; GO:0009273; P:cell wall biosynthesis (sensu Bacteria); IEA.
 DR InterPro; IPR005311; PBP_dimer.
 DR InterPro; IPR01460; PBP_bind_lptpt.
 DR Pfam; PF03717; PBP_dimer; 1.
 DR Pfam; PF00905; Transpeptidase; 1.
 KW Complete proteome.
 SQ SEQUENCE 500 AA; 54890 MW; E09B1C5EPD06E554 CRC64;

Query Match 45.4%; Score 44; DB 2; Length 500;
 Best Local Similarity 47.4%; Pred. No. 1.4e+02;
 Matches 9; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 2 IKG-PTLRQWLKSRHTS 18
 Db 92 LKGLKTLNLSWLAGRHSS 110

RESULT 23

Q9P888 PRELIMINARY; PRT; 648 AA.
 AC Q9P888;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative MFS membrane transporter (Fragment).
 GN Name=mtf;
 OS Gibberella fujikuroi (Bakane and foot rot disease fungus) (Fusarium
 OS moniliforme).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella;
 OC Gibberella fujikuroi complex.
 OX NCBI_TaxID=5127;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=mb567;
 RX MEDLINE=21416226; PubMed=11525413;
 RA Voss T., Schulte J., Tudzyński B.;

RT "A new MFS transporter gene next to the gibberellin biosynthesis gene
 RT cluster of Gibberella fujikuroi is not involved in gibberellin
 RT secretion.";
 RT Curr. Genet. 39:377-383(2001).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; A1272424; CAB75959.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005511; F:sugar porter activity; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0008643; P:carbohydrate transport; IEA.
 DR InterPro; IPR005828; Sub transporter.
 DR InterPro; IPR003663; Sugar_transpt.
 DR InterPro; IPR005829; Sug_transporter.
 DR Pfam; PF00083; Sugar_tr; 1.
 DR PRINTS; PR00171; SUGRTNSPORT.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
 KW Sugar transport; Transmembrane; Transport.

FT	NON TERM	1	1	45.4%	Score 44;	DB 2;	Length 648;
SEQ	SEQUENCE	648 AA;	72248 MW;	4C90EEB49B25A9FC CRC64;	Best Local Similarity	77.8%;	Pred. No. 1.9e+02;
Matches	7;	Conservative	2;	Mismatches	0;	Indels	0;
QY	9 QWLSKREHT	17					
Db	122 QWLSKREHT	130					
RESULT	24						
Q6VG40	PRELIMINARY;	PRT:	1017 AA.				
AC	Q6VG40;						
DT	05-JUL-2004 (TREMBLrel. 27, Created)						
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)						
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)						
DE	Pol protein (fragment).						
OC	Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).						
OC	Viruses; Retroid viruses; Retroviridae; Lentiviruses.						
OX	NCBI_TaxID=11723;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=22927551; PubMed=14610175;						
RX	DOI=10.1128/JVI.77.23.12523-12534.2003;						
RA	Cougnard V., Abela B., Pourrut X., Mpondi-Ngole E., Loul S.,						
RA	Delaporte E., Peeters M.;						
RT	"Identification of a new simian immunodeficiency virus lineage with a						
RT	vpv gene present among different cercopithecus monkeys (C. mona, C.						
RT	cephus, and C. mitis) from Cameroon."						
RL	J. Virol. 77.12523-12534(2003).						
CC	-1- SIMILARITY: belongs to peptidase family A2.						
DR	EMBL; AY340701; AAR02377.1; -.						
DR	HSSP; P12497; 1B9F.						
DR	GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.						
DR	GO; GO:0003677; F:DNA binding; IEA.						
DR	GO; GO:0008907; F:integrase activity; IEA.						
DR	GO; GO:0008233; F:peptidase activity; IEA.						
DR	GO; GO:0004523; F:ribonuclease H activity; IEA.						
DR	GO; GO:0003723; F:RNA binding; IEA.						
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.						
DR	GO; GO:0016740; F:transferase activity; IEA.						
DR	GO; GO:0008270; F:zinc ion binding; IEA.						
DR	GO; GO:0015074; F:DNA integration; IEA.						
DR	GO; GO:0006310; F:DNA recombination; IEA.						
DR	GO; GO:0006508; F:proteolysis and peptidolysis; IEA.						
DR	GO; GO:0006278; F:RNA-dependent DNA replication; IEA.						
DR	InterPro; IPR010137; Integrase C.						
DR	InterPro; IPR003308; Integrase_Zn_N.						
DR	InterPro; IPR001995; Peptidase_A2.						
DR	InterPro; IPR009007; Pept_Asp_AS.						
DR	InterPro; IPR001969; Pept_Asp_AS.						
DR	InterPro; IPR002156; RNaseH.						
DR	InterPro; IPR001584; Rve.						
DR	InterPro; IPR000477; Rvase.						
DR	InterPro; IPR010659; RVT_connect.						
DR	InterPro; IPR010661; RVT_thumb.						
DR	Pfam; PF02022; Integrase_Zn_1.						
DR	Pfam; PF00075; RNaseH_1.						
DR	Pfam; PF00665; rve; 1.						
DR	Pfam; PF00077; RVD; 1.						
DR	Pfam; PF00078; RVT_1; 1.						
DR	Pfam; PF06815; RVT_connect; 1.						
DR	Pfam; PF06817; RVT_thumb; 1.						
DR	PROSITE; PS00141; ASP_PROTEASE; 1.						
DR	PROSITE; PS00175; ASP_PROT_RETROV; 1.						
KW	Aspartyl protease; Hydrolase; Protease; RNA-directed DNA polymerase;						
KW	Transferase.						
FT	NON TER	1					
SEQ	SEQUENCE	1017 AA;	114690 MW;	ALCFE26C001B6B35 CRC64;			

Query Match	45.4%	Score 44:	DB 2:	Length 1017:
Best Local Similarity	61.5%	Prod. No. 3.2e+02:		
Matches	8:	Conservative	2:	Mismatches 3: Indels 0: Gaps 0:

QY	3	KGPTLRQMLKSR	15
DB	180	EGPRLKQKPLSR	192

RESULT 25			
POL_SIVS4			
ID_POL_SIVS4	STANDARD;	PRT;	1019 AA.
AC	P12502:		
DT	01-OCT-1989 (Rel. 12, Created)		
DT	01-OCT-1989 (Rel. 12, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Pol polyprotein [Contains: Protease (Retropepin) (EC 3.4.23.-);		
DE	Reverse transcriptase/ribonuclease H (EC 2.7.7.49) (EC 3.1.26.4) (RT);		
DE	Integrase (IN)].		
DE	Name=POL;		
OS	Simian immunodeficiency virus (P236/sm14 isolate) (sooty mangabey).		
OC	Viruses; Retroid viruses; Retroviridae; Lentiviruses.		
OX	NCBI_TaxID=11737;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
FX	MEDLINE=89262053; PubMed=2786147; DOI=10.1038/3339389a0;		
RA	Hirsch V.M., Olmstead R.A., Murphy-Corb M., Purcell R.H.,		
RT	Johnson P.R.;		
RL	"An African primate lentivirus (SIVam) closely related to HIV-2.";		
CC	Nature 339:389-392(1989).		
CC	-1- FUNCTION: During replicative cycle of retroviruses, the reverse-		
CC	transcribed viral DNA is integrated into the host chromosome by		
CC	the viral integrase enzyme. RNase H activity is associated with		
CC	the reverse transcriptase.		
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-		
CC	phosphonomoester.		
CC	-1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate		
CC	+ (dN) (N).		
CC	-1- PTM: Cleavage sites that yield the mature proteins remain to be		
CC	determined.		
CC	-1- SIMILARITY: Belongs to the retroviruses Pol polyprotein family.		
CC	-1- SIMILARITY: Contains 1 integrase-type zinc finger.		
CC	-1- SIMILARITY: Contains 1 peptidase A2 domain.		
CC	-1- SIMILARITY: Contains 1 reverse transcriptase domain.		
CC	-1- SIMILARITY: Contains 1 RNase H domain.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; X14307; -; NOT_ANNOTATED_CDS.		
DR	HSSP; P04584; 1M02.		
DR	MEROPS; A02.002; -.		
DR	HIV; X14307; POLSSMH4.		
DR	InterPro; IPR001037; Integrase_C.		
DR	InterPro; IPR003308; Integrase_Zn_N.		
DR	InterPro; IPR001995; Peptidase_A2.		
DR	InterPro; IPR009007; Pept_AspArtic.		
DR	InterPro; IPR001969; Pept_Asp_AS.		
DR	InterPro; IPR002156; RNaseH.		
DR	InterPro; IPR001584; Rve.		
DR	InterPro; IPR004777; RVTse.		
DR	InterPro; IPR010659; RVT_connect.		
DR	InterPro; IPR010661; RVT_chumb.		
DR	Pfam; PF00552; Integrase; 1.		
DR	Pfam; PF002022; Integrase_Zn; 1.		
DR	Pfam; PF00075; RNaseH; 1.		
DR	Pfam; PF00665; rve; 1.		
DR	Pfam; PF00077; RVP; 1.		

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DR Pfam; PF00078; RVT; 1.
DR Pfam; PF06815; RVT_connect; 1.
DR Pfam; PF06817; RVT_thumb; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
DR PROSITE; PS50879; RNASE_H_1.
DR PROSITE; PS50878; RT_POL; 1.
DR PROSITE; PS50876; 2F_INTEGRASE; 1.
DR AIDS; Aspartyl protease; DNA integration; DNA recombination;
KM Aldose; Aspartyl protease; Metal-binding; Multifunctional enzyme;
KW Nucleonuclease; Polypeptide; RNA-directed DNA polymerase; Transferase; Zinc;
Zinc-finger.
FT CHAIN 1 167 Protease.
FT DOMAIN 211 401 Reverse transcriptase.
FT ZN_FING 600 723 RNase H.
FT ZN_FING 729 770 Integrase-type.
FT ACT_SITE 93 93 By similarity.
SQ SEQUENCE 1019 AA; 115465 MW; 8D3DE0B85FC92B1C CRC64;

Query Match 45.4%; Score 44; DB 1; Length 1019;
Best Local Similarity 61.5%; Pred. No. 3.2e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 KGPTRLROWLKSRE 15
Db 184 EGPTRLROWPLSKE 196

RESULT 26
P89154 PRELIMINARY; PRT; 1019 AA.
AC P89154;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pol polyprotein (Fragment).
GN Name=pol;
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SV5MS43;
RX MEDLINE=97151152; PubMed=8995688;
RA Hirsch V., Adger-Johnson D., Campbell B., Goldstein S., Brown C.,
RA Elkins W.R., Montefiori D.C.;
RT "A molecularly cloned, pathogenic, neutralization-resistant simian
RT immunodeficiency virus, SV5MS43-3."
RT J. Virol. 71:1608-1620(1997).
RL [2]
RN SEQUENCE FROM N.A.
RC STRAIN=SV5MS43;
RA Hirsch V.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: Belongs to peptidase family A2.
DR EMBL; U72748; AAC56559.1; -.
DR PIR; T11560; T11560.
DR HSSP; P04584; 1MU2.
DR MEMOPS; A02_002; -.
DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008907; F:integrase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0015074; P:DNA integration; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR001037; Integrase_C.
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DR InterPro; IPR003308; Integrase_Zn_N.
DR InterPro; IPR001995; Peptidase_A2.
DR InterPro; IPR009007; Pept_AspArtic.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; RVTase.
DR InterPro; IPR010659; RVT_connect.
DR InterPro; IPR010661; RVT_thumb.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF02022; Integrase_Zn; 1.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; RVP; 1.
DR Pfam; PF00078; RVP; 1.
DR Pfam; PF00078; RVT_1; 1.
DR Pfam; PF06815; RVT_connect; 1.
DR Pfam; PF06817; RVT_thumb; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
DR Aspartyl protease; Hydrolase; Polypeptide; Protease;
KW RNA-directed DNA polymerase; Transferase.
FT NON_TER 1 1
SQ SEQUENCE 1019 AA; 115595 MW; 26F1EF4594E59537 CRC64;

Query Match 45.4%; Score 44; DB 2; Length 1019;
Best Local Similarity 61.5%; Pred. No. 3.2e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 KGPTRLROWLKSRE 15
Db 184 EGPTRLROWPLSKE 196

RESULT 27
O7ZBR5 PRELIMINARY; PRT; 1019 AA.
AC O7ZBR5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pol (Fragment).
GN Name=pol;
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92628501; PubMed=12743298;
RX DOI=10.1126/JVI.77.11.6405-6418.2003;
RA Denghani H., Puffer B.A., Doms R.W., Hirsch V.M.;
RT "Unique pattern of convergent envelope evolution in simian
RT immunodeficiency virus-infected rapid progressor macaques: association
RT with CD4-independent usage of CCR5."
RT J. Virol. 77:6405-6418(2003).
RL -1 SIMILARITY: Belongs to peptidase family A2.
DR EMBL; AY221515; AA067309.1; -.
DR HSSP; P04584; 1MU2.
DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008907; F:integrase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0015074; P:DNA integration; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR001037; Integrase_C.
DR InterPro; IPR003308; Integrase_Zn_N.
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DR InterPro: IPR001995; Peptidase_A2.
DR InterPro: IPR009007; Pept_Aspartic.
DR InterPro: IPR001969; Pept_Asp_AS.
DR InterPro: IPR002156; RNaseH.
DR InterPro: IPR001584; Rve.
DR InterPro: IPR000477; RVTase.
DR InterPro: IPR010659; RVT_connect.
DR InterPro: IPR010661; RVT_chumb.
DR InterPro: IPR005829; Sug_transporter.
DR Pfam: PF02022; Integrase_Zn; 1.
DR Pfam: PF00075; RNaseH; 1.
DR Pfam: PF00665; Rve; 1.
DR Pfam: PF00077; RVP; 1.
DR Pfam: PF00078; RVT_1; 1.
DR Pfam: PF06815; RVT_connect; 1.
DR Pfam: PF06817; RVT_chumb; 1.
DR PROSITE: PS00141; ASP_PROTASE; 1.
DR PROSITE: PS50175; ASP_PROT_RETROV; 1.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN 1.
KW Aspartyl protease; Hydrolase; Protease; RNA-directed DNA polymerase;
KW Transferrase.
FT NON_TER
SQ SEQUENCE 1019 AA; 115613 MW; 6002D54F14648CBC CRC64;

Query Match 45.4%; Score 44; DB 2; Length 1019;
Best Local Similarity 61.5%; Pred. No. 3.2e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KGPTLRQWLKRSRE 15
Db 184 EGPTLRQWLKRSKE 196

RESULT 28
Q7ZBR7 PRELIMINARY; PRT; 1019 AA.
AC Q7ZBR7;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Pol (fragment).
GN Name-pol;
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22628501; PubMed=12743298;
RX DOI=10.1128/JVI.77.11.6405-6418.2003;
RA Deighan H., Puffer B.A., Doms R.W., Hirsch V.M.;
RT "Unique pattern of convergent envelope evolution in simian
RT immunodeficiency virus-infected rapid progressor macaques: association
RT with CD4-independent usage of CCR5.";
RL J. Virol. 77:6405-6418(2003).
CC -1 SIMILARITY: Belongs to peptidase family A2.
DR EMBL; AY21514; AAC67307.1; -.
DR HSSP; P04584; 1M02.
DR GO: GO:0004190; F:aspartic-type endopeptidase activity; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0008907; F:integrase activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004523; F:ribonuclease H activity; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0015074; F:DNA integration; IEA.
DR GO: GO:0006310; P:DNA recombination; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO: GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro: IPR001037; Integrase_C.
DR InterPro: IPR003308; Integrase_Zn_N.
DR InterPro: IPR001995; Peptidase_A2.
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DR InterPro: IPR009007; Pept_Aspartic.
DR InterPro: IPR001969; Pept_Asp_AS.
DR InterPro: IPR002156; RNaseH.
DR InterPro: IPR001584; Rve.
DR InterPro: IPR000477; RVTase.
DR InterPro: IPR010659; RVT_connect.
DR InterPro: IPR010661; RVT_chumb.
DR InterPro: IPR005829; Sug_transporter.
DR Pfam: PF02022; Integrase_Zn; 1.
DR Pfam: PF00075; RNaseH; 1.
DR Pfam: PF00665; Rve; 1.
DR Pfam: PF00077; RVP; 1.
DR Pfam: PF00078; RVT_1; 1.
DR Pfam: PF06815; RVT_connect; 1.
DR Pfam: PF06817; RVT_chumb; 1.
DR PROSITE: PS00141; ASP_PROTASE; 1.
DR PROSITE: PS50175; ASP_PROT_RETROV; 1.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN 1.
KW Aspartyl protease; Hydrolase; Protease; RNA-directed DNA polymerase;
KW Transferrase.
FT NON_TER
SQ SEQUENCE 1019 AA; 115340 MW; A866525DFP1BE26F CRC64;

Query Match 45.4%; Score 44; DB 2; Length 1019;
Best Local Similarity 61.5%; Pred. No. 3.2e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KGPTLRQWLKRSRE 15
Db 184 EGPTLRQWLKRSKE 196

RESULT 29
POL_HV2D2 STANDARD; PRT; 1058 AA.
AC P15833;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Pol polyprotein [Contains: Protease (Retropepin) (EC 3.4.23.47);
DE Reverse transcriptase/ribonuclease H (EC 2.7.7.49) (EC 3.1.26.4) (RT);
DE Integrase (IN)].
GN Name-pol;
OS Human immunodeficiency virus type 2 (isolate D205.7) (HIV-2).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11716;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90081881; PubMed=2594088; DOI=10.1038/342948a0;
RX Dietrich U., Adamski M., Kreutz R., Seipp A., Kuehnelt H.,
RX Ruebsamen-Waigmann H.;
RT "A highly divergent HIV-2-related isolate.";
RL Nature 342:948-950(1989).
CC -1 FUNCTION: During replicative cycle of retroviruses, the reverse-
CC transcribed viral DNA is integrated into the host chromosome by
CC the viral integrase enzyme. RNase H activity is associated with
CC the reverse transcriptase.
CC -1 CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphononucleoside.
CC -1 CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + [DNA] (N).
CC -1 CATALYTIC ACTIVITY: Endopeptidase for which the P1 residue is
CC preferably hydrophobic.
CC -1 PM: Cleavage sites that yield the mature proteins remain to be
CC determined.
CC -1 SIMILARITY: Belongs to the retroviruses Pol polyprotein family.
CC -1 SIMILARITY: Contains 1 integrase-type zinc finger.
CC -1 SIMILARITY: Contains 1 peptidase A2 domain.
CC -1 SIMILARITY: Contains 1 reverse transcriptase domain.
CC -1 SIMILARITY: Contains 1 RNase H domain.
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CC EMBL; X61240; -; NOT_ANNOTATED_CDS.
 DR PIR; S08436; S08436.
 DR HSSP; P04584; 1MU2.
 DR MEROPS; A02.002; -.
 DR HIV; X16109; POLS2D205.
 DR InterPro; IPR001037; Integrase_C.
 DR InterPro; IPR003308; Integrase_Zn_N.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR InterPro; IPR009007; Pept_AspAlic.
 DR InterPro; IPR001995; Peptidase_A2.
 DR InterPro; IPR002156; RNaseH.
 DR InterPro; IPR001584; Rve.
 DR InterPro; IPR010659; RVT_connect.
 DR InterPro; IPR010661; RVT_thumb.
 DR InterPro; IPR000477; RVTse.
 DR Pfam; PF00552; Integrase; 1.
 DR Pfam; PF02022; Integrase_Zn; 1.
 DR Pfam; PF00075; RNaseH; 1.
 DR Pfam; PF00665; Rve; 1.
 DR Pfam; PF00077; RVP; 1.
 DR Pfam; PF00078; RVT; 1.
 DR Pfam; PF06815; RVT_connect; 1.
 DR Pfam; PF06815; RVT; 1.
 DR Pfam; PF06817; RVT_thumb; 1.
 DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR PROSITE; PS50879; RNase_H; 1.
 DR PROSITE; PS50876; ZF_INTEGRASE; 1.
 DR AIDS; Asparacyl protease; DNA integration; DNA recombination;
 KW Nucleonuclease; Hydrolase; Metal-binding; Multifunctional enzyme;
 KW Nucleonuclease; Polypeptide; RNA-directed DNA polymerase; Transferase; Zinc;
 KW Zinc-finger.
 FT CHAIN 106 204 Protease.
 FT DOMAIN 248 437 Reverse transcriptase.
 FT DOMAIN 636 759 RNase H.
 FT ZN_FING 765 806 Integrase-type.
 FT ACT_SITE 130 130 By similarity.
 SQ SEQUENCE 1058 AA; 11964 MW; 914D5433694B57F4 CRC64;
 Query Match 45.4%; Score 44; DB 1; Length 1058;
 Best Local Similarity 66.7%; Pred. No. 3.3e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 4 GPTLRQWLKSRH 15
 DB 222 GPKIRQWPLSRH 233
 RESULT 30
 Q8D674 PRELIMINARY; PRT; 1928 AA.
 AC Q8D674;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE ATP-dependent exodNase, alpha subunit.
 GN OrderedLocuNames=VV20663;
 OS Vibrio vulnificus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=672;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choy H.E.,
 RT "Complete genome sequence of Vibrio vulnificus CMCP6.";

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE016810; ANO07605.1; -.
 DR HSSP; P14565; 1PAD.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
 DR ATP-binding; Complete proteome.
 KW SEQUENCE 1928 AA; 216321 MW; 01D807F50782E486 CRC64;
 SQ SEQUENCE 1928 AA; 216321 MW; 01D807F50782E486 CRC64;
 Query Match 45.4%; Score 44; DB 2; Length 1928;
 Best Local Similarity 61.5%; Pred. No. 6.5e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 GPTLRQWLKSRH 16
 DB 686 GWTLRQMDKGRH 698
 RESULT 31
 Q6MDL6 PRELIMINARY; PRT; 561 AA.
 AC Q6MDL6;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocuNames=pc0609;
 OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
 OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
 OX NCBI_TaxID=264201;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
 RA Farnham B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
 RA Rettel T., Mewes H.-W., Wagner M.;
 RT "Genome sequence of an amoeba symbiont and its use for reconstructing
 RT the evolutionary history of Chlamydiae."
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX908798; CAF2333.1; -.
 DR InterPro; IPR008938; ARM.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 561 AA; 63263 MW; 7219CF0B6CA98EDA CRC64;
 Query Match 44.8%; Score 43.5; DB 2; Length 561;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
 Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 3 KGP--TLRQWLKSRH 17
 DB 470 KGPYAEOLRQWVKTQRET 487
 RESULT 32
 Q88L07 PRELIMINARY; PRT; 657 AA.
 AC Q88L07;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Soluble lytic transglycosylase, putative.
 GN OrderedLocuNames=PP2130;
 OS Pseudomonas putida (strain KT2440).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=160488;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=2243060; PubMed=12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,

RA Brinkac L.M., Beanan M.J., Deboy R.T., Daugherty S.C., Kolonay J.F.,
 RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
 RA Hance I., Chris Lee P., Holtzapfe E.K., Scanlan D., Tran K.,
 RA Moazzaz A., Ullarback T.R., Rizzo M., Lee K., Kosack D., Mestl D.,
 RA Kiewler H., Lauber J., Stjepandic D., Hohnselt J., Straetz M., Heim S.,
 RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Thewissen B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile *Pseudomonas putida* KT2440.";
 RL Environ. Microbiol. 4:799-808(2002).
 DR EMBL: AE016782; AAN67743.1; -.
 DR HSSP: P03810; IOSA.
 DR TIGR: PP2130; -.
 DR InterPro: IPR008939; Muramidase_bact.
 DR InterPro: IPR008258; SLT.
 DR Pfam: PF01464; SLT.1.
 KM Complete proteome.
 SQ SEQUENCE 657 AA; 75337 MW; 03403C8F6D912790 CRC64;

Query Match 44.8%; Score 43.5; DB 2; Length 657;
 Best Local Similarity 56.2%; Pred. No. 2.4e+02;
 Matches 9; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 4 GP-TLRQWLKSRHETS 18
 Db 594 GPGRVQWLKGAHLIS 609

RESULT 33
 Q98183 PRELIMINARY; PRT; 63 AA.
 ID Q98183; 012598; 012879;
 AC Q98183; 012598; 012879;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)
 DE M0C12L (Hypothetical protein B-M.N.L.2).
 GN Name=M0C12L; Synonyms=B-M.N.L.2;
 OS Molluscum contagiosum virus subtype 1 (MCV1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Molluscipoxvirus.
 OC NCBI_Taxid=10280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96325459; Pubmed=8670425;
 RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
 RA Moss B.;
 RT "Genome sequence of a human tumorigenic poxvirus: prediction of
 RT specific host response-evasion genes.";
 RL Science 273:813-816(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97093414; Pubmed=8938976;
 RA Martin-Gallardo A., Moratilla M., Funes J.M., Agromayor M., Nunez A.,
 RA Varas A.J., Collado M., Valencia A., Lopez-Esteban J.L.,
 RA Esteban M.;
 RT "Sequence analysis of a Molluscum contagiosum virus DNA region which
 RT includes the gene encoding protein kinase 2 and other genes with
 RT unique organization.";
 RL Virus Genes 13:19-29(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97352177; Pubmed=9208457; DOI=10.1023/A:1007991508159;
 RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
 RA Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.;
 RT "A random DNA sequencing, computer-based approach for the generation
 RT of a gene map of molluscum contagiosum virus.";
 RL Virus Genes 14:73-80(1997).
 DR EMBL: U60315; AAC55140.1; -.
 DR PIR: T30614; T30614.
 KW Hypothetical protein.
 SQ SEQUENCE 63 AA; 7088 MW; 1C96B36D3E5D8F27 CRC64;

Query Match 44.3%; Score 43; DB 2; Length 63;
 Best Local Similarity 41.2%; Pred. No. 21;
 Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IKGPTLRQWLKSRHETS 18
 Db 41 VIGETLRQWLKSRHETS 57

RESULT 34
 Q8VLU9 PRELIMINARY; PRT; 113 AA.
 ID Q8VLU9;
 AC Q8VLU9;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative nitrate reductase (Fragment).
 GN Name=narg;
 OS Uncultured bacterium.
 OC Bacteria; environmental samples.
 OC NCBI_Taxid=77133;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gregory L.G.;
 RL Thesis (2000), Department of School of Biological Sciences, University
 RL of East Anglia, Norwich, United Kingdom.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gregory L.G.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Spiro S.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ314989; CAC85822.1; -.
 DR HSSP: P03152; 1016.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 FT NON_TER 1 1
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12691 MW; 34F772F88634988D CRC64;

Query Match 44.3%; Score 43; DB 2; Length 113;
 Best Local Similarity 35.3%; Pred. No. 40;
 Matches 6; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IKGPTLRQWLKSRHETS 18
 Db 15 IRGVLMLMKRKAHESA 31

RESULT 35
 Q48532 PRELIMINARY; PRT; 124 AA.
 ID Q48532;
 AC Q48532;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Excreted protein (Fragment).
 GN Name=exca;
 OS Leptochrix discophora.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Leptochrix.
 OC NCBI_Taxid=89;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS-1;
 RA Corstjens P.L.;
 RL Thesis (1993), Biochemistry, Leiden University.
 DR EMBL: Z25772; CAA81034.1; -.
 DR GO: GO:0005215; P:transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR006059; SBP_bac_1.
 DR Pfam: PF01547; SBP_bac_1; 1.

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FT  NON TER      1      1
RT  NON TER      124     124
SQ  SEQUENCE     124 AA; 13393 MW; 33F814295B8BF475 CRC64;

Query Match      44.3%; Score 43; DB 2; Length 124;
Best Local Similarity 54.8%; Pred. No. 44;
Matches          6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY  2 IKGPTLRQWLK 12
    |||:::|
    40 IKGPSIOEMAK 50

RESULT 36
ID  OGAM22      PRELIMINARY;      PRT;      215 AA.
AC  OGAM22;
DT  25-OCT-2004 (TrEMBLrel. 28, Created)
DT  25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT  25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE  Related to hemolysin II.
OS  OrderedLocustNames=DP1874;
OC  Desulfotalea psychrophila.
OC  Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
OC  Desulfobulbaceae; Desulfotalea.
OX  NCBI_TaxID=84980;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=LSv54 / DSM 12343;
RX  PubMed=15305914;
RA  Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
RA  Bauer M., Zibat A., Lombardot T., Becker I., Aman V., Gellner K.,
RA  Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Aman R.,
RA  Klenk H.-P.;
RT  "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT  from permanently cold Arctic sediments.";
RL  Environ. Microbiol. 6:887-902(2004).
DR  EMBL; CR522870; CAG36603.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  InterPro; IPR004254; HlyIII_related.
DR  Pfam; PF03006; HlyIII; 1.
KM  Complete proteome.
SQ  SEQUENCE 215 AA; 23870 MW; F73016495673A459 CRC64;

Query Match      44.3%; Score 43; DB 2; Length 215;
Best Local Similarity 50.0%; Pred. No. 82;
Matches          7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY  3 KGPTLRQWLKSRH 16
    |||:::|
    73 KKPVLARKLRRCDH 86

Db

RESULT 37
ID  PSAL_SPTOL      STANDARD;      PRT;      216 AA.
AC  Q41385;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Photosystem I reaction center subunit XI, chloroplast precursor (PSI-
DE  L) (PSI subunit V).
GN  Name=PSAL;
OS  Spinacia oleracea (Spinach).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
OC  Caryophyllales; Amaranthaceae; Spinacia.
OX  NCBI_TaxID=3562;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=cv. Monatal.
RX  MEDLINE=93344519; PubMed=8343606;
RA  Flieger K., Oelmüller R., Herrmann R.G.;

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RT  "Isolation and characterization of cDNA clones encoding a 18.8 kDa
RT  polypeptide, the product of the gene psal, associated with photosystem
RT  I reaction center from spinach.";
RL  Plant Mol. Biol. 22:703-709(1993).
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
CC  thylakoid membrane (Probable).
CC  -1- SIMILARITY: Belongs to the psal family.
CC  -----
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CC  -----
DR  EMBL; X64445; CAA5775.1; -.
DR  PIR; S35151; S35151.
DR  HSSP; P25902; 1UBO.
DR  InterPro; IPR003757; PSI_Psal.
DR  Pfam; PF02605; Psal; 1.
DR  ProDom; PD005947; PSI_Psal; 1.
KM  Chloroplast; Photosynthesis; Photosystem I; Thylakoid;
KT  Transit peptide; Transmembrane.
FT  TRANSIT 1 47 Chloroplast (Potential).
FT  CHAIN 48 216 Photosystem I reaction center subunit XI.
FT  DOMAIN 48 134 Stromal (Potential).
FT  TRANSMEM 135 155 Potential.
FT  DOMAIN 156 188 Lumenal (Potential).
FT  TRANSMEM 189 209 Potential.
FT  DOMAIN 210 216 Stromal (Potential).
SQ  SEQUENCE 216 AA; 22937 MW; 603DCA983C7C383B CRC64;

Query Match      44.3%; Score 43; DB 1; Length 216;
Best Local Similarity 52.9%; Pred. No. 82;
Matches          9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY  2 IKGPTLRQWLKSRH 18
    |||:::|
    27 ISGPALRGFPSPRRHTS 43

Db

RESULT 38
ID  Q87115      PRELIMINARY;      PRT;      217 AA.
AC  Q87115;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Pol protein (Fragment).
GN  Name=pol;
OS  Chimpanzee immunodeficiency virus (SIV/cpz) (CIV).
OC  Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX  NCBI_TaxID=11723;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=SIVagmsABD37;
RX  MEDLINE=94298785; PubMed=8026477;
RA  Hirsch V.M., Allan J.S., Shaw G.M., Sharp P.M., Hahn B.H.;
RT  "Mosaic genome structure of simian immunodeficiency virus from west
RT  African green monkeys.";
RL  EMBO J. 13:2935-2947(1994).
DR  EMBL; U04018; AAA21512.1; -.
DR  GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
DR  GO; GO:0003723; F:RNA binding; IEA.
DR  GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR  GO; GO:0016740; F:transferase activity; IEA.
DR  GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR  GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR  InterPro; IPR001995; Peptidase A2.
DR  InterPro; IPR009007; Rept Aspartic.
DR  InterPro; IPR000477; RTase.

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DR Pfam; PF00077; RVP; 1.
DR Pfam; PF00078; RVT; 1; 1.
DR PROSITE; PS50175; ASP_PROT_RETROV; 1.
KW RNA-directed DNA polymerase; transferase.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 217 AA; 24503 MW; C1162E4BF18204B8 CRC64;

Query Match 44.3%; Score 43; DB 2; Length 217;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 GPTLRQWLKSR 15
DB 87 GPTLRQWLKSR 98

RESULT 39
O9KC77 PRELIMINARY; PRT; 233 AA.
ID O9KC77;
AC O9KC77;
DT 01-OCT-2000 (TREMBlrel. 15; Created)
DT 01-OCT-2000 (TREMBlrel. 15; Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26; Last annotation update)
DE Initiation of chromosome replication.
GN Name=dnad; OrderedLocustNames=BH1697;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
RX MEDLINE=2051582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001512; BAB05416.1; -.
DR PIR; A83862; A83862.
DR InterPro; IPR006343; Dnad_phage.
DR InterPro; IPR009058; Wing_Hlx_DNA_bnd.
DR Pfam; PF04271; Dnad; 1.
DR TIGRFAMs; TIGR01446; Dnad_dom; 1.
KM Complete proteome.
SQ SEQUENCE 233 AA; 27045 MW; D25E82126AD97CC3 CRC64;

Query Match 44.3%; Score 43; DB 2; Length 233;
Best Local Similarity 43.8%; Pred. No. 89;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 2 IKGPTLRQWLKSRHT 17
DB 144 IEGTSLRMWDQDHT 159

RESULT 40
PYRF_GLOVI STANDARD; PRT; 237 AA.
ID PYRF_GLOVI;
AC Q7NK22;
DT 29-MAR-2004 (Rel. 43; Created)
DT 29-MAR-2004 (Rel. 43; Last sequence update)
DT 05-JUN-2004 (Rel. 44; Last annotation update)
DE Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)
DE (OMPDecase) (OMPDecase).
GN Name=pyrf; OrderedLocustNames=g111658;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7421;

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RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Miumuro M., Miyashita H., Tsuchiya T.,
RA Saeamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145(2003)
CC -1- CATALYTIC ACTIVITY: Orotidine 5'-phosphate = UMP + CO(2).
CC -1- PATHWAY: Pyrimidine biosynthesis; sixth (last) step.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: Belongs to the OMP decarboxylase family. Subfamily 1.
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DR EMBL; AP006573; BAC89599.1; -.
DR HAMAP; MF_01200; -.
DR InterPro; IPR001754; OMPDecase.
DR Pfam; PF00215; OMPDecase; 1.
DR TIGRFAMs; TIGR01740; pyrf; 1.
DR PROSITE; PS00156; OMPDecase; 1.
KM Complete proteome; Decarboxylase; lyase; Pyrimidine biosynthesis.
FT ACT SITE 62
FT ACT SITE 62
SQ SEQUENCE 237 AA; 24470 MW; 0959AC5628E8258C CRC64;

Query Match 44.3%; Score 43; DB 1; Length 237;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 TIRGPTLRQWLKSR 14
DB 40 TIRGPTLRQWLKSR 53

RESULT 41
O8XSK8 PRELIMINARY; PRT; 238 AA.
ID O8XSK8;
AC O8XSK8;
DT 01-MAR-2002 (TREMBlrel. 20; Created)
DT 01-MAR-2002 (TREMBlrel. 20; Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24; Last annotation update)
DE Hypothetical protein RSP0463.
GN Name=RS00951; OrderedLocustNames=RS0463;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Guzy J., Mangenot S.,
RA Ariat M., Billault A., Brotier P., Camus J.C., Cactolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunne S., Demange N.,
RA Gaepin C., Lavie W., Moisan A., Robert C., Saurin W., Schiek T.,
RA Siguler P., Thebaud P., Whalen W., Winkler P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646078; CAD17614.1; -.
KM Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 238 AA; 25530 MW; ABA94D28568858E7 CRC64;

Query Match 44.3%; Score 43; DB 2; Length 238;
Best Local Similarity 61.5%; Pred. No. 92;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY 5 PTIROWLKSREHT 17
 DB 221 PIRNGWLKRLHET 233

RESULT 42
 YMO8 PARTE STANDARD; PRT; 241 AA.
 AC P15609;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Hypoetical 28.6 kDa protein (ORF8).
 OS Paramaecium tetraurelia.
 OG Mitochondrion.
 OC Eukaryote; Alveolata; Ciliophora; Oligohymenophorea; Periculida;
 OC Paramaecium.
 OX NCBI_TaxID=5888;
 RN PIR; S07399; 5888; 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Strock 51;
 RX MEDLINE=90174913; PubMed=2308823;
 RA Pritchard A.E., Sellhauer J.U., Mahalingam R., Sable C.L.,
 RA Vanuit S.E., Cummings D.U.;
 RT "Nucleotide sequence of the mitochondrial genome of Paramaecium";
 RL Nucleic Acids Res. 18:173-180(1990).
 CC -1- SIMILARITY: Belongs to the ribosomal protein S13p family.
 CC -----
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 CC -----
 CC EMBL; X15917; CAA34049.1; -;
 DR PIR; S07740; S07740.
 DR InterPro: IPR010979; Ribosomal_H2TH.
 DR InterPro: IPR001892; Ribosomal_S13.
 DR Pfam; PF00416; Ribosomal_S13_1.
 DR PROSITE; PS00646; RIBOSOMAL_S13_1; FALSE_NEG.
 DR PROSITE; PS50159; RIBOSOMAL_S13_2; 1.
 KM Hypothetical protein; Mitochondrion.
 SQ SEQUENCE 241 AA; 26648 MW; 7410BAA96B37FA6F CRC64;
 Query Match 44.3%; Score 43; DB 1; Length 241;
 Best Local Similarity 41.2%; Pred. No. 93;
 Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 2 IKGPTLROWLKSREHTS 18
 DB 26 VKGPTLKEFLKRFPRYNA 42

RESULT 43
 RIBF MYCPN STANDARD; PRT; 269 AA.
 AC P75587;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Putative riboflavin biosynthesis protein ribf [includes: Riboflavin
 DE kinase (EC 2.7.7.2) (P4D pyrophosphorylase); FMN adenylyltransferase
 DE (EC 2.7.7.2) (P4D pyrophosphorylase); FMN synthetase)].
 GN Name=ribf; OrderedLocNames=MpN158; ORFNames=WP673;
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;

RX MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
 RA Himmelfreisch R., Hilbert H., Plegens H., Pirkl E., Li B.-C.,
 RA Hermann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -1- CATALYTIC ACTIVITY: ATP + riboflavin = ADP + FMN.
 CC -1- CATALYTIC ACTIVITY: ATP + FMN = diphosphate + P4D.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AE000062; AAB96321.1; -;
 DR PIR; S73999; S73999.
 DR HSSP; Q96966; INB9.
 DR InterPro: IPR002606; P4D_Synth.
 DR Pfam; PF01687; P4D_Synth; 1.
 DR Pfam; PF06574; Flavokinase; 1.
 DR Prodom; PD003662; P4D_Synth; 1.
 DR TIGRPFAM; TIGR00083; Ribf; 1.
 KM Complete proteome; P4D; FMN; Multifunctional enzyme;
 KM Nucleotidyltransferase; Transferase.
 SQ SEQUENCE 269 AA; 30435 MW; 2E63D7BC7A8FA12D CRC64;
 Query Match 44.3%; Score 43; DB 1; Length 269;
 Best Local Similarity 58.3%; Pred. No. 1e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TIKGPTLROWLK 12
 DB 124 TLSSSTIROWLK 135

RESULT 44
 Q8UN03 PRELIMINARY; PRT; 340 AA.
 ID Q8UN03;
 DT 01-MAR-2002 (TRENBEREL. 20, Created)
 DT 01-MAR-2002 (TRENBEREL. 20, Last sequence update)
 DT 01-MAR-2004 (TRENBEREL. 26, Last annotation update)
 DE Reverse transcriptase (Fragment).
 GN Name=pol;
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
 OC Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Diamond T.L., Lee K.Y., Kimata J.T., Kim B.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF458220; AAL59620.1; -;
 DR HSSP; P04584; LMU2.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
 DR Pfam; PF00078; RVT_1; 1.
 DR Pfam; PF06815; RVT_connect; 1.
 DR Pfam; PF06817; RVT_chumb; 1.
 KM RNA-directed DNA polymerase; Transferase.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 340 AA; 39547 MW; 7777BFD2A057EA6B CRC64;
 Query Match 44.3%; Score 43; DB 2; Length 340;
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 4 GPTLROWLKSRE 15

Db 18 GPKLRQWPLSKR 29

RESULT 45

08UN04 PRELIMINARY; PRT; 340 AA.

AC 08UN04; 01-MAR-2002 (TRENBLrel. 20, Created)

DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Reverse transcriptase (Fragment).

GN Name-Pol;

OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11723;

RN [1]

RP SEQUENCE FROM N.A.

RA Diamond T.L., Lee K.Y., Kimata J.T., Kim B.;

RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL; AF458219; AAL59619.1; -.

DR HSSP; P04584; IMU2.

DR GO; GO:0003723; F:RNA binding; IEA.

DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006278; F:RNA-dependent DNA replication; IEA.

DR Pfam; PF00078; RVT_1; 1.

DR Pfam; PF06815; RVT_connect; 1.

DR Pfam; PF06817; RVT_chumb; 1.

DR RNA-directed DNA polymerase; Transferase.

FT NON_TER 1

FT 340

FT NON_TER 1

FT 340

SEQUENCE 340 AA; 39545 MM; F9F3BPD3F4005252 CRC64;

Query Match 44.3%; Score 43; DB 2; Length 340;

Best Local Similarity 66.7%; Pred. No. 1.4e+02;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 GPTLRQWPLSKR 15

DB 18 GPKLRQWPLSKR 29

Search completed: September 1, 2005, 16:21:06

Job time : 70.946 secs

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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:02 ; Search time 82.7482 Seconds
(without alignments)
84.131 Million cell updates/sec

Title: US-10-083-768-10

Perfect score: 98
Sequence: 1 SIBGPTLRWMLSRTPHS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	2	AAW09460 Thrombopo
2	98	100.0	18	2	AAW09498 Thrombopo
3	98	100.0	18	2	AAW36649 Thrombopo
4	98	100.0	18	2	AAW33027 Thrombopo
5	98	100.0	18	2	AAW36652 Thrombopo
6	98	100.0	18	3	AAW17026 Thrombopo
7	98	100.0	18	4	AAW25868 Human chr
8	98	100.0	18	4	AAW25824 Human chr
9	98	100.0	18	4	AAU25871 Human chr
10	98	100.0	18	5	ABW72912 TPO mimet
11	98	100.0	18	7	ADJ73064 CHI delet
12	98	100.0	18	8	ADJ52699 CHI delet
13	98	100.0	18	8	ADJ51660 CHI delet
14	98	100.0	18	5	ABP51693 TPO mimet
15	98	100.0	18	5	ABP51691 TPO mimet
16	98	100.0	18	5	ADQ16625 TPO mimet
17	98	100.0	18	8	ADQ16629 TPO mimet
18	98	100.0	18	7	ADN59830 TPO mimet
19	98	100.0	18	7	ADN59708 TPO mimet
20	98	100.0	18	5	ABP51670 TPO mimet
21	98	100.0	18	5	ADQ16585 TPO mimet
22	98	100.0	18	5	ABP51687 TPO mimet
23	98	100.0	18	5	ABP51689 TPO mimet
24	98	100.0	18	5	ABP51688 TPO mimet
25	98	100.0	18	5	ABP51686 TPO mimet

26	66	67.3	18	5	ABP51684 TPO mimet
27	66	67.3	18	5	ABP51690 TPO mimet
28	66	67.3	18	5	ABP51675 TPO mimet
29	66	67.3	18	8	ADQ16611 TPO mimet
30	66	67.3	18	8	ADQ16619 TPO mimet
31	66	67.3	18	8	ADQ16621 TPO mimet
32	66	67.3	18	8	ADQ16646 TPO mimet
33	66	67.3	18	8	ADQ16615 TPO mimet
34	66	67.3	18	8	ADQ16617 TPO mimet
35	66	67.3	18	8	ADQ16623 TPO mimet
36	66	67.3	18	8	ADQ16708 TPO mimet
37	66	67.3	18	8	ADQ16710 TPO mimet
38	66	67.3	128	8	ADQ16705 Modified
39	66	67.3	225	8	ADQ16704 Modified
40	66	67.3	472	5	ABP51695 SGI.1-TPO
41	66	67.3	472	8	ADQ16647 TPO mimet
42	62	63.3	14	5	ABP16959 TPO mimet
43	62	63.3	14	5	ABP16959 TPO mimet
44	62	63.3	14	7	ADJ73005 TPO mimet
45	62	63.3	14	8	ADJ52640 CHI delet
46	62	63.3	14	8	ADJ51601 CHI delet
47	60	61.2	28	8	ADQ16709 TPO mimet
48	60	61.2	28	8	ADQ16709 TPO mimet
49	60	61.2	29	7	ADJ73011 TPO mimet
50	60	61.2	29	7	ADJ73006 TPO mimet
51	60	61.2	29	8	ADJ52646 CHI delet
52	60	61.2	29	8	ADJ52641 CHI delet
53	60	61.2	29	8	ADJ51602 CHI delet
54	60	61.2	29	8	ADJ51602 CHI delet
55	60	61.2	31	7	ADJ73009 TPO mimet
56	60	61.2	31	7	ADJ73010 TPO mimet
57	60	61.2	31	8	ADJ52644 CHI delet
58	60	61.2	31	8	ADJ52645 CHI delet
59	60	61.2	31	8	ADJ51606 CHI delet
60	60	61.2	14	6	ABG71748 Anticbody
61	60	61.2	14	6	ABG71748 Anticbody
62	59	60.2	13	2	AAW09463 Thrombopo
63	59	60.2	14	2	AAW09468 Thrombopo
64	59	60.2	14	2	AAW33030 Thrombopo
65	59	60.2	14	2	AAW33034 Thrombopo
66	59	60.2	14	2	AAW36774 Thrombopo
67	59	60.2	14	2	ADJ24843 AF 12505
68	59	60.2	14	2	AAW36779 Thrombopo
69	59	60.2	14	3	AAW36779 Thrombopo
70	59	60.2	14	3	AAW36779 Thrombopo
71	59	60.2	14	3	AAW36779 Thrombopo
72	59	60.2	14	4	AAU25827 Human chr
73	59	60.2	14	4	AAU25827 Human chr
74	59	60.2	14	4	AAU25827 Human chr
75	59	60.2	14	5	ABP51669 Thrombopo
76	59	60.2	14	5	ABP51669 Thrombopo
77	59	60.2	14	6	ABG71747 TPO recep
78	59	60.2	14	7	ABR62907 Erythro
79	59	60.2	14	7	ADN59652 Thrombopo
80	59	60.2	14	7	ADN59652 Thrombopo
81	59	60.2	14	8	ADN59652 Thrombopo
82	59	60.2	14	8	ADN59652 Thrombopo
83	59	60.2	14	8	ADN59652 Thrombopo
84	59	60.2	14	8	ADN59652 Thrombopo
85	59	60.2	14	8	ADN59652 Thrombopo
86	59	60.2	14	8	ADN59652 Thrombopo
87	59	60.2	14	8	ADN59652 Thrombopo
88	59	60.2	14	8	ADN59652 Thrombopo
89	59	60.2	14	8	ADN59652 Thrombopo
90	59	60.2	14	8	ADN59652 Thrombopo
91	59	60.2	14	8	ADN59652 Thrombopo
92	59	60.2	14	8	ADN59652 Thrombopo
93	59	60.2	14	8	ADN59652 Thrombopo
94	59	60.2	14	8	ADN59652 Thrombopo
95	59	60.2	14	8	ADN59652 Thrombopo
96	59	60.2	14	8	ADN59652 Thrombopo
97	59	60.2	14	8	ADN59652 Thrombopo
98	59	60.2	14	8	ADN59652 Thrombopo

99 59 60.2 15 8 ADM72485 Adm72485 TPO mimet
100 59 60.2 15 8 ADM72479 Adm72479 TPO mimet

ALIGNMENTS

```

RESULT 1
AAW09460
ID AAW09460 standard; protein; 18 AA.
XX
AC AAW09460;
XX
DT 10-SEP-1997 (first entry)
XX
DE Thrombopoietin receptor binding compound peptide.
XX
KM Haematology; thrombocytopenia; TPO; TR; proliferation;
XX bone marrow transfusion; chemotherapy; radiation therapy.
XX
OS Synthetic.
XX
Key Location/Qualifiers
FT Misc-difference 1..18
FT /note= "Preferably linkages are selected from: -
FT CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-; -C(O)NR6
FT ; -NRC(O)NH; where R is hydrogen or lower alkyl and R6 is
FT lower alkyl"
FT 1
FT /note= "Preferably N-terminus is selected from: -NRR1; -
FT NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NHR; succinimide;
FT benzoyloxycarbonyl-NH; benzoyloxycarbonyl-NH with 1-3
FT substitutions on the phenyl ring selected from lower
FT alkyl, lower alkoxy, chloro, bromo; where R and R1 are
FT independently selected from hydrogen and lower alkyl"
FT 18
FT /note= "Preferably C-terminus is -C(O)R2 where R2 is
FT selected from hydroxy, lower alkoxy, and -NR3R4, where R3
FT and R4 are independently selected from hydrogen and lower
FT alkyl, and where the nitrogen atom of the -NR3R4 group
FT can optionally be the amine group of the N-terminus of
FT the peptide forming a cyclic peptide"
XX
PN MO9640189-A1.
XX
PD 19-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US008998.
XX
PR 07-JUN-1995; 95US-00472371.
PR 07-JUN-1995; 95US-00473604.
PR 07-JUN-1995; 95US-00476168.
PR 07-JUN-1995; 95US-00478128.
PR 07-JUN-1995; 95US-00484090.
PR 07-JUN-1995; 95US-00485301.
XX
PA (GLAXO ) GLAXO GROUP LTD.
XX
PI Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX
DR WPI; 1997-051883/05.
XX
PT Thrombopoietin receptor-binding/activating peptide(s) and peptide
PT mimetic(s) - useful in treatment of haematological disorders, esp.
PT thrombocytopenia resulting from chemotherapy, etc.
XX
PS Claim 18; Page 89; 106pp; English.
XX
CC The present sequence is a compound which binds to thrombopoietin (TPO)
CC receptor (TR). It has a molecular weight of < 8000 Da, and a binding
CC affinity to TR as expressed by an IC50 of no more than about 100 nM. The
CC compound (especially if modified, see features table) can be used for

```

CC treating patients suffering from haematological disorders and
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC marrow transfusions. The peptide may also be used to maintain the
CC proliferation and growth of TPO-dependent cell lines and for use in
CC biological research, for detecting TPO receptors on living cells
XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIEGPTLRWLTSTRTPHS 18
|||
1 SIEGPTLRWLTSTRTPHS 18

RESULT 2
AAW09498
ID AAW09498 standard; protein; 18 AA.
XX

AC AAW09498;

DT 10-SEP-1997 (first entry)

DE Thrombopoietin receptor binding peptide.

KM Haematology; thrombocytopenia; TPO; TR; proliferation;
KW bone marrow transfusion; chemotherapy; radiation therapy.

OS Synthetic.

PN MO9640189-A1.

PD 19-DEC-1996.

PF 05-JUN-1996; 96WO-US008998.

PR 07-JUN-1995; 95US-00472371.

PR 07-JUN-1995; 95US-00473604.

PR 07-JUN-1995; 95US-00476168.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00484090.

PR 07-JUN-1995; 95US-00485301.

XX (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-051883/05.

PT Thrombopoietin receptor-binding/activating peptide(s) and peptide
PT mimetic(s) - useful in treatment of haematological disorders, esp.
PT thrombocytopenia resulting from chemotherapy, etc.

XX PS Disclosure; Page 27; 106pp; English.

XX CC The present sequence is a peptide which binds to thrombopoietin (TPO)
XX CC receptor (TR). The compound can be used for treating patients suffering
XX CC from haematological disorders and thrombocytopenia resulting from
XX CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide
XX CC may also be used to maintain the proliferation and growth of TPO-
XX CC dependent cell lines and for use in biological research, for detecting
XX CC TPO receptors on living cells
XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIEGPTLRWLTSTRTPHS 18

Db 1 SIEGPTLRMLTSRTPHS 18

RESULT 3

ID AAM36649 standard; peptide; 18 AA.

AC AAM36649;

DT 11-MAR-1998 (first entry)

DB Thrombopoietin receptor binding peptide.

KW Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopaenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

OS Synthetic.

PN WO9640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PA (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barret RM, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;

PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

DR WPI; 1997-052226/05.

XX Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopaenia resulting from chemotherapy, etc.

XX Disclosure; Page 27; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be

CC used to treat disorders which are susceptible to treatment with a

CC thrombopoietin agonist, preferably haematological disorders and

CC thrombocytopaenia resulting from chemotherapy, radiation therapy or bone

CC marrow transfusions. It can also be used diagnostically, e.g. to

CC investigate the mechanism of thrombopoietin signal transduction and

CC receptor activation, or to maintain the proliferation and growth of

CC thrombopoietin dependent cell lines

XX Sequence 18 AA:

Query Match 100.0%; Score 98; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.1e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIEGPTLRMLTSRTPHS 18

DB 1 SIEGPTLRMLTSRTPHS 18

RESULT 4

ID AAM33027 standard; peptide; 18 AA.

AC AAM33027;

DT 11-MAR-1998 (first entry)

DB Thrombopoietin receptor binding peptide.

KW Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopaenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

OS Synthetic.

PN WO9640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PA (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barret RM, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;

PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

DR WPI; 1997-052226/05.

XX Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopaenia resulting from chemotherapy, etc.

XX Claim 19; Page 89; 106pp; English.

XX The present peptide binds the thrombopoietin receptor (TR), has a

CC molecular weight of less than 8000 Da and a TR binding affinity as

CC expressed by an IC50 of no more than about 100 microm. It can be used to

CC treat disorders which are susceptible to treatment with a thrombopoietin

CC agonist, preferably haematological disorders and thrombocytopaenia

CC resulting from chemotherapy, radiation therapy or bone marrow

CC transfusions. It can also be used diagnostically, e.g. to investigate the

CC mechanism of thrombopoietin signal transduction and receptor activation,

CC or to maintain the proliferation and growth of thrombopoietin dependent

XX cell lines

XX Sequence 18 AA:

Query Match 100.0%; Score 98; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.1e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIEGPTLRMLTSRTPHS 18

DB 1 SIEGPTLRMLTSRTPHS 18

RESULT 5

ID AAM36652 standard; peptide; 18 AA.

AC AAM36652;

DT 11-MAR-1998 (first entry)

DB Thrombopoietin receptor binding peptide.

KW Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopaenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

OS Synthetic.

PN WO9640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

XX 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 PI Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Matcheakis LC, Schatz PJ, Wagstrom CR, Wighton NC;
 XX WPI; 1997-052226/05.
 DR
 XX Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 XX Disclosure; Page 27; 106pp; English.
 PS
 XX The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopaenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transplants. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 100.0%; Score 98; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIEGPTLRWLTSTRPHS 18
 Db 1 SIEGPTLRWLTSTRPHS 18
 XX
 RESULT 6
 ID AAB17026 standard; peptide; 18 AA.
 XX
 AC AAB17026;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE TPO-mimetic peptide sequence SEQ ID NO:82.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTAA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US025044.
 XX
 PR 23-OCT-1998; 98US-0105371P.
 PR 22-OCT-1999; 99US-00428082.
 XX
 XX (AMGEN-) AMGEN INC.
 PA
 XX Feige U, Liu C, Cheetham J, Boone TC;
 PI WPI; 2000-350702/30.
 XX
 PT Novel composition of matter comprising an Fc domain and pharmacologically

PT active peptides, useful for treating cancer and autoimmune diseases.
 XX
 PS Claim 19; Page 222; 608pp; English.
 XX
 CC The present invention describes composition of matter (1) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (1) is:
 CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)-C-P1, -(L1)-C-P1-(L2)-d-P2, -(L1)-C-P1-
 CC (L2)-d-P2-(L3)-e-P3, or -(L1)-C-P1-(L2)-d-P2-(L3)-e-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 100.0%; Score 98; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SIEGPTLRWLTSTRPHS 18
 Db 1 SIEGPTLRWLTSTRPHS 18
 XX
 RESULT 7
 ID AAU25868 standard; peptide; 18 AA.
 XX
 AC AAU25868;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #54.
 XX
 KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 PA
 PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;
 XX yin Q;
 XX WPI; 2001-564142/63.
 DR
 XX
 PT Activating thrombopoietin receptors in cells, used to treat

PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 XX
 PS Disclosure, Col 20; 128pp; English.

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent hematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX

SO Sequence 18 AA:

Query Match 100.0%; Score 98; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STEGPTLRWLTSTRPHS 18
 |||
 DB 1 STEGPTLRWLTSTRPHS 18

RESULT 8

AAU25824
 ID AAU25824 standard; peptide; 18 AA.

AC AAU25824;

DT 17-DEC-2001 (first entry)

DE Human thrombopoietin receptor (TPO-R) activator peptide #10.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; hematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX

OS Homo sapiens.

PN US6251864-B1.

PD 26-JUN-2001.

PF 01-MAR-2000; 2000US-00516704.

XX 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PR 07-JUN-1996; 96WO-US009623.

XX 15-AUG-1996; 96US-00699027.

PA (GLAXO) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;
 PI Balaubramanian P, Wagstrom CR, Hendren RW, Depirince RB, Podduturi S;
 PI Yin Q;

XX WPI; 2001-564142/63.

PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 XX
 PS Disclosure, Col 67-68; 128pp; English.

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent hematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX

SO Sequence 18 AA:

Query Match 100.0%; Score 98; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STEGPTLRWLTSTRPHS 18
 |||
 DB 1 STEGPTLRWLTSTRPHS 18

RESULT 9

AAU25871
 ID AAU25871 standard; peptide; 18 AA.

AC AAU25871;

DT 17-DEC-2001 (first entry)

DE Human thrombopoietin receptor (TPO-R) activator peptide #57.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; hematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX

OS Homo sapiens.

PN US6251864-B1.

PD 26-JUN-2001.

PF 01-MAR-2000; 2000US-00516704.

XX 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PR 07-JUN-1996; 96WO-US009623.

XX 15-AUG-1996; 96US-00699027.

PA (GLAXO) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;
 PI Balaubramanian P, Wagstrom CR, Hendren RW, Depirince RB, Podduturi S;
 PI Yin Q;

XX WPI; 2001-564142/63.

XX Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprising contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 PS Disclosure; Col 20; 128pp; English.
 XX
 CC Sequences AMU5815-AMU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent hematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX
 SQ Sequence 18 AA;
 XX
 QY
 DB 1 SIEGPTLRWLTSTRTPHS 18
 1 SIEGPTLRWLTSTRTPHS 18
 RESULT 10
 ID ABB72912 standard; peptide, 18 AA.
 XX
 AC ABB72912;
 XX
 DT 05-APR-2002 (first entry)
 XX
 DE TPO mimetic peptide SEQ ID NO:82.
 XX
 KW Modified peptide; mimetic; Fe domain; fusion; immunoglobulin G; IgG; EPO;
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
 KW TPO mimetic peptide; EPO mimetic peptide; BMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antineumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianemic; anorectic; antiinfectivity; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 PN WO200183525-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US014310.
 XX
 PR 03-MAY-2000; 2000US-00563286.
 XX
 PA (AMGB-) AMGEN INC.
 XX

PI Feige U, Liu C, Cheatham JC, Boone TC, Gudas JM;
 XX
 DR WPI; 2002-130313/17.
 XX
 PT Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 XX
 PS Claim 39; Page 44; 176pp; English.
 XX
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antineumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianemic, anorectic, antiinfectivity, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL5695 to ABL5777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 18 AA;
 XX
 QY
 DB 1 SIEGPTLRWLTSTRTPHS 18
 1 SIEGPTLRWLTSTRTPHS 18
 RESULT 11
 ID ADJ73064 standard; peptide, 18 AA.
 XX
 AC ADJ73064;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE TPO mimetic peptide sequence SeqID 518.
 XX
 KW mimetic; CDR mimetibody; gene therapy; transgenic; immune;
 KW cardiovascular; infectious; malignant; neurological disease; anaemia;
 KW immunomodulator; cardiac; antimicrobial; cytostatic; neuroprotective;
 KW TPO.
 XX
 XX Synthetic.
 OS
 XX
 PN WO2003084477-A2.
 XX
 PD 16-OCT-2003.
 XX
 PF 24-MAR-2003; 2003WO-US009139.
 XX
 PR 29-MAR-2002; 2002US-0368791P.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Heavner GA, Knight DM, Scallion BJ, Grayeb J;
 XX

DR WPI; 2003-804237/75.

PT New CDR mimetibody comprising a portion of a heavy or light chain variable region comprising human framework or ligand binding region useful for preparing a composition for treating e.g., immune, cardiovascular or neurologic disease.

PS Disclosure; SEQ ID NO 518; 97pp; English.

CC This invention relates to novel mammalian CDR mimetibodies, specific
CC portions or variants thereof. Specifically, it refers to an antibody
CC fragment where a protein has been inserted into, or replaces a portion
CC of, one or more CDR regions, such that each CDR mimetibody comprises at
CC least one portion of a heavy chain or light chain variable region, which
CC itself comprises at least one human framework region and at least one
CC 15 and binding region (LBR). The present invention describes human
CC mimetibodies, including modified immunoglobulins and cleavage products
CC that can be useful in gene therapy and the generation of transgenic
CC plants and animals. Furthermore, the CDR mimetibody is useful for
CC preparing compositions for modulating, creating or reducing the symptoms
CC of immune, cardiovascular, infectious, malignant and/or neurologic
CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC peptide sequence is a TPO mimetic peptide sequence used to make a
CC mimetibody of the invention.

SQ Sequence 18 AA;

Query Match	100.0%	Score 98	DB 7	Length 18
Best Local Similarity	100.0%	Pred. NO.	1.1e-08	
Matches 18, Conservative	0	Mismatches	0	Indels 0
				Gaps 0

Qy 1 SIEGPTLREWLTSRTPHS 18
|||
Db 1 SIEGPTLREWLTSRTPHS 18

RESULT 12
ADJ52699

ID ADJ52699 standard; peptide; 18 AA.

AC ADJ52699;

DT 06-MAY-2004 (first entry)

DE CHI deleted mimetibody-related peptide SeqID518.

KM CHL delayed mimetbody; immunosuppressive; cardiovascular; cardiac
KM hypertensive; neuroprotective; immunotropic; antibacterial; vinicide;
KM fungicide; gene therapy; immune disorder; cardiovascular disease;
KM arylthymal; hypertension; heart failure; neurodegenerative;
KM multiple sclerosis; dementia; Alzheimer's disease; anaemia;
KM cancerous condition; infectious disease; bacterial infection;
KM viral infection; fungal infection.

OS	Unidentified
OS	Synthetic.

PN WO2004002417-A2.

PD 08-JAN-2004.

PF 27-JUN-2003; 2003WO-US020347.

PR 28-JUN-2002; 2002US-0392431P.

PA (CENZ) CENTOCOR INC.

PI Heavner GA, Knight DM, Ghrayeb J, Scallion BJ, Nessor TC;

PI Kucolowski KA;

DR WPI; 2004-082870/08.

PT New CH1-deleted mimetobody polypeptides and nucleic acids, useful for modulating, treating, alleviating, preventing an immune, cardiovascular, PT or neurodegenerative disease or disorder, anemia, cancer, or infectious PT diseases.

PS Claim 2; SEQ ID NO 518; 129pp; English.

This invention relates to CHI deleted mimetibodies (and the DNA sequences which encode them), compositions, methods and uses. The invention may be useful for the development of compounds with an immunosuppressive, cardiovascular, cardiac, hypotensive, neuroprotective, neurotropic, antibacterial, virucide or fungicide activity. In addition, the disclosed sequences may prove useful for gene therapy. The CHI-deleted mimetibody is useful for diagnosing or treating a disease condition in a cell, tissue, organ or animal, specifically for modulating, treating, alleviating, preventing the incidence or reducing the symptoms of an immune, cardiovascular (for example arrhythmia, hypertension or heart failure), or neurodegenerative (for example multiple sclerosis, dementia or Alzheimer's disease) diseases or disorders, anaemia, cancerous conditions, or infectious diseases (for example bacterial, viral or fungal infection). The present sequence is that of a peptide which may be used during the creation of a mimetibody of the invention.

Sequence 18 AA:

Query Match	100.0%	Score 98;	DB 8;	length 18;
Best Local Similarity	100.0%	Pred. No. 1.1e-08;		
Matches 18; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1 SIEGPTLREWLTSRTPHS 18
Db	1 SIEGPTLREWLTSRTPHS 18

RESULT 1
ADJ51660

ID ADJ51660 standard; peptide; 18 AA.

AC ADJ51660 ;

DT 06-MAY-2004 (first entry)

CHI deleted mimetibody-related peptide SeqID518.

KM CHI deleted mimetibody; osteopathic; cardiovascular-Gen;
 KM dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
 KM gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KM antiallergic; muscular-Gen; cytostatic; antinflammatory; neuroleptic;
 KM ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor
 KM TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KM dental disorder; oral disorder; dermatological disorder; ear disorder;
 KM nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KM gastrointestinal disorder; gynaecological disorder; hepatic disorder;
 KM obstructive disorder; haematologic disorder; immunological disorder;
 KM allergic disorder; infectious disorder; musculoskeletal disorder;
 KM oncological disorder; neurological disorder; nutritional disorder;
 KM ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KM renal disorder; pulmonary disorder.

OS Unidentified.
OS Synthetic.

PN WO2004002424-A2

PD 08-JAN-2004.

PF 30-JUN-2003; 2003WO-US020495

PR 28-JUN-2002; 2002US-0392431P

XX

XX

PI Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nespor TC;
PI Kutoolski KA;
XX WPI; 2004-082872/08.
XX
XX
XX New CHI deleted mimetibody polypeptide and nucleic acid, useful for
PT diagnosing, preventing or treating cardiovascular, dermatologic,
PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
PT nutritional disorders.
XX
XX
XX Claim 15; SEQ ID NO 518; 123pp; English.
XX
XX This invention relates to CHI deleted mimetibodies (and the DNA sequences
XX which encode them), compositions, methods and uses. The invention may be
XX useful for the development of compounds with an osteopathic,
XX cardiovascular-gen, dermatological-gen, auditory, endocrine-gen,
XX gastrointestinal-gen, gynaecological-gen, hepatotropic, haemostatic,
XX immunomodulatory, antiallergic, muscular-gen, cytostatic,
XX antiinflammatory, neuroleptic, ophthalmological, nephrotropic or
XX respiratory-gen activity acting as a tumour necrosis factor (TNF)-
XX modulator or cytokine-agonist. The methods and compositions of the
XX present invention are useful for the diagnosis, prevention and/or
XX treatment of diseases or conditions associated with aberrant expression
XX or activity of the CHI deleted mimetibody, such as a bone or joint,
XX cardiovascular, dental or oral, dermatological, ear, nose or throat,
XX endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
XX obstructive, haematologic, immunological, allergic, infectious,
XX musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
XX pediatric, psychiatric, renal or pulmonary disorders. The present
XX sequence is that of a peptide which may be used during the creation of a
XX mimetibody of the invention.
XX
XX
XX Sequence 18 AA;
SQ

Query Match 100.0%; Score 98; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SIEGPTLRWMTSRTPHS 18
DB 1 SIEGPTLRWMTSRTPHS 18

RESULT 14
ABP51693
ID ABP51693 standard; peptide; 18 AA.
XX
XX AC ABP51693;
XX
XX DT 01-OCT-2002 (first entry)
XX
XX DE TPO mimetic peptide SEQ ID NO:49.
XX
XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
XX complementarity determining region; immunoglobulin; antianaemic;
XX haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX PN WO200246238-A2.
XX
XX PD 13-JUN-2002.
XX
XX PF 05-DEC-2001; 2001WO-US047656.
XX
XX PR 05-DEC-2000; 2000US-0251448P.
XX
XX PR 04-MAY-2001; 2001US-0288889P.
XX
XX PR 29-MAY-2001; 2001US-0294068P.
XX
XX PA (ALEX-) ALEXION PHARM INC.
XX
XX PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX WPI; 2002-566610/60.
DR N-PSDB; ABQ73371.
XX
XX
XX A novel immunogen molecule comprising a region in which amino acid
PT residues corresponding to at least a portion of the complementary
PT determining region are replaced or fused with an erythropoietin or
PT thrombopoietin mimetic.
XX
XX
XX Claim 20; Fig 5; 113pp; English.
XX
XX The present invention describes an immunoglobulin molecule or its fragment
XX (I) comprising a region where amino acid residues corresponding to at
XX least a portion of the complementarity determining region (CDR) are
XX replaced or fused with biologically active peptides e.g. a peptide
XX mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
XX that is flanked with proline at its carboxy terminus. (I) has
XX antianaemic, haemostatic and nephrotropic activities, and can be used as
XX a stimulator of proliferation, differentiation and maturation of
XX haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
XX for stimulating proliferation, differentiation or growth of
XX promegakaryocytes or megakaryocytes, which results in increased platelet
XX production. (I) with a region where amino acid residues corresponding to
XX a portion of CDR is replaced with an EPO mimetic, or which has one or
XX more of its CDRs fused to an EPO mimetic, is useful for increasing the
XX production of red blood cells, where (I) is contacted with haematopoietic
XX stem cells or their progenitors. (I) is useful for diagnostics or
XX therapeutics, in cell isolation strategies, and for treating patients
XX suffering from deficiency in cell populations caused by disease,
XX disorders or treatments related to the suppression of haematopoiesis.
XX ABQ73288 to ABQ73377 and ABP51696 to ABP51696 represent sequences used in
XX the exemplification of the present invention
XX
XX
XX Sequence 18 AA;
SQ

Query Match 68.4%; Score 67; DB 5; Length 18;
Best Local Similarity 68.8%; Pred. No. 0.0011;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 SIEGPTLRWMTSRTP 16
DB 2 TIEGPTLRWMTSRTP 17

RESULT 15
ABP51691
ID ABP51691 standard; peptide; 18 AA.
XX
XX AC ABP51691;
XX
XX DT 01-OCT-2002 (first entry)
XX
XX DE TPO mimetic peptide SEQ ID NO:45.
XX
XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
XX complementarity determining region; immunoglobulin; antianaemic;
XX haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
XX
XX OS Homo sapiens.
XX
XX OS Synthetic.
XX
XX PN WO200246238-A2.
XX
XX PD 13-JUN-2002.
XX
XX PF 05-DEC-2001; 2001WO-US047656.
XX
XX PR 05-DEC-2000; 2000US-0251448P.
XX
XX PR 04-MAY-2001; 2001US-0288889P.
XX
XX PR 29-MAY-2001; 2001US-0294068P.
XX
XX PA (ALEX-) ALEXION PHARM INC.
XX
XX PI

XX
PI Bowdish KS, Barbas-Frederickson S, Renshaw M;
XX
XX WPI; 2002-566610/60.
DR N-PSDB; ABQ73369.
XX
XX A novel immunogen molecule comprising a region in which amino acid
PT residues corresponding to at least a portion of the complementary
PT determining region are replaced or fused with an erythropoietin or
PT thrombopoietin mimetic.
XX
XX Claim 20; Fig 5; 113pp; English.
XX
XX The present invention describes an immunoglobulin molecule or its fragment
CC comprising a region where amino acid residues corresponding to at
CC least a portion of the complementary determining region (CDR) are
CC replaced or fused with biologically active peptides e.g. a peptide
CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC that is flanked with proline at its carboxy terminus. (I) has
CC antianaemic, haemostatic and nephrotoxic activities, and can be used as
CC a stimulator of proliferation, differentiation and maturation of
CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
CC for stimulating proliferation, differentiation or growth of
CC promegakaryocytes or megakaryocytes, where (I) is contacted with
CC promegakaryocytes or megakaryocytes, which results in increased platelet
CC production. (I) with a region where amino acid residues corresponding to
CC a portion of CDR is replaced with an EPO mimetic, or which has one or
CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC production of red blood cells, where (I) is contacted with haematopoietic
CC stem cells or their progenitors. (I) is useful for diagnostics or
CC therapeutics, in cell isolation strategies, and for treating patients
CC suffering from deficiency in cell populations caused by disease,
CC disorders or treatments related to the suppression of haematopoiesis.
CC ABQ73288 to ABQ73377 and ABP51659 to ABP51696 represent sequences used in
CC the exemplification of the present invention
XX
XX Sequence 18 AA;
SQ

Query Match 68.4%; Score 67; DB 5; Length 18;
Best Local Similarity 68.8%; Pred. No. 0.0011;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIEGPTLRWLTSTRTP 16
:|||||:|:|
Db 2 TIEGPTLRQWLARAP 17

RESULT 16
ADQ16625
ID ADQ16625 standard; peptide; 18 AA.
XX
AC ADQ16625;
XX
DT 09-SEP-2004 (first entry)
XX
XX TPO mimetic peptide with random flanking residues SEQ ID NO:45.
DE
XX immunoglobulin; complementarity determining region; CDR; peptide mimetic;
KM erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
KM immunotherapy; thrombocytopenia.
XX
XX Unidentified.
OS
XX WO2004050017-A2.
PN
XX 17-JUN-2004.
PD
XX 17-NOV-2003; 2003WO-US036894.
PF
XX 02-DEC-2002; 2002US-00307724.
PR
XX (ALEX-) ALEXION PHARM INC.
PA
XX
XX

PI Bowdish KS, Frederickson S, Renshaw M;
XX
XX WPI; 2004-460973/43.
DR N-PSDB; ADQ16626.
XX
XX New immunoglobulin molecule comprising a region, where two
PT complementary determining regions (CDRs) are replaced with EPO mimetic
PT or a TPO mimetic, useful for treating thrombocytopenia.
XX
XX Example 1; SEQ ID NO 45; 107pp; English.
XX
XX The invention relates to a novel immunoglobulin molecule or its fragment
CC comprising a region where amino acid residues corresponding to at least a
CC portion of a two complementarity determining regions (CDRs) are replaced
CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC invention has immunosuppressive activity, and may have a use in
CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC treating thrombocytopenia as a result of chemotherapy, bone marrow
CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC The present sequence represents a TPO mimetic peptide with flanking
CC residues.
XX
XX Sequence 18 AA;
SQ

Query Match 68.4%; Score 67; DB 8; Length 18;
Best Local Similarity 68.8%; Pred. No. 0.0011;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIEGPTLRWLTSTRTP 16
:|||||:|:|
Db 2 TIEGPTLRQWLARAP 17

RESULT 17
ADQ16629
ID ADQ16629 standard; peptide; 18 AA.
XX
AC ADQ16629;
XX
DT 09-SEP-2004 (first entry)
XX
XX TPO mimetic peptide with random flanking residues SEQ ID NO:49.
DE
XX immunoglobulin; complementarity determining region; CDR; peptide mimetic;
KM erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
KM immunotherapy; thrombocytopenia.
XX
XX Unidentified.
OS
XX WO2004050017-A2.
PN
XX 17-JUN-2004.
PD
XX 17-NOV-2003; 2003WO-US036894.
PF
XX 02-DEC-2002; 2002US-00307724.
PR
XX (ALEX-) ALEXION PHARM INC.
PA
XX Bowdish KS, Frederickson S, Renshaw M;
PI
XX WPI; 2004-460973/43.
DR N-PSDB; ADQ16630.
XX
XX New immunoglobulin molecule comprising a region, where two
PT complementary determining regions (CDRs) are replaced with EPO mimetic
PT or a TPO mimetic, useful for treating thrombocytopenia.
XX
XX Example 1; SEQ ID NO 49; 107pp; English.
XX
XX The invention relates to a novel immunoglobulin molecule or its fragment
CC comprising a region where amino acid residues corresponding to at least a

CC portion of a two complementarily determining regions (CDRs) are replaced
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 CC invention has immunosuppressive activity, and may have a use in
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow
 CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide with flanking
 CC residues.

XX Sequence 18 AA;

XX Query Match 68.4%; Score 67; DB 8; Length 18;

XX Best Local Similarity 68.8%; Pred. No. 0.0011; Mismatches 2; Indels 0; Gaps 0;

XX Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

XX RESULT 18

XX ADNS9830 standard; peptide; 22 AA.

XX ADNS9830;

XX 01-JUL-2004 (first entry)

XX TMP peptide TMP12.

XX Haemostatic; antihaemic; immunosuppressive; platelet;
 XX transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 XX TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 XX thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
 XX autoimmune haemolytic anaemia; Hughes's syndrome;
 XX lupoid thrombocytopenia; linker.

XX Homo sapiens.

XX WO2003031589-A2.

XX 17-APR-2003.

XX 11-OCT-2002; 2002WO-US032552.

XX 11-OCT-2001; 2001US-0328666P.

XX 10-OCT-2002; 2002US-00269806.

XX (AMGE-) AMGEN INC.

XX Min H, Sliney KC, Hartley C;

XX WPI; 2003-403101/38.

XX Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.

XX Example 6; Page 83; 126pp; English.

XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.,
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,
 CC autoimmune haemolytic anaemia, Hughes's syndrome and lupoid

CC thrombocytopenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior.
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a TMP peptide of the invention to which a two amino acid "cap"
 CC has been added to the carboxy terminal to increase peptide affinity.

XX Sequence 22 AA;

XX Query Match 67.9%; Score 66.5; DB 7; Length 22;

XX Best Local Similarity 72.2%; Pred. No. 0.0017; Mismatches 3; Indels 1; Gaps 1;

XX Matches 13; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

XX RESULT 19

XX ADNS9708 standard; peptide; 25 AA.

XX ADNS9708;

XX 01-JUL-2004 (first entry)

XX Thrombopoietin mimetic peptide TMP12, seq id 57.
 XX Haemostatic; antihaemic; immunosuppressive; platelet;
 XX transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 XX TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 XX thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
 XX autoimmune haemolytic anaemia; Hughes's syndrome;
 XX lupoid thrombocytopenia.

XX Homo sapiens.

XX WO2003031589-A2.

XX 17-APR-2003.

XX 11-OCT-2002; 2002WO-US032552.

XX 11-OCT-2001; 2001US-0328666P.

XX 10-OCT-2002; 2002US-00269806.

XX (AMGE-) AMGEN INC.

XX Min H, Sliney KC, Hartley C;

XX WPI; 2003-403101/38.

XX Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.

XX Disclosure; SEQ ID NO 57; 126pp; English.

XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or

CC platelets in a patient. The TMP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,
 CC autoimmune haemolytic anaemia, Hughes's syndrome and lupoid
 CC thrombocytopenia. The TMP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryopoietic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a TMP fragment.

XX Sequence 25 AA;

Query Match 67.3%; Score 66.5; DB 7; Length 25;
 Best Local Similarity 72.2%; Pred. No. 0.002;
 Matches 13; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 2 IEGPTLRWLTSTR-TPHS 18
 DB 6 IEGPTLRWLTSTR-TPHS 23

RESULT 20

ABP51670
 ID ABP51670 standard; peptide; 15 AA.

AC ABP51670;

DT 01-OCT-2002 (first entry)

XX Thrombopoietin (TPO) agonist mimetic peptide SEQ ID NO:2.

XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;

KM complementarity determining region; immunoglobulin; antianaemic;

KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX Homo sapiens.

OS Synthetic.

XX WO200246238-A2.

XX 13-JUN-2002.

XX 05-DEC-2001; 2001WO-US047656.

XX 05-DEC-2000; 2000US-0251448P.

XX 04-MAY-2001; 2001US-0288889P.

XX 29-MAY-2001; 2001US-0294068P.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX WPI; 2002-566610/60.

XX A novel immunogen molecule comprising a region in which amino acid

PT residues corresponding to at least a portion of the complementary

PT determining region are replaced or fused with an erythropoietin or

PT thrombopoietin mimetic.

XX Claim 19; Page 6; 113pp; English.

XX The present invention describes an immunoglobulin molecule or its fragment

CC (1) comprising a region where amino acid residues corresponding to at

CC least a portion of the complementary determining region (CDR) are

CC replaced or fused with biologically active peptides e.g. a peptide

CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (1) has
 CC antianaemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (1) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (1) is contacted with
 CC promegakaryocytes or megakaryocytes, which results in increased platelet
 CC production. (1) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (1) is contacted with haematopoietic
 CC stem cells or their progenitors. (1) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP5169 to ABP5169 represent sequences used in
 CC the exemplification of the present invention

XX Sequence 15 AA;

Query Match 67.3%; Score 66; DB 5; Length 15;
 Best Local Similarity 73.3%; Pred. No. 0.0013;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEGPTLRWLTSTRTP 16
 DB 1 IEGPTLRWLTSTRTP 15

RESULT 21

ADQ16585
 ID ADQ16585 standard; peptide; 15 AA.

AC ADQ16585;

DT 09-SEP-2004 (first entry)

XX TPO mimetic peptide SEQ ID NO:2.

XX immunoglobulin; complementarity determining region; CDR; peptide mimetic;

KM erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;

KW immunotherapy; thrombocytopenia.

XX Unidentified.

XX WO2004050017-A2.

XX 17-JUN-2004.

XX 17-NOV-2003; 2003WO-US036894.

XX 02-DEC-2002; 2002US-00307724.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Frederickson S, Renshaw M;

XX WPI; 2004-460973/43.

XX New immunoglobulin molecule comprising a region, where two

PT complementarity determining regions (CDRs) are replaced with EPO mimetic

PT or a TPO mimetic, useful for treating thrombocytopenia.

XX Disclosure; SEQ ID NO 2; 107pp; English.

XX The invention relates to a novel immunoglobulin molecule or its fragment

CC comprising a region where amino acid residues corresponding to at least a

CC portion of a two complementarity determining regions (CDRs) are replaced

CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and

CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the

CC invention has immunosuppressive activity, and may have a use in

CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or

CC treating thrombocytopenia as a result of chemotherapy, bone marrow
CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC The present sequence represents a TPO mimetic peptide.
XX
XX

SQL Sequence 15 AA;

Query Match 67.3%; Score 66; DB 8; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.0013;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEGPLREWLTSRTP 16
1 IEGPLRQWLAAARP 15
DB

RESULT 22

ABP51687
ID ABP51687 standard; peptide; 18 AA.

AC ABP51687;

DT 01-OCT-2002 (first entry)

XX TPO mimetic peptide SEQ ID NO:37.

DE TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
KW complementarity determining region; immunoglobulin; antianaemic;
KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
XX
XX

OS Homo sapiens.

OS Synthetic.

PN WO200246238-A2.

PD 13-JUN-2002.

PF 05-DEC-2001; 2001WO-US047656.

PR 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

XX (ALEX-) ALEXION PHARM INC.

PA Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX WPI; 2002-566610/60.

DR N-PSDB; ABQ73365.

PT A novel immunogen molecule comprising a region in which amino acid
PT residues corresponding to at least a portion of the complementary
PT determining region are replaced or fused with an erythropoietin or
PT thrombopoietin mimetic.

XX Claim 20; Fig 5; 113pp; English.

PS The present invention describes an immunoglobulin molecule or its fragment
XX (I) comprising a region where amino acid residues corresponding to at
XX least a portion of the complementary determining region (CDR) are
XX replaced or fused with biologically active peptides e.g. a peptide
XX mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
XX that is flanked with proline at its carboxy terminus. (I) has
XX antianaemic, haemostatic and nephrotropic activities, and can be used as
XX a stimulator of proliferation, differentiation and maturation of
XX haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
XX for stimulating proliferation, differentiation or growth of
XX promegakaryocytes or megakaryocytes, where (I) is contacted with
XX promegakaryocytes or megakaryocytes, which results in increased platelet
XX production. (I) with a region where amino acid residues corresponding to
XX a portion of CDR is replaced with an EPO mimetic, or which has one or
XX more of its CDRs fused to an EPO mimetic, is useful for increasing the
XX production of red blood cells, where (I) is contacted with haematopoietic
XX stem cells or their progenitors. (I) is useful for diagnostics or

CC therapeutics, in cell isolation strategies, and for treating patients
CC suffering from deficiency in cell populations caused by disease,
CC disorders or treatments related to the suppression of haematopoiesis.
CC ABQ73288 to ABQ73377 and ABP51689 to ABP51696 represent sequences used in
CC the exemplification of the present invention
XX
XX

SQL Sequence 18 AA;

Query Match 67.3%; Score 66; DB 5; Length 18;
Best Local Similarity 73.3%; Pred. No. 0.0016;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEGPLREWLTSRTP 16
3 IEGPLRQWLAAARP 17
DB

RESULT 23

ABP51689
ID ABP51689 standard; peptide; 18 AA.

AC ABP51689;

DT 01-OCT-2002 (first entry)

XX TPO mimetic peptide SEQ ID NO:41.

DE TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
KW complementarity determining region; immunoglobulin; antianaemic;
KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
XX
XX

OS Homo sapiens.

OS Synthetic.

PN WO200246238-A2.

PD 13-JUN-2002.

PF 05-DEC-2001; 2001WO-US047656.

PR 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

XX (ALEX-) ALEXION PHARM INC.

PA Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX WPI; 2002-566610/60.

DR N-PSDB; ABQ73367.

PT A novel immunogen molecule comprising a region in which amino acid
PT residues corresponding to at least a portion of the complementary
PT determining region are replaced or fused with an erythropoietin or
PT thrombopoietin mimetic.

XX Claim 20; Fig 5; 113pp; English.

PS The present invention describes an immunoglobulin molecule or its fragment
XX (I) comprising a region where amino acid residues corresponding to at
XX least a portion of the complementary determining region (CDR) are
XX replaced or fused with biologically active peptides e.g. a peptide
XX mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
XX that is flanked with proline at its carboxy terminus. (I) has
XX antianaemic, haemostatic and nephrotropic activities, and can be used as
XX a stimulator of proliferation, differentiation and maturation of
XX haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
XX for stimulating proliferation, differentiation or growth of
XX promegakaryocytes or megakaryocytes, where (I) is contacted with
XX promegakaryocytes or megakaryocytes, which results in increased platelet
XX production. (I) with a region where amino acid residues corresponding to
XX a portion of CDR is replaced with an EPO mimetic, or which has one or
XX more of its CDRs fused to an EPO mimetic, is useful for increasing the

CC production of red blood cells, where (I) is contacted with haematopoietic
 CC stem cells or their progenitors. (I) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP51696 represent sequences used in
 CC the exemplification of the present invention

XX SQ Sequence 18 AA;

Query Match 67.3%; Score 66; DB 5; Length 18;
 Best Local Similarity 73.3%; Pred. No. 0.0016;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEQPTLRWLTGRTP 16
 |||||:|:|:
 Db 3 IEQPTLRQWLAARAP 17

RESULT 24

ABP51688 ID ABP51688 standard; peptide; 18 AA.

XX AC ABP51688;

XX DT 01-OCT-2002 (first entry)

XX DE TPO mimetic peptide SEQ ID NO:39.

XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 KW complementarity determining region; immunoglobulin; antianaemic;
 KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

OS Homo sapiens.
 OS Synthetic.

XX PN WO200246238-A2.

XX PD 13-JUN-2002.

XX PF 05-DEC-2001; 2001WO-US047656.

XX PR 05-DEC-2000; 2000US-0251448P.

XX PR 04-MAY-2001; 2001US-0288889P.

XX PR 29-MAY-2001; 2001US-0294068P.

XX PA (ALEX-) ALEXION PHARM INC.

XX PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX DR WPI; 2002-566610/60.

XX DR N-PSDB; ABQ73366.

XX PT A novel immunogen molecule comprising a region in which amino acid
 PT residues corresponding to at least a portion of the complementary
 PT determining region are replaced or fused with an erythropoietin or
 PT thrombopoietin mimetic.

XX PS Claim 20; Fig 5; 113pp; English.

XX The present invention describes an immunoglobulin molecule or its fragment
 CC (I) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (I) has
 CC antianaemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (I) is contacted with
 CC promegakaryocytes or megakaryocytes, which results in increased platelet
 CC production. (I) with a region where amino acid residues corresponding to

CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (I) is contacted with haematopoietic
 CC stem cells or their progenitors. (I) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP51696 represent sequences used in
 CC the exemplification of the present invention

XX SQ Sequence 18 AA;

Query Match 67.3%; Score 66; DB 5; Length 18;
 Best Local Similarity 73.3%; Pred. No. 0.0016;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEQPTLRWLTGRTP 16
 |||||:|:|:
 Db 3 IEQPTLRQWLAARAP 17

RESULT 25

ABP51686 ID ABP51686 standard; peptide; 18 AA.

XX AC ABP51686;

XX DT 01-OCT-2002 (first entry)

XX DE TPO mimetic peptide SEQ ID NO:35.

XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 KW complementarity determining region; immunoglobulin; antianaemic;
 KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

OS Homo sapiens.
 OS Synthetic.

XX PN WO200246238-A2.

XX PD 13-JUN-2002.

XX PF 05-DEC-2001; 2001WO-US047656.

XX PR 05-DEC-2000; 2000US-0251448P.

XX PR 04-MAY-2001; 2001US-0288889P.

XX PR 29-MAY-2001; 2001US-0294068P.

XX PA (ALEX-) ALEXION PHARM INC.

XX PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX DR WPI; 2002-566610/60.

XX DR N-PSDB; ABQ73364.

XX PT A novel immunogen molecule comprising a region in which amino acid
 PT residues corresponding to at least a portion of the complementary
 PT determining region are replaced or fused with an erythropoietin or
 PT thrombopoietin mimetic.

XX PS Claim 20; Fig 5; 113pp; English.

XX The present invention describes an immunoglobulin molecule or its fragment
 CC (I) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (I) has
 CC antianaemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (I) is contacted with

CC promegakaryocytes or megakaryocytes, which results in increased platelet
 CC production. (I) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (I) is contacted with haematopoietic
 CC stem cells or their progenitors. (I) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease.
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP5169 to ABP51696 represent sequences used in
 CC the exemplification of the present invention
 CC XX

SO Sequence 18 AA;

Query Match 67.3%; Score 66; DB 5; Length 18;
 Best Local Similarity 73.3%; Pred. No. 0.0016;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEGPTLRWLTSTRP 16
 |||||:|:|
 Db 3 IEGPTLRQWLARAP 17

RESULT 26

ABP51684
 ID ABP51684 standard; peptide; 18 AA.

AC ABP51684;

DT 01-OCT-2002 (first entry)

DE TPO mimetic peptide SEQ ID NO:31.

KW TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 KW complementarity determining region; immunoglobulin; antianaemic;
 KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

OS Homo sapiens.

OS Synthetic.

PN WO200246238-A2.

PD 13-JUN-2002.

PF 05-DEC-2001; 2001WO-US047656.

PR 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

PA (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

DR WPI; 2002-566610/60.

DR N-PSDB; ABQ73362.

PT A novel immunogen molecule comprising a region in which amino acid
 PT residues corresponding to at least a portion of the complementary
 PT determining region are replaced or fused with an erythropoietin or
 PT thrombopoietin mimetic.

PS Claim 20; Fig 5; 113pp; English.

CC The present invention describes an immunoglobulin molecule or its fragment
 CC (I) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (I) has
 CC antianaemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful

CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (I) is contacted with
 CC promegakaryocytes or megakaryocytes, which results in increased platelet
 CC production. (I) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (I) is contacted with haematopoietic
 CC stem cells or their progenitors. (I) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease.
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP5169 to ABP51696 represent sequences used in
 CC the exemplification of the present invention
 CC XX

SO Sequence 18 AA;

Query Match 67.3%; Score 66; DB 5; Length 18;
 Best Local Similarity 73.3%; Pred. No. 0.0016;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEGPTLRWLTSTRP 16
 |||||:|:|
 Db 3 IEGPTLRQWLARAP 17

RESULT 27

ABP51690
 ID ABP51690 standard; peptide; 18 AA.

AC ABP51690;

DT 01-OCT-2002 (first entry)

DE TPO mimetic peptide SEQ ID NO:43.

KW TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 KW complementarity determining region; immunoglobulin; antianaemic;
 KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

OS Homo sapiens.

OS Synthetic.

PN WO200246238-A2.

PD 13-JUN-2002.

PF 05-DEC-2001; 2001WO-US047656.

PR 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

PA (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

DR WPI; 2002-566610/60.

DR N-PSDB; ABQ73368.

PT A novel immunogen molecule comprising a region in which amino acid
 PT residues corresponding to at least a portion of the complementary
 PT determining region are replaced or fused with an erythropoietin or
 PT thrombopoietin mimetic.

PS Claim 20; Fig 5; 113pp; English.

CC The present invention describes an immunoglobulin molecule or its fragment
 CC (I) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (I) has
 CC antianaemic, haemostatic and nephrotropic activities, and can be used as

CC a stimulator of proliferation, differentiation and maturation of
CC haematopoietic cells; and a stimulator of haematopoiesis. (1) is useful
CC for stimulating proliferation, differentiation or growth of
CC promegakaryocytes or megakaryocytes, where (1) is contacted with
CC promegakaryocytes or megakaryocytes, which results in increased platelet
CC production. (1) with a region where amino acid residues corresponding to
CC a portion of CDR is replaced with an EPO mimetic, or which has one or
CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC production of red blood cells, where (1) is contacted with haematopoietic
CC stem cells or their progenitors. (1) is useful for diagnostics or
CC therapeutics, in cell isolation strategies, and for treating patients
CC suffering from deficiency in cell populations caused by disease,
CC disorders or treatments related to the suppression of haematopoiesis.
CC ABQ73288 to ABQ73377 and ABP5169 to ABP51696 represent sequences used in
CC the exemplification of the present invention

SQ Sequence 18 AA;

Query Match 67.3%; Score 66; DB 5; Length 18;
Best Local Similarity 73.3%; Pred. No. 0.0016; 2; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 2;

QY 2 IEGPTLRWLTSTPT 16
| | | | | : | : | |
Db 3 IEGPTLRWLTSTPT 17

RESULT 28

ID ABP51675
ABP51675 standard; peptide; 18 AA.

AC ABP51675;

DT 01-OCT-2002 (first entry)

DE TPO mimetic antibody related peptide graft SEQ ID NO:66.

KW TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;

KW complementarity determining region; immunoglobulin; antianaemic;

KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

OS Homo sapiens.

OS Synthetic.

PN WO200246238-A2.

PD 13-JUN-2002.

PF 05-DEC-2001; 2001WO-US047656.

PR 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX WPI; 2002-566610/60.

XX A novel immunogen molecule comprising a region in which amino acid

XX residues corresponding to at least a portion of the complementary

XX determining region are replaced or fused with an erythropoietin or

XX thrombopoietin mimetic.

XX Example 4; Page 55; 113pp; English.

XX The present invention describes an immunoglobulin molecule or its fragment

XX (1) comprising a region where amino acid residues corresponding to at

XX least a portion of the complementary determining region (CDR) are

XX replaced or fused with biologically active peptides e.g. a peptide

XX mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,

XX that is flanked with proline at its carboxy terminus. (1) has

CC antianaemic, haemostatic and nephrotropic activities, and can be used as
CC a stimulator of proliferation, differentiation and maturation of
CC haematopoietic cells; and a stimulator of haematopoiesis. (1) is useful
CC for stimulating proliferation, differentiation or growth of
CC promegakaryocytes or megakaryocytes, where (1) is contacted with
CC promegakaryocytes or megakaryocytes, which results in increased platelet
CC production. (1) with a region where amino acid residues corresponding to
CC a portion of CDR is replaced with an EPO mimetic, or which has one or
CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC production of red blood cells, where (1) is contacted with haematopoietic
CC stem cells or their progenitors. (1) is useful for diagnostics or
CC therapeutics, in cell isolation strategies, and for treating patients
CC suffering from deficiency in cell populations caused by disease,
CC disorders or treatments related to the suppression of haematopoiesis.
CC ABQ73288 to ABQ73377 and ABP5169 to ABP51696 represent sequences used in
CC the exemplification of the present invention

SQ Sequence 18 AA;

Query Match 67.3%; Score 66; DB 5; Length 18;
Best Local Similarity 73.3%; Pred. No. 0.0016; 2; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 2;

QY 2 IEGPTLRWLTSTPT 16
| | | | | : | : | |
Db 3 IEGPTLRWLTSTPT 17

RESULT 29

ID ADQ16611
ADQ16611 standard; peptide; 18 AA.

AC ADQ16611;

DT 09-SEP-2004 (first entry)

DE TPO mimetic peptide with random flanking residues SEQ ID NO:31.

KW immunoglobulin; complementarity determining region; CDR; peptide mimetic;

KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;

KW immunotherapy; thrombocytopenia.

OS Unidentified.

PN WO2004050017-A2.

PD 17-JUN-2004.

PF 17-NOV-2003; 2003WO-US036894.

PR 02-DEC-2002; 2002US-00307724.

PR (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Frederickson S, Renshaw M;

XX WPI; 2004-460973/43.

XX N-PSDB; ADQ16612.

XX New immunoglobulin molecule comprising a region, where two

XX complementary determining regions (CDRs) are replaced with EPO mimetic

XX or a TPO mimetic, useful for treating thrombocytopenia.

XX Example 1; SEQ ID NO 31; 107pp; English.

XX The invention relates to a novel immunoglobulin molecule or its fragment

XX comprising a region where amino acid residues corresponding to at least a

XX portion of a two complementarity determining regions (CDRs) are replaced

XX with a peptide mimetic selected from an erythropoietin (EPO) mimetic and

XX a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the

XX invention has immunosuppressive activity, and may have a use in

XX immunotherapy. The immunoglobulin molecule is useful for diagnosing or

XX treating thrombocytopenia as a result of chemotherapy, bone marrow

CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide with flanking
 CC residues.

XX Sequence 18 AA;

Query Match 67.3%; Score 66; DB 8; Length 18;
 Best Local Similarity 73.3%; Pred. No. 0.0016;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEGPTLRWLTSTRP 16
 |||||:|:|
 Db 3 IEGPTLRQWLAARAP 17

RESULT 30

ADQ16619
 ID ADQ16619 standard; peptide; 18 AA.

XX ADQ16619;

XX 09-SEP-2004 (first entry)

DE TPO mimetic peptide with random flanking residues SEQ ID NO:39.

XX immunoglobulin; complementarity determining region; CDR; peptide mimetic;

KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;

XX immunotherapy; thrombocytopenia.

XX Unidentified.

XX WO2004050017-A2.

XX 17-JUN-2004.

XX 17-NOV-2003; 2003WO-US036894.

XX 02-DEC-2002; 2002US-00307724.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Frederickson S, Renshaw M;

XX WPI; 2004-460973/43.

XX N-PSDB; ADQ16620.

XX New immunoglobulin molecule comprising a region, where two

XX complementarity determining regions (CDRs) are replaced with EPO mimetic

XX or a TPO mimetic, useful for treating thrombocytopenia.

XX Example 1; SEQ ID NO 39; 107pp; English.

XX The invention relates to a novel immunoglobulin molecule or its fragment

XX comprising a region where amino acid residues corresponding to at least a

XX portion of a two complementarity determining regions (CDRs) are replaced

XX with a peptide mimetic selected from an erythropoietin (EPO) mimetic and

XX a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the

XX invention has immunosuppressive activity, and may have a use in

XX immunotherapy. The immunoglobulin molecule is useful for diagnosing or

XX treating thrombocytopenia as a result of chemotherapy, bone marrow

XX transplantation, or chronic diseases such as idiopathic thrombocytopenia.

XX The present sequence represents a TPO mimetic peptide with flanking

RESULT 31
 ADQ16621
 ID ADQ16621 standard; peptide; 18 AA.

XX ADQ16621;

XX 09-SEP-2004 (first entry)

DE TPO mimetic peptide with random flanking residues SEQ ID NO:41.

XX immunoglobulin; complementarity determining region; CDR; peptide mimetic;

KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;

XX immunotherapy; thrombocytopenia.

XX Unidentified.

XX WO2004050017-A2.

XX 17-JUN-2004.

XX 17-NOV-2003; 2003WO-US036894.

XX 02-DEC-2002; 2002US-00307724.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Frederickson S, Renshaw M;

XX WPI; 2004-460973/43.

XX N-PSDB; ADQ16622.

XX New immunoglobulin molecule comprising a region, where two

XX complementarity determining regions (CDRs) are replaced with EPO mimetic

XX or a TPO mimetic, useful for treating thrombocytopenia.

XX Example 1; SEQ ID NO 41; 107pp; English.

XX The invention relates to a novel immunoglobulin molecule or its fragment

XX comprising a region where amino acid residues corresponding to at least a

XX portion of a two complementarity determining regions (CDRs) are replaced

XX with a peptide mimetic selected from an erythropoietin (EPO) mimetic and

XX a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the

XX invention has immunosuppressive activity, and may have a use in

XX immunotherapy. The immunoglobulin molecule is useful for diagnosing or

XX treating thrombocytopenia as a result of chemotherapy, bone marrow

XX transplantation, or chronic diseases such as idiopathic thrombocytopenia.

XX The present sequence represents a TPO mimetic peptide with flanking

XX residues.

XX Sequence 18 AA;

Query Match 67.3%; Score 66; DB 8; Length 18;

Best Local Similarity 73.3%; Pred. No. 0.0016;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEGPTLRWLTSTRP 16

|||||:|:|

Db 3 IEGPTLRQWLAARAP 17

|||||:|:|

IMMUNOGLOBULIN; COMPLEMENTARITY DETERMINING REGION; CDR; PEPTIDE MIMETIC;

KM erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 KW immunotherapy; thrombocytopenia.
 XX Unidentified.
 XX WO2004050017-A2.
 PN 17-JUN-2004.
 PD 17-JUN-2004.
 XX 17-NOV-2003; 2003WO-US036894.
 PF 02-DEC-2002; 2002US-00307724.
 PR (ALEX-) ALEXION PHARM INC.
 PA Bowdish KS, Frederickson S, Renshaw M;
 PI WPI; 2004-460973/43.
 DR N-PSDB; ADQ16645.
 XX New immunoglobulin molecule comprising a region, where two
 PT complementarity determining regions (CDRs) are replaced with EPO mimetic
 PT or a TPO mimetic, useful for treating thrombocytopenia.
 XX Example 4; SEQ ID NO 66; 107pp; English.
 PS
 XX The invention relates to a novel immunoglobulin molecule or its fragment
 CC comprising a region where amino acid residues corresponding to at least a
 CC portion of a two complementarity determining regions (CDRs) are replaced
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 CC invention has immunosuppressive activity, and may have a use in
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow
 CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide of the invention.
 XX Sequence 18 AA;
 SQ
 XX
 XX Query Match 67.3%; Score 66; DB 8; Length 18;
 XX Best Local Similarity 73.3%; Pred. No. 0.0016;
 XX Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 IEGPTLRQWLTSRTP 16
 DB 3 IEGPTLRQWLTSRTP 16
 DE TPO mimetic peptide with random flanking residues SEQ ID NO:35.
 KW immunoglobulin; complementarity determining region; CDR; peptide mimetic;
 KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 KW immunotherapy; thrombocytopenia.
 XX Unidentified.
 OS
 XX WO2004050017-A2.
 PN 17-JUN-2004.
 PD 17-JUN-2004.
 PF 17-NOV-2003; 2003WO-US036894.
 PR 02-DEC-2002; 2002US-00307724.
 PS (ALEX-) ALEXION PHARM INC.
 PA

XX Bowdish KS, Frederickson S, Renshaw M;
 PI WPI; 2004-460973/43.
 DR N-PSDB; ADQ16616.
 XX New immunoglobulin molecule comprising a region, where two
 PT complementarity determining regions (CDRs) are replaced with EPO mimetic
 PT or a TPO mimetic, useful for treating thrombocytopenia.
 XX Example 1; SEQ ID NO 35; 107pp; English.
 PS
 XX The invention relates to a novel immunoglobulin molecule or its fragment
 CC comprising a region where amino acid residues corresponding to at least a
 CC portion of a two complementarity determining regions (CDRs) are replaced
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 CC invention has immunosuppressive activity, and may have a use in
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow
 CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide with flanking
 CC residues.
 XX Sequence 18 AA;
 SQ
 XX
 XX Query Match 67.3%; Score 66; DB 8; Length 18;
 XX Best Local Similarity 73.3%; Pred. No. 0.0016;
 XX Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 IEGPTLRQWLTSRTP 16
 DB 3 IEGPTLRQWLTSRTP 16
 DE TPO mimetic peptide with random flanking residues SEQ ID NO:37.
 KW immunoglobulin; complementarity determining region; CDR; peptide mimetic;
 KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 KW immunotherapy; thrombocytopenia.
 XX Unidentified.
 OS
 XX WO2004050017-A2.
 PN 17-JUN-2004.
 PD 17-JUN-2004.
 PF 17-NOV-2003; 2003WO-US036894.
 PR 02-DEC-2002; 2002US-00307724.
 PS (ALEX-) ALEXION PHARM INC.
 PA Bowdish KS, Frederickson S, Renshaw M;
 PI WPI; 2004-460973/43.
 DR N-PSDB; ADQ16618.
 XX New immunoglobulin molecule comprising a region, where two
 PT complementarity determining regions (CDRs) are replaced with EPO mimetic
 PT or a TPO mimetic, useful for treating thrombocytopenia.
 XX Example 1; SEQ ID NO 37; 107pp; English.
 PS
 XX The invention relates to a novel immunoglobulin molecule or its fragment

CC comprising a region where amino acid residues corresponding to at least a
CC portion of a two complementarity determining regions (CDRs) are replaced
CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC invention has immunosuppressive activity, and may have a use in
CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC treating thrombocytopenia as a result of chemotherapy, bone marrow
CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC The present sequence represents a TPO mimetic peptide with flanking
CC residues.
CC
XX
SQ Sequence 18 AA;

Query Match 67.3%; Score 66; DB 8; Length 18;
Best Local Similarity 73.3%; Pred. No. 0.0016;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEGPTLRWLTSTRTP 16
|||||:|:|
Db 3 IEGPTLRQWLARAP 17

RESULT 35

ADQ16623
ID ADQ16623 standard; peptide; 18 AA.

AC ADQ16623;

DT 09-SEP-2004 (first entry)

DE TPO mimetic peptide with random flanking residues SEQ ID NO:43.

KW immunoglobulin; complementarity determining region; CDR; peptide mimetic;
KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
KW immunotherapy; thrombocytopenia.

OS Unidentified.

PN WO2004050017-A2.

PD 17-JUN-2004.

PF 17-NOV-2003; 2003WO-US036894.

PR 02-DEC-2002; 2002US-00307724.

PA (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Frederickson S, Renshaw M;

DR WPI; 2004-460973/43.

DR N-PSDB; ADQ16624.

PT New immunoglobulin molecule comprising a region, where two
PT complementarity determining regions (CDRs) are replaced with EPO mimetic
PT or a TPO mimetic, useful for treating thrombocytopenia.
XX
PS Example 1; SEQ ID NO 43; 107bp; English.

CC The invention relates to a novel immunoglobulin molecule or its fragment
CC comprising a region where amino acid residues corresponding to at least a
CC portion of a two complementarity determining regions (CDRs) are replaced
CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC invention has immunosuppressive activity, and may have a use in
CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC treating thrombocytopenia as a result of chemotherapy, bone marrow
CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC The present sequence represents a TPO mimetic peptide with flanking
CC residues.
CC
XX
SQ Sequence 18 AA;

Query Match 67.3%; Score 66; DB 8; Length 18;
Best Local Similarity 73.3%; Pred. No. 0.0016;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEGPTLRWLTSTRTP 16
|||||:|:|
Db 3 IEGPTLRQWLARAP 17

RESULT 36

ADQ16708
ID ADQ16708 standard; protein; 22 AA.

AC ADQ16708;

DT 09-SEP-2004 (first entry)

DE Immunoglobulin heavy chain CDR2 with TPO clone HR2-20 SEQ ID NO:128.

KW immunoglobulin; complementarity determining region; CDR; peptide mimetic;
KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
KW immunotherapy; thrombocytopenia.

OS Synthetic.

PN WO2004050017-A2.

PD 17-JUN-2004.

PF 17-NOV-2003; 2003WO-US036894.

PR 02-DEC-2002; 2002US-00307724.

PA (ALEX-) ALEXION PHARM INC.

PI Bowdish KS, Frederickson S, Renshaw M;

DR WPI; 2004-460973/43.

PT New immunoglobulin molecule comprising a region, where two
PT complementarity determining regions (CDRs) are replaced with EPO mimetic
PT or a TPO mimetic, useful for treating thrombocytopenia.
XX
PS Example 9; SEQ ID NO 128; 107bp; English.

CC The invention relates to a novel immunoglobulin molecule or its fragment
CC comprising a region where amino acid residues corresponding to at least a
CC portion of a two complementarity determining regions (CDRs) are replaced
CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC invention has immunosuppressive activity, and may have a use in
CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC treating thrombocytopenia as a result of chemotherapy, bone marrow
CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC The present sequence represents an immunoglobulin heavy chain CDR2 with
CC TPO peptide inserted.
XX
SQ Sequence 22 AA;

Query Match 67.3%; Score 66; DB 8; Length 22;
Best Local Similarity 68.8%; Pred. No. 0.0021;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEGPTLRWLTSTRTP 17
|||||:|:|
Db 6 IEGPTLRQWLARAP 21

RESULT 37

ADQ16710
ID ADQ16710 standard; protein; 22 AA.

AC ADQ16710;


```
XX 09-SEP-2004 (first entry)
DT Immunoglobulin heavy chain CDR2 with TPO clone HR2-28 SEQ ID NO:130.
DE immunoglobulin; complementarity determining region; CDR; peptide mimetic;
XX erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
XX immunotherapy; thrombocytopenia.
OS Synthetic.
XX WO2004050017-A2.
XX 17-JUN-2004.
XX 17-NOV-2003; 2003WO-US036894.
XX 02-DEC-2002; 2002US-00307724.
XX (ALEX-) ALEXION PHARM INC.
XX Bowdish KS, Frederickson S, Renshaw M;
XX WPI; 2004-460973/43.
XX New immunoglobulin molecule comprising a region, where two
PT complementarity determining regions (CDRs) are replaced with EPO mimetic
PT or a TPO mimetic, useful for treating thrombocytopenia.
XX Example 9; SEQ ID NO 130; 107pp; English.
XX The invention relates to a novel immunoglobulin molecule or its fragment
CC comprising a region where amino acid residues corresponding to at least a
CC portion of a two complementarity determining regions (CDRs) are replaced
CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC invention has immunosuppressive activity, and may have a use in
CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC treating thrombocytopenia as a result of chemotherapy, bone marrow
CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC The present sequence represents an immunoglobulin heavy chain CDR2 with
CC TPO peptide inserted.
XX
SQ Sequence 22 AA;
Query Match 67.3%; Score 66; DB 8; Length 22;
Best Local Similarity 73.3%; Pred. No. 0.0021;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 IEGPTLRWLTSTRTP 16
| | | | | | | | | | | |
| | | | | | | | | | | |
Db 6 IEGPTLRQWLARAP 20
| | | | | | | | | | | |
| | | | | | | | | | | |
RESULT 38
ADQ16705
ID ADQ16705 standard; protein; 128 AA.
XX
AC ADQ16705;
XX
DE 09-SEP-2004 (first entry)
XX
DE Modified immunoglobulin clone 116 HC variable region SEQ ID NO:125.
XX immunoglobulin; complementarity determining region; CDR; peptide mimetic;
XX erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
XX immunotherapy; thrombocytopenia.
XX Synthetic.
XX WO2004050017-A2.
XX
XX 17-JUN-2004.
```

```
XX 17-NOV-2003; 2003WO-US036894.
XX
XX 02-DEC-2002; 2002US-00307724.
XX (ALEX-) ALEXION PHARM INC.
XX Bowdish KS, Frederickson S, Renshaw M;
XX WPI; 2004-460973/43.
XX New immunoglobulin molecule comprising a region, where two
PT complementarity determining regions (CDRs) are replaced with EPO mimetic
PT or a TPO mimetic, useful for treating thrombocytopenia.
XX Claim 9; SEQ ID NO 125; 107pp; English.
XX
XX The invention relates to a novel immunoglobulin molecule or its fragment
CC comprising a region where amino acid residues corresponding to at least a
CC portion of a two complementarity determining regions (CDRs) are replaced
CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
CC invention has immunosuppressive activity, and may have a use in
CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
CC treating thrombocytopenia as a result of chemotherapy, bone marrow
CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
CC The present sequence represents immunoglobulin clone 116 heavy chain
CC variable region.
XX
SQ Sequence 128 AA;
Query Match 67.3%; Score 66; DB 8; Length 128;
Best Local Similarity 73.3%; Pred. No. 0.015;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 IEGPTLRWLTSTRTP 16
| | | | | | | | | | | |
| | | | | | | | | | | |
Db 102 IEGPTLRQWLARAP 116
| | | | | | | | | | | |
| | | | | | | | | | | |
RESULT 39
ADQ16704
ID ADQ16704 standard; protein; 225 AA.
XX
AC ADQ16704;
XX
DE 09-SEP-2004 (first entry)
XX
DE Modified immunoglobulin clone 116 heavy chain SEQ ID NO:124.
XX immunoglobulin; complementarity determining region; CDR; peptide mimetic;
XX erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
XX immunotherapy; thrombocytopenia.
XX Synthetic.
XX WO2004050017-A2.
XX
XX 17-JUN-2004.
XX 17-NOV-2003; 2003WO-US036894.
XX 02-DEC-2002; 2002US-00307724.
XX (ALEX-) ALEXION PHARM INC.
XX Bowdish KS, Frederickson S, Renshaw M;
XX WPI; 2004-460973/43.
XX New immunoglobulin molecule comprising a region, where two
PT complementarity determining regions (CDRs) are replaced with EPO mimetic
PT or a TPO mimetic, useful for treating thrombocytopenia.
```

XX Example 8; SEQ ID NO 124; 107pp; English.

PS The invention relates to a novel immunoglobulin molecule or its fragment

XX comprising a region where amino acid residues corresponding to at least a

CC portion of a two complementarity determining regions (CDRs) are replaced

CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and

CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the

CC invention has immunosuppressive activity, and may have a use in

CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or

CC treating thrombocytopenia as a result of chemotherapy, bone marrow

CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.

CC The present sequence represents immunoglobulin clone 116 heavy chain.

XX Sequence 225 AA;

SO

Query Match 67.3%; Score 66; DB 8; Length 225;

Best Local Similarity 73.3%; Pred. No. 0.028;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEGPLREWLTSRTP 16

DB 102 IEGPLRQWLAAAP 116

RESULT 40

ABP51695

ID ABP51695 standard; protein; 472 AA.

XX

AC ABP51695;

XX

DT 01-OCT-2002 (first entry)

XX

DE 5G1.1-TPO heavy chain amino acid sequence SEQ ID NO:67.

XX

KW TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;

KM complementarity determining region; immunoglobulin; antianaemic;

XX haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

OS Homo sapiens.

OS Synthetic.

XX

PN WO200246238-A2.

XX

PD 13-JUN-2002.

XX

PF 05-DEC-2001; 2001WO-US047656.

XX

PR 05-DEC-2000; 2000US-0251448P.

XX

PR 04-MAY-2001; 2001US-0288889P.

XX

PR 29-MAY-2001; 2001US-0294068P.

XX

PA (ALEX-) ALEXION PHARM INC.

XX

PI Bowdish KS, Barbas-Frederickson S, Renshaw M;

XX

DR WPI; 2002-566610/60.

XX

DR N-PSDB; ABQ73374.

XX

PT A novel immunogen molecule comprising a region in which amino acid

PT residues corresponding to at least a portion of the complementary

PT determining region are replaced or fused with an erythropoietin or

PT thrombopoietin mimetic.

XX

XX Example 4; Fig 13A; 113pp; English.

XX

CC The present invention describes an immunoglobulin molecule or its fragment

CC (I) comprising a region where amino acid residues corresponding to at

CC least a portion of the complementary determining region (CDR) are

CC replaced or fused with biologically active peptides e.g. a peptide

CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,

CC that is flanked with proline at its carboxy terminus. (I) has

CC antianaemic, haemostatic and nephrotropic activities, and can be used as

CC a stimulator of proliferation, differentiation and maturation of

CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful

CC for stimulating proliferation, differentiation or growth of

CC promegakaryocytes or megakaryocytes, where (II) is contacted with

CC promegakaryocytes or megakaryocytes, which results in increased platelet

CC production. (I) with a region where amino acid residues corresponding to

CC a portion of CDR is replaced with an EPO mimetic, or which has one or

CC more of its CDRs fused to an EPO mimetic, is useful for increasing the

CC production of red blood cells, where (I) is contacted with haematopoietic

CC stem cells or their progenitors. (I) is useful for diagnostics or

CC therapeutics, in cell isolation strategies, and for treating patients

CC suffering from deficiency in cell populations caused by disease,

CC disorders or treatments related to the suppression of haematopoiesis.

CC ABQ73288 to ABQ73377 and ABP51695 to ABP51696 represent sequences used in

CC the exemplification of the present invention

XX

SO Sequence 472 AA;

Query Match 67.3%; Score 66; DB 5; Length 472;

Best Local Similarity 73.3%; Pred. No. 0.063;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IEGPLREWLTSRTP 16

DB 120 IEGPLRQWLAAAP 134

RESULT 41

ADQ16647

ID ADQ16647 standard; protein; 472 AA.

XX

AC ADQ16647;

XX

DT 09-SEP-2004 (first entry)

XX

DE Immunoglobulin antibody 5G1.1-TPO heavy chain SEQ ID NO:67.

XX

KW immunoglobulin; complementarity determining region; CDR; peptide mimetic;

KM erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;

XX immunotherapy; thrombocytopenia.

XX

OS Synthetic.

OS

XX

PN WO2004050017-A2.

XX

PD 17-JUN-2004.

XX

PF 17-NOV-2003; 2003WO-US036894.

XX

PR 02-DEC-2002; 2002US-00307724.

XX

XX (ALEX-) ALEXION PHARM INC.

XX

PI Bowdish KS, Frederickson S, Renshaw M;

XX

DR WPI; 2004-460973/43.

XX

DR N-PSDB; ADQ16648.

XX

PT New immunoglobulin molecule comprising a region, where two

PT complementarity determining regions (CDRs) are replaced with EPO mimetic

PT or a TPO mimetic, useful for treating thrombocytopenia.

XX

XX Example 4; SEQ ID NO 67; 107pp; English.

XX

CC The invention relates to a novel immunoglobulin molecule or its fragment

CC comprising a region where amino acid residues corresponding to at least a

CC portion of a two complementarity determining regions (CDRs) are replaced

CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and

CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the

CC invention has immunosuppressive activity, and may have a use in

CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or

CC treating thrombocytopenia as a result of chemotherapy, bone marrow

CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.

CC The present sequence represents an immunoglobulin antibody heavy chain of
 CC the invention.
 XX
 SQ Sequence 472 AA;
 Query Match 67.3%; Score 66; DB 8; Length 472;
 Best Local Similarity 73.3%; Pred. No. 0.063;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 IEGPTLRWLTSTRTP 16
 DB 120 IEGPTLRQWLAARAP 134
 RESULT 42
 AAB16969
 ID AAB16969 standard; peptide; 14 AA.
 AC AAB16969;
 NC
 DE 31-OCT-2000 (first entry)
 DT
 XX TPO-mimetic peptide sequence SEQ ID NO:25.
 DE Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antineoplastic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.
 OS Synthetic.
 XX
 OS
 PN MO200024782-A2.
 PD
 XX 04-MAY-2000.
 PD
 XX 25-OCT-1999; 99MO-US025044.
 PF
 XX 23-OCT-1998; 98US-0105371P.
 PR 22-OCT-1999; 99US-00428082.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 PI Peige U, Liu C, Cheatham J, Boone TC;
 PI WPI; 2000-350702/30.
 DR
 XX Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 PT
 XX
 PS Claim 19; Page 203; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)-e-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)-c-P1, -(L1)-c-P1-(L2)-d-P2, -(L1)-c-P1-
 CC (L2)-d-P2-(L3)-e-P3, or -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antineoplastic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions,
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAB69443 to AAB69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX

SQ Sequence 14 AA;
 Query Match 63.3%; Score 62; DB 3; Length 14;
 Best Local Similarity 84.6%; Pred. No. 0.0055;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 IEGPTLRWLTSTR 14
 DB 1 IEGPTLRWLAAR 13
 RESULT 43
 ABB72855
 ID ABB72855 standard; peptide; 14 AA.
 AC ABB72855;
 NC
 DE 05-APR-2002 (first entry)
 DT
 XX TPO mimetic peptide SEQ ID NO:25.
 DE Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IGG; EPO;
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antineoplastic; antitumour; immunosuppressive;
 KW cytostatic; antineoplastic; antineoplastic; antidiabetic; ophthalmological;
 KW antineoplastic; anorectic; antineoplastic; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO2001B3525-A2.
 PD
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US014310.
 PF
 XX 03-MAY-2000; 2000US-00563286.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 PI Peige U, Liu C, Cheatham JC, Boone TC, Gudae JM;
 PI WPI; 2002-130313/17.
 DR
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 PT
 XX
 PS Claim 39; Page 43; 176pp; English.
 XX
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antineoplastic, antineoplastic, antidiabetic, ophthalmological,
 CC antineoplastic, anorectic, antineoplastic, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC

CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopenia, aplastic anemia, metastatic
CC tumor which result in thrombocytopenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABB35695 to ABB35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention

XX Sequence 14 AA;

Query Match 63.3%; Score 62; DB 5; Length 14;
Best Local Similarity 84.6%; Pred. No. 0.0055;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 IEQPTLRWLTSR 14
| | | | | | | | | | : |
Db 1 IEQPTLRWLAAR 13

RESULT 44

ID ADJ73005 standard; peptide; 14 AA.

AC ADJ73005;

DT 06-MAY-2004 (first entry)

DE TPO mimetic peptide sequence SegID 459.

XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;

KW cardiovascular; infectious; malignant; neurologic disease; anaemia;

KM immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;

KX TPO.

OS Synthetic.

PN WO2003084477-A2.

PD 16-OCT-2003.

PF 24-MAR-2003; 2003WO-US009139.

PR 29-MAR-2002; 2002US-0368791P.

PA (CENZ) CENTOCOR INC.

PI Heavner GA, Knight DM, Scallion BJ, Ghayeb J;

DR WPI; 2003-804237/75.

PT New CDR mimetibody comprising a portion of a heavy or light chain
PT variable region comprising human framework or ligand binding region,
PT useful for preparing a composition for treating e.g., immune,
PT cardiovascular or neurologic disease.

PS Disclosure; SEQ ID NO 459; 97pp; English.

XX This invention relates to novel mammalian CDR mimetibodies, specific
CC portions or variants thereof. Specifically, it refers to an antibody
CC fragment where a protein has been inserted into, or replaces a portion
CC of, one or more CDR regions, such that each CDR mimetibody comprises at
CC least one portion of a heavy chain or light chain variable region, which
CC itself comprises at least one human framework region and at least one
CC ligand binding region (LBR). The present invention describes human
CC mimetibodies, including modified immunoglobulins and cleavage products
CC that can be useful in gene therapy and the generation of transgenic
CC plants and animals. Furthermore, the CDR mimetibody is useful for
CC preparing compositions for modulating, treating or reducing the symptoms
CC of immune, cardiovascular, infectious, malignant and/or neurologic
CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC peptide sequence is a TPO mimetic peptide sequence used to make a
CC mimetibody of the invention.

SQ Sequence 14 AA;

Query Match 63.3%; Score 62; DB 7; Length 14;
Best Local Similarity 84.6%; Pred. No. 0.0055;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 IEQPTLRWLTSR 14
| | | | | | | | | | : |
Db 1 IEQPTLRWLAAR 13

RESULT 45
ADJ52640
ID ADJ52640 standard; peptide; 14 AA.

AC ADJ52640;

DT 06-MAY-2004 (first entry)

DE CHI deleted mimetibody-related peptide SegID459.

XX CHI deleted mimetibody; immunosuppressive; cardiovascular; cardiant;

KW hypotensive; neuroprotective; nootropic; antibacterial; virucide;

KM fungicide; gene therapy; immune disorder; cardiovascular disease;

KW arrhythmia; hypertension; heart failure; neurodegenerative;

KM multiple sclerosis; dementia; Alzheimer's disease; anaemia;

KW cancerous condition; infectious disease; bacterial infection;

OS Unidentified.

PN WO2004002417-A2.

PD 08-JAN-2004.

PF 27-JUN-2003; 2003WO-US020347.

PR 28-JUN-2002; 2002US-0392431P.

PA (CENZ) CENTOCOR INC.

PI Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Neseppor TC;

DR Kulooski KA;

XX WPI; 2004-082870/08.

PT New CHI-deleted mimetibody polypeptides and nucleic acids, useful for
PT modulating, treating, alleviating, preventing an immune, cardiovascular,
PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
PT diseases.

PS Claim 2; SEQ ID NO 459; 129pp; English.

XX This invention relates to CHI deleted mimetibodies (and the DNA sequences
CC which encode them), compositions, methods and uses. The invention may be
CC useful for the development of compounds with an immunosuppressive,
CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
CC antibacterial, virucide or fungicide activity. In addition, the disclosed
CC sequences may prove useful for gene therapy. The CHI-deleted mimetibody
CC is useful for diagnosing or treating a disease condition in a cell,
CC tissue, organ or animal, specifically for modulating, treating,
CC alleviating, preventing the incidence or reducing the symptoms of an
CC immune, cardiovascular (for example arrhythmia, hypertension or heart
CC failure), or neurodegenerative (for example multiple sclerosis, dementia
CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
CC conditions, or infectious diseases (for example bacterial, viral or
CC fungal infection). The present sequence is that of a peptide which may be
CC used during the creation of a mimetibody of the invention.

XX Sequence 14 AA;

Query Match 63.3%; Score 62; DB 8; Length 14;

	Best Local Similarity	84.6%	Pred. No.	0.0055;						
	Matches	11;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
Oy	2	IEGPTLRWMLTSR	14		:					
Db	1	IEGPTLRWMLAAR	13							

Search completed: September 1, 2005, 16:12:12
Job time : 82.7482 secs

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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:57:33 ; Search time 13.7266 Seconds
(without alignments)
126.171 Million cell updates/sec

Title: US-10-083-768-10

Perfect score: 98
Sequence: 1 SIEGPTLRWLTSTRTPHS 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 79:***
1: p1r1:***
2: p1r2:***
3: p1r3:***
4: p1r4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	52.0	753	1	D72660
2	48.5	49.5	410	1	DEPSXA
3	48.5	49.5	410	2	C83365
4	48	49.0	150	2	C75456
5	48	49.0	664	2	G89894
6	47	48.0	154	2	F64026
7	47	48.0	430	1	B69659
8	46.5	47.4	330	2	C69593
9	46.5	47.4	527	2	B64633
10	46	46.9	664	2	H83962
11	46	46.9	1028	2	A59253
12	45.5	46.4	331	2	AD1246
13	45.5	46.4	331	2	AH1608
14	45	45.9	132	1	S15618
15	45	45.9	473	2	B84853
16	45	45.9	886	2	S22383
17	45	45.9	1036	2	S22383
18	44.5	45.9	2354	2	T13288
19	44	44.9	200	2	T23485
20	44	44.9	207	2	T37464
21	44	44.9	310	2	C90277
22	44	44.9	400	2	C87021
23	43.5	44.4	327	2	B82277
24	43	43.9	347	2	T06371
25	43	43.9	399	1	B70936
26	43	43.9	491	2	C98275
27	43	43.9	491	2	AC3009
28	43	43.9	514	2	T44502
29	43	43.9	648	1	H69878

30	43	43.9	1094	2	F70697
31	43	43.9	2896	2	T30939
32	42.5	43.4	371	1	DEBSPA
33	42.5	43.4	436	2	JC4742
34	42.5	43.4	586	2	B84271
35	42	42.9	236	2	AH1884
36	42	42.9	305	2	G87394
37	42	42.9	263	2	D70601
38	42	42.9	310	2	JL0119
39	42	42.9	317	2	JL0118
40	42	42.9	323	2	S06946
41	42	42.9	430	2	B82096
42	42	42.9	448	2	B45438
43	42	42.9	564	2	T37934
44	42	42.9	721	2	A39707
45	42	42.9	807	2	H75634
46	42	42.9	970	2	A72028
47	42	42.9	970	2	G86595
48	42	42.9	1028	2	S41749
49	42	42.9	1028	2	S37146
50	41.5	42.3	125	1	A46315
51	41.5	42.3	330	2	C83995
52	41.5	42.3	4006	2	T09070
53	41	41.8	109	2	S69853
54	41	41.8	285	2	AC1537
55	41	41.8	306	2	T45453
56	41	41.8	336	2	S41643
57	41	41.8	346	2	B84377
58	41	41.8	346	2	B90073
59	41	41.8	389	2	B69096
60	41	41.8	410	2	G90362
61	41	41.8	413	2	AI0598
62	41	41.8	482	2	D75346
63	41	41.8	521	2	T01923
64	41	41.8	754	2	D88734
65	41	41.8	897	2	B69202
66	41	41.8	1019	2	T11560
67	41	41.8	1040	2	T08190
68	41	41.8	1123	2	T51517
69	41	41.8	1172	2	AD2310
70	41	41.8	1299	2	AH2090
71	40.5	41.3	255	2	A45881
72	40.5	41.3	371	2	AD1206
73	40.5	41.3	371	2	AC1563
74	40.5	41.3	446	1	IOB80C
75	40.5	41.3	1420	2	A32869
76	40.5	41.3	2476	2	T34022
77	40	40.8	195	2	B56688
78	40	40.8	195	2	A85481
79	40	40.8	195	2	A90630
80	40	40.8	195	2	AE0057
81	40	40.8	220	2	AC0318
82	40	40.8	251	2	T14548
83	40	40.8	251	2	F95295
84	40	40.8	279	2	G83041
85	40	40.8	289	2	J00059
86	40	40.8	312	2	F86876
87	40	40.8	327	2	B71900
88	40	40.8	331	2	B48445
89	40	40.8	337	1	DEJUGC
90	40	40.8	338	2	T47218
91	40	40.8	378	2	D83381
92	40	40.8	413	2	H75357
93	40	40.8	466	2	B86411
94	40	40.8	492	2	C84142
95	40	40.8	524	2	E71881
96	40	40.8	561	2	C75543
97	40	40.8	694	2	A96571
98	40	40.8	719	2	B95325
99	40	40.8	722	2	T37970
100	40	40.8	749	2	H82691

probable arabinosy
hemocyanin G-type
pyruvate dehydroge
transposase - Cory
glutamy1-ERNA synt
hypothetical prote
hypothetical prote
UTP-glucose-1-phos
Fc gamma (1Gg) rec
Fc gamma (1Gg) rec
Fc gamma (1Gg) rec
Fc gamma (1Gg) rec
conserved hypotet
erythrocyte membra
myosin-1C - mouse
preprotein translo
protein translocas
myosin heavy chain
myosin I heavy cha
E4 protein - human
branched-chain alp
probable tenascin
hypothetical prote
hypothetical prote
UTP-glucose-1-phos
syrm protein - Rhl
protein export [im
hypothetical prote
cortinoid/iron-sul
hypothetical prote
probable phosphol
glucamyl-ERNA (Gln)
hypothetical prote
protein F32P10.1 l
valine-ERNA ligase
pol polyprotein -
hypothetical prote
telomerase reverse
hypothetical prote
two-component hybr
MHC class II histo
pyruvate dehydroge
pyruvate dehydroge
replication initia
apolipoprotein(a)
zonahesin - pig
molybdopterin bios
molybdopterin bios
molybdopterin bio
molybdopterin bios
probable nicotinat
beta-fructofuranos
glucanate 5-dehydr
probable N-hydroxy
hypothetical 31.6K
hypothetical prote
hypothetical prote
glyceraldhyde-3-P
glyceraldhyde-3-P
hypothetical prote
tRNA (5-methylamin
protein P3M18.4 [i
hypothetical prote
hypothetical prote
6-aminohexanoate-c
hypothetical prote
conserved hypotet
probable G2-specif
topoisomerase IV B

C/Species: *Staphylococcus aureus*
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C/Accession: G89894
 R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A/Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A/Reference number: A89758; MUID:21311952; PMID:11418146
 A/Accession: G89894
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-664 <KIR>
 A/Cross-references: UNIPROT:Q99UP8; GB:BA000018; PID:913701020; PIDN:BA042315.1; GSRDB:G
 A/Experimental source: strain N315
 C/Genetics:
 A/Gene: SA1063

Query Match 49.0%; Score 48; DB 2; Length 664;
 Best Local Similarity 58.8%; Pred. No. 12;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 IEQPTLRWLTSTRPHS 18
 Db 90 IEQPTLRWLTSTRPHS 106

RESULT 6
 F64026
 hypothetical protein H11355 - *Haemophilus influenzae* (strain Rd KW20)
 C/Species: *Haemophilus influenzae*
 C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
 C/Accession: F64026
 R./Geyrhofer, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kierlavage, J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fritchman, J.L.; Geoghegan, N.S.M.
 Science 268, 496-512, 1995
 A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A./Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
 A/Reference number: A64000; MUID:95350630; PMID:7542800
 A/Accession: F64026
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-154 <TIGR>
 A/Cross-references: UNIPROT:P44168; GB:U02814; GB:L42023; NID:91574809; PIDN:AA023002.1;
 C/Superfamily: uncharacterized conserved protein

Query Match 48.0%; Score 47; DB 2; Length 154;
 Best Local Similarity 61.1%; Pred. No. 3.5;
 Matches 11; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

OY 3 EGPTRREM-LTSRTPHS 18
 Db 105 EGPTRREM-LTSRTPHS 122

RESULT 7
 E69659
 molybdopter in biosynthesis protein moea - *Bacillus subtilis*
 C/Species: *Bacillus subtilis*
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
 C/Accession: E69659
 R./Kuster, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A/Authors: Foulger, D.; Henaut, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holstappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A./Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauei, Y. M.; Ogawa, K.; Ogawara, N.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A./Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekowska, A.; Sero

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.
 A/Authors: Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Danchin, A.
 A/Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A/Reference number: A69580; MUID:98044033; PMID:9384377
 A/Accession: E69659
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-430 <KUN>
 A/Cross-references: UNIPROT:Q31703; GB:Z99111; GB:AL009126; NID:92633699; PIDN:CAB13301
 A/Experimental source: strain 168
 C/Genetics:
 A/Gene: moea
 C/Superfamily: Molybdenum cofactor molybdenum incorporation protein Moea

Query Match 48.0%; Score 47; DB 1; Length 430;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 5 PTLREWLTSRTPHS 18
 Db 323 PTLREWLTSRTPHS 336

RESULT 8
 C69593
 3-methyl-2-oxobutanoate dehydrogenase (lipoamide) (EC 1.2.4.4) Et alpha chain b6mBA - 1
 N/Alternate names: branched-chain alpha-oxo acid dehydrogenase Et alpha chain
 C/Species: *Bacillus subtilis*
 C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C/Accession: C69593; S32486
 R./Kuster, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A/Authors: Foulger, D.; Henaut, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holstappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A./Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauei, Y. M.; Ogawa, K.; Ogawara, N.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A./Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekowska, A.; Sero
 A/Authors: Tanakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, A./Authors: Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Danchin, A.
 A/Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A/Reference number: A69580; MUID:98044033; PMID:9384377
 A/Accession: C69593
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-330 <KUN>
 A/Cross-references: UNIPROT:P37940; GB:Z99116; GB:AL009126; NID:92634723; PIDN:CAB14336
 A/Experimental source: strain 168
 R./Wang, G.F.; Kuriki, T.; Roy, K.L.; Kaneda, T.
 Eur. J. Biochem. 213, 1091-1099, 1993
 A/Title: The primary structure of branched-chain alpha-oxo acid dehydrogenase from *Bacillus subtilis*.
 A/Reference number: S32486; MUID:93279308; PMID:8504804
 A/Accession: S32486
 A/Molecule type: DNA
 A/Residues: 1-330 <MAN>
 A/Cross-references: GB:M97391; GB:M96937; NID:9142610; PIDN:AAA22278.1; PID:9142611
 A/Experimental source: strain 1688
 C/Genetics:
 A/Gene: b6mBA
 C/Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bi
 F/Keyworf: fatty acid biosynthesis; oxido-reductase; phosphoprotein
 F/113-190/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 47.4%; Score 46.5; DB 2; Length 330;
 Best Local Similarity 64.7%; Pred. No. 9.8;
 Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 3 EGPTRREM-LTSRTPHS 18

Db 237 EGPTLERTSYRTPHS 253

RESULT 9
B64633
hypothetical protein HP0906 - *Helicobacter pylori* (strain 26695)

C/Species: *Helicobacter pylori*
C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C/Accession: B64633
R/Tomb, J.F.; White, O.; Karlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenrae, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L. Nature 388, 539-547, 1997
A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.
A/Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A/Reference number: A64520; MUID:97394467; PMID:9252185
A/Accession: B64633

A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-527 <TOM>
A/Cross-references: UNIPROT:Q25564; GB:AE000600; GB:AE000511; NID:92314042; PIDN:AAD0795

Query Match 47.4%; Score 46.5; DB 2; Length 527;
Best Local Similarity 44.4%; Pred. No. 17;
Matches 8; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

QY 3 EGPTLREMTSR--TPH 17
: |||::|: |||
Db 98 QAPTLKCMNHKKVTPH 115

RESULT 10
H83962
serine/threonine protein kinase BH2504 [imported] - *Bacillus halodurans* (strain C-125)

C/Species: *Bacillus halodurans*
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: H83962
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: H83962

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-664 <STO>
A/Cross-references: UNIPROT:Q9K920; GB:AP001515; GB:BA000004; NID:910174886; PIDN:BA0062
A/Experimental source: strain C-125
C/Genetics:
A/Gene: BH2504

Query Match 46.9%; Score 46; DB 2; Length 664;
Best Local Similarity 53.3%; Pred. No. 26;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 IEGPTLREMTSRTP 16
: |||::|: |||
Db 90 VEGPTLKEHLQQRKP 104

RESULT 11
A59253
myosin I beta - human
C/Species: *Homo sapiens* (man)
C/Date: 15-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C/Accession: A59253
R/Crozat, F.; Amraoui, A.E.; Blanchard, S.; Lenoir, M.; Ripoll, C.; Vago, P.; Hamel, C.;
Genomics 40, 332-341, 1997
A/Title: Cloning of the genes encoding two murine and human cochlear unconventional type
A/Reference number: A59253; MUID:97237053; PMID:9119401
A/Accession: A59253
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA

A/Residues: 1-1028 <CRO>
A/Cross-references: UNIPROT:Q00159; GB:X98507; NID:91926310; PIDN:CAA67131.1; PID:919263
A/Experimental source: dev stage adult; tissue type kidney
C/Genetics:
A/Gene: myo-1b
A/Map position: 17p3.2-p13.3
C/Superfamily: brush border myosin heavy chain I; myosin motor domain homology
F.14-683/Domain: myosin motor domain homology <MMO>

Query Match 46.9%; Score 46; DB 2; Length 1028;
Best Local Similarity 71.4%; Pred. No. 42;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIEGPTLREMTSR 14
: |||::|: |||
Db 308 SVEGPTLREMTSR 321

RESULT 12
AD1246

branched-chain alpha-keto acid dehydrogenase E1 chain (2-oxoisovalerate dehydrogenase a1
C/Species: *Listeria monocytogenes*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AD1246
R/Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karet, U. Science 294, 849-852, 2001
A/Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A/Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AD1246

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-311 <GLA>
A/Cross-references: UNIPROT:Q8Y7B4; GB:NC_003210; PIDN:CAC99450.1; PID:916410788; GSPDB:
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: lmoJ372

C/Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain, thiamin pyrophosphate-bin
Query Match 46.4%; Score 45.5; DB 2; Length 331;
Best Local Similarity 64.7%; Pred. No. 14;
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 3 EGPTLREMTSR-TPHS 18
: |||::|: |||
Db 234 EGPTLERTSYRTPHS 250

RESULT 13
AH1608
branched-chain alpha-keto acid dehydrogenase E1 chain (2-oxoisovalerate dehydrogenase a1
C/Species: *Listeria innocua*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AH1608
R/Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karet, U. Science 294, 849-852, 2001
A/Authors: Kreft, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A/Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AH1608
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-311 <GLA>
A/Cross-references: UNIPROT:Q928Y3; GB:AL592022; PIDN:CMC96640.1; PID:916413882; GSPDB:G
A/Experimental source: strain Clj11262
C/Genetics:
A/Gene: lln1409

C/Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bi

Query Match

Best Local Similarity 46.4%; Score 45.5; DB 2; Length 331;
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 3 EGPTLRWLTSLR-TPHS 18
|||||:|||||

Db 234 EGPTLRWLTSLRTPHS 250

RESULT 14

S15618
E4 protein - human papillomavirus type 2a

C/Species: human papillomavirus type 2a

A/Note: host Homo sapiens (man)

C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004

C/Accession: S15618

R/Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.

Virus Res. 18, 81-98, 1990

A/Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and

A/Reference number: S15614; PMID:9186899; PMID:1964523

A/Accession: S15618

A/Molecule type: DNA

A/Residues: 1132 <HR>

A/Cross-references: UNIPROT:P25483; EMBL:X55964

C/Superfamily: papillomavirus type 2 E4 protein

C/Keywords: early protein

Query Match

Best Local Similarity 45.9%; Score 45; DB 1; Length 132;
Matches 13; Conservative 2; Mismatches 1; Indels 16; Gaps 2;

QY 1 SIEGPTLR-----W-----LTSRTP 16
|||:|||||

Db 90 SIEGPTLRSEKSKSVTTSGLSVTLTAQTP 121

RESULT 15

E84853
hypothetical protein At2g42400 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C/Accession: E84853

R/Lin, X.; Kall, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffett, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

eues, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; PMID:20083487; PMID:10617197

A/Accession: E84853

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1473 <STO>

A/Cross-references: UNIPROT:Q9SLB9; GB:A802093; NID:94567312; PTDN:AD23723.1; GSPDB:GN

C/Genetics:

A/Map position: 2

Query Match 45.9%; Score 45; DB 2; Length 473;
Best Local Similarity 70.0%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 IEQPTLRWLT 11
|||:|||||

Db 343 VEGETIREWL 352

RESULT 16

A32758
beta-amyloid-like protein precursor - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 08-Dec-1989 #sequence_revision 08-Dec-1989 #text_change 09-Jul-2004

C/Accession: A32758

R/Rosen, D.R.; Martin-Morris, L.; Luo, L.; White, K.

Proc. Natl. Acad. Sci. U.S.A. 86, 2478-2482, 1989

A/Title: A Drosophila gene encoding a protein resembling the human beta-amyloid protein

A/Reference number: A32758; PMID:8918450; PMID:2494667

A/Accession: A32758

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1886 <ROS>

A/Cross-references: UNIPROT:P14599; GB:J04516; NID:9158371; PID:9158372

C/Genetics:

A/Genes: FlyBase:Appl

A/Cross-references: FlyBase:FBgn0000108

C/Keywords: transmembrane protein

Query Match

Best Local Similarity 45.9%; Score 45; DB 2; Length 886;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 GPTLRWLTSLRTPHS 18
|||:|||||

Db 829 GVAVAKWRTSRSPHA 843

RESULT 17

S22383
axonin 1 precursor - chicken

N/Alternate names: neural cell adhesion molecule AxCAM

C/Species: Gallus gallus (chicken)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: S22383; S34107; S69332; S22128

R/Zuellig, R.A.; Rader, C.; Schroeder, A.; Kalousek, M.B.; von Bohnen und Halbach, F.;

Bur, J. Biochem. 204, 453-463, 1992

A/Title: The axonally secreted cell adhesion molecule, axonin-1. Primary structure, imm

A/Reference number: S22383; PMID:92174898; PMID:1311675

A/Accession: S22383

A/Molecule type: mRNA

A/Residues: 1-1036 <ZUPL>

A/Cross-references: UNIPROT:P28685; EMBL:X63101; NID:962852; PTDN:CAA44815.1; PID:96285

A/Accession: S34107

A/Molecule type: protein

A/Residues: 29-49;51-80;84-95;100-117;120-128;130-141;143-176;243-254;256-296;303-336;3

R/Giger, R.J.; Vogt, L.; Zuellig, R.A.; Rader, C.; Henenhan-Beatty, A.; Wolfer, D.P.; Sol

Bur, J. Biochem. 227, 617-628, 1995

A/Title: The gene of chicken axonin-1. Complete structure and analysis of the promoter.

A/Reference number: S69332; PMID:95172044; PMID:7867620

A/Accession: S69332

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1002-1036 <GIG>

A/Cross-references: EMBL:X79607

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994

C/Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology

C/Keywords: cell adhesion

F.1.23/Domain: signal sequence #status predicted <SIG>

F.24-1036/Product: axonin 1 #status predicted <MAT>

F.336-392/Domain: immunoglobulin homology <IMM>

Query Match 45.9%; Score 45; DB 2; Length 1036;
Best Local Similarity 29.4%; Pred. No. 61;
Matches 10; Conservative 3; Mismatches 1; Indels 20; Gaps 1;

QY 5 PTLRE-----WLSRTPHS 18
|||||:|||||

Db 728 PTLRDYONGDFGYILSPKKGTOGWLTVARVPHA 761

RESULT 18

T13288
mel-41 protein - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C/Accession: T13288

R.Hart, K.L.; Santerre, A.; Sekelesky, J.J.; McKim, K.S.; Boyd, J.B.; Hawley, R.S.
Cell 82, 815-821, 1995
A>Title: The mei-41 gene of *D. melanogaster* is a structural and functional homolog of th
A:Reference number: Z11072; MUID:95401271; PMID:7671309
A:Accession: T13288
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2354 <HAR>
A:Cross-references: UNIPROT:Q24135; EMBL:U34925; NID:g998351; PID:g998351; PIDN:AA046881
C:Genetics:
A:Gene: mei-41
A:Cross-references: FlyBase:FBgn004367
A:Introns: 650/3; 748/3; 2313/3
C:Function:
A:Description: involved in cell cycle checkpoint and meiotic recombination

Query Match 45.9%; Score 45; DB 2; Length 2354;
Best Local Similarity 56.2%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 5 PTLREWLTSR--TPHS 18
| : ||| | |||
Db 2159 PVFQEWLRGRFAPPHS 2174

RESULT 19
T23485
hypothetical protein K08F4.11 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T23485
R:Hemby, C.
Submitted to the EMBL Data Library, January 1996
A:Reference number: Z19746
A:Accession: T23485
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-200 <WLL>
A:Cross-references: EMBL:Z68879; PIDN:CAA93088.1; GSPDB:GN00022; CESP:K08F4.11
A:Experimental source: clone K08F4
C:Genetics:
A:Gene: CESP:K08F4.11
A:Map position: 4
A:Introns: 45/1; 76/1; 111/3
C:Superfamily: glutathione transferase

Query Match 44.9%; Score 44; DB 2; Length 200;
Best Local Similarity 61.5%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IEQPTLRWLTSLR 14
||| : |||
Db 183 IETPKLEWLAKR 195

RESULT 20
T37464
probable glutathione transferase (EC 2.5.1.18) GST3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37464
R:Rawe, W.N.; Eschbach, M.L.; Walter, R.D.; Henkle-Duehren, K.
Submitted to the EMBL Data Library, June 1997
A:Description: Parquat mediates differential gene expression in *C. elegans*.
A:Reference number: Z21702
A:Accession: T37464
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <TRM>
A:Cross-references: UNIPROT:O16116; EMBL:AF010241; PIDN:AA065419.1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: GST3

C:Superfamily: glutathione transferase
C:Keywords: transferase

Query Match 44.9%; Score 44; DB 2; Length 207;
Best Local Similarity 61.5%; Pred. No. 15;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IEQPTLRWLTSLR 14
||| : |||
Db 190 IETPKLEWLAKR 202

RESULT 21
C90277
hypothetical protein tmoA [imported] - *Sulfolobus solfataricus*
C:Species: *Sulfolobus solfataricus*
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: C90277
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A:Description: *Sulfolobus solfataricus* complete genome.
A:Reference number: A99139
A:Accession: C90277
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-310 <KUB>
A:Cross-references: UNIPROT:Q97YT0; GB:AE006641; NID:g13814426; PIDN:AAK41474.1; GSPDB:G
A:Genetics:
A:Gene: tmoA

Query Match 44.9%; Score 44; DB 2; Length 310;
Best Local Similarity 47.4%; Pred. No. 23;
Matches 9; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 SIEGPTLRWLTSLRTPH 17
| ||| : |||
Db 141 SFRGPTPDERKWLNEKYPH 159

RESULT 22
C87021
serine-threonine protein kinase [imported] - *Mycobacterium leprae*
C:Species: *Mycobacterium leprae*
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: C87021
R:Coile, S.T.; Eiglsmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthey, S.; Fellwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A>Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: C87021
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-400 <STO>
A:Cross-references: UNIPROT:O69568; GB:AL450380; NID:g13092968; PIDN:CAC31278.1; GSPDB:G
C:Genetics:
A:Gene: M0897
C:Superfamily: *Mycobacterium tuberculosis* probable serine/threonine-specific protein kin

Query Match 44.9%; Score 44; DB 2; Length 400;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 IEQPTLRWLTSLRTP 16
||| ||| | |
Db 86 IEQTLREHLAERGP 100

RESULT 23

B82277
 Probable transposase VC0817 [similarity] - *Vibrio cholerae* (strain N16961 serogroup O1)
 C:Species: *Vibrio cholerae*
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: E82277; T09435
 R:Heidelberg, J.F.; Eichen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardon, D.; Ermolova, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellars, F. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A:Reference number: AB2035; PMID:20406833; PMID:10952301
 A:Accession: E82277
 A:Molecule type: DNA
 A:Residues: 1-327 <HE1>
 A:Cross-references: UNIPROT:Q9KTS1; GB:AE004166; GB:AE003852; NID:g9655259; PIDN:AAF9398
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 R:Karol, D.K.R.; Johnson, J.A.; Bailey, C.C.; Boedeker, E.C.; Kaper, J.B.; Reeves, P. Proc. Natl. Acad. Sci. U.S.A. 95, 3134-3139, 1998
 A:Title: A *Vibrio cholerae* pathogenicity island associated with epidemic and pandemic strains
 A:Reference number: Z16672; PMID:98169509; PMID:9501228
 A:Accession: T09435
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 3327 <KAR>
 A:Cross-references: EMBL:AF034434; NID:g3004923; PIDN:AACT2272.1; PID:g3004924
 A:Experimental source: strain N16961
 C:Genetics:
 A:Gene: VC0817
 A:Map position: 1
 A:Note: part of the pathogenicity island (VPI); associated with epidemic and pandemic strains

Query Match 44.4%; Score 43.5; DB 2; Length 327;
 Best Local Similarity 36.7%; Pred. No. 29;
 Matches 11; Conservative 1; Mismatches 5; Indels 13; Gaps 1;

OY 2 IEGLTLEWLTSTRT 18
 DB 32 ISRPLTKMKAKRYKQCGIAGLESQSRPHS 61

RESULT 24
 T06371
 Probable UDP-glucuronosyltransferase (EC 2.4.1.-) - garden pea
 C:Species: *Pisum sativum* (garden pea)
 C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T06371
 R:Woo, H.H.; Orbach, M.J.; Hawes, M.C.
 Submitted to the EMBL Data Library, November 1997
 A:Description: Lethal effects on root development by genetic alteration of glucuronide transferase
 A:Reference number: Z15633
 A:Accession: T06371
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-347 <WOO>
 A:Cross-references: UNIPROT:Q8U5C7; EMBL:AF034743; NID:g2827991; PIDN:AA899950.1; PID:g2827991
 A:Experimental source: cv. Little Marvel
 C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 43.9%; Score 43; DB 2; Length 347;
 Best Local Similarity 50.0%; Pred. No. 38;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 3 EGPFLREMLTSTRT 18
 DB 149 EEPCECLEMNSKEPNS 164

RESULT 25
 B70936
 Probable serine/threonine-specific protein kinase (EC 2.7.1.-) 2 - *Mycobacterium tuberculosis*
 C:Species: *Mycobacterium tuberculosis*
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: B70936

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felkell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A:Reference number: A70500; PMID:98295987; PMID:9634230
 A:Accession: B70936
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-399 <COL>
 A:Cross-references: UNIPROT:O53510; GB:AL021957; GB:AL123456; NID:g3242293; PIDN:CAAL748
 A:Experimental source: strain H37Rv
 C:Genetics:
 A:Gene: PMU
 C:Superfamily: *Mycobacterium tuberculosis* probable serine/threonine-specific protein kinase
 C:Keywords: phosphotransferase
 F:17-270/Domain: protein kinase homology <KIN>

Query Match 43.9%; Score 43; DB 1; Length 399;
 Best Local Similarity 66.7%; Pred. No. 44;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 IEGLTLEWLTSTRT 16
 DB 99 IEGLTLEWLTSTRT 113

RESULT 26
 C98275
 polyketide synthase and peptidase synthetase (AB032549) [imported] - *Agrobacterium tumefaciens*
 C:Species: *Agrobacterium tumefaciens*
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
 C:Accession: C98275
 R:Goodier, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
 A:Reference number: A97359; PMID:21608551; PMID:11743194
 A:Accession: C98275
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-491 <KUR>
 A:Cross-references: UNIPROT:Q8U999; GB:AE007870; PIDN:AAK89725.1; PID:g15159639; GSPDB:1A0309
 A:Genetic:
 A:Gene: AGR_L 2319
 A:Map position: linear chromosome
 C:Superfamily: ornithine-oxo-acid aminotransferase

Query Match 43.9%; Score 43; DB 2; Length 491;
 Best Local Similarity 61.5%; Pred. No. 55;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 EGPFLREMLTSTRT 15
 DB 383 DGPTLDEGLMART 395

RESULT 27
 AC3009
 polyketide synthase and peptidase synthetase mcyl [imported] - *Agrobacterium tumefaciens*
 C:Species: *Agrobacterium tumefaciens*
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AC3009
 R:Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, J.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.T.; W. W.
 A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A:Reference number: AB2577; PMID:21608550; PMID:11743193
 A:Accession: AC3009

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-491 <KUR>
A:Cross-references: UNIPROT:Q8U999, GB:AE008689, PIDN:AL44489.1, PID:g17742095, GSPDB:C
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: mcyE
A:Map position: linear chromosome
C:Superfamily: ornithine-oxo-acid aminotransferase

Query Match 43.9%; Score 43; DB 2; Length 491;
Best Local Similarity 61.5%; Pred. No. 55;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 EGPTRWMTSRT 15
:|||||:|:|
Db 383 DGPTLQEGINART 395

RESULT 28
T44602
phosphonate monoester hydrolase (EC 3.1.3.-) PEH [validated] - Burkholderia caryophylli
C:Species: Burkholderia caryophylli
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44602
R:Dotson, S.B.; Smith, C.E.; Ling, C.S.; Barry, G.F.; Kishore, G.M.
J. Biol. Chem. 271, 25754-25761, 1996
A:Title: Identification, characterization and cloning of a phosphonate monoester hydrolase
A:Reference number: Z22807; MUID:96421555; PMID:8824203
A:Accession: T44602
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-514 <DOT>
A:Cross-references: UNIPROT:Q45087, EMBL:U44852, NID:g1177863, PIDN:AA04467.1, PID:g117
A:Experimental source: strain PG2982
A:Note: part of this sequence, including the amino end of the mature protein was confirm
C:Genetics:
A:Gene: pehA
C:Complex: homotrimer [validated, MUID:96421555]
C:Function:
A:Description: EC 3.1.3.- [validated, MUID:96421555]; phosphonate monoester hydrolase; h
A:Pathway: glyceryl phosphate utilization
A:Note: may also function in vivo as phosphodiesterase
C:Superfamily: animal sulfatase
C:Keywords: homotrimer; phosphoric monoester hydrolase
F:1-514/Product: phosphonate monoester hydrolase #status experimental <MAT>

Query Match 43.9%; Score 43; DB 2; Length 514;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 PTLREWLTSTRPS 18
||:|||||:
Db 375 PTLREWLTSTRPS 388

RESULT 29
H69878
probable protein kinase (EC 2.7.1.-) yloP - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: H69878
R:Kunze, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Beret
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Enlrich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
koetter, F.; Koningsreth, G.; Krogh, S.; Kumano, M.; Kurita, K.; Kapitus, A.; Lardinois,
A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, R.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumaeta, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A65860; MUID:96044033; PMID:9384377
A:Accession: H69878
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-648 <KUN>
A:Cross-references: UNIPROT:Q34507, GB:Z29112, GB:AL009126, NID:G2633902, PIDN:CAB13450.
A:Experimental source: strain 168
C:Genetics:
A:Gene: yloP
C:Superfamily: Bacillus subtilis probable protein kinase yloP; protein kinase homology
C:Keywords: ATP; phosphotransferase; protein kinase
F:9-269/Domain: protein kinase homology <KIN>

Query Match 43.9%; Score 43; DB 1; Length 648;
Best Local Similarity 46.7%; Pred. No. 75;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEGPTREWLTSRTP 16
:|||||:|:|
Db 91 VEGMTLKEYITRANGP 105

RESULT 30
F70697
probable arabinosyltransferase - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: F70697
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70697
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1094 <COL>
A:Cross-references: UNIPROT:F72060, GB:Z80343, GB:AL123456, NID:G3261648, PIDN:CAB02473.
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: emdA
C:Superfamily: probable arabinosyl transferase

Query Match 43.9%; Score 43; DB 2; Length 1094;
Best Local Similarity 61.5%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 GPTLRWLTSTRTP 16
|||||:|:|
Db 230 GRTLRDWLTSTRTP 242

RESULT 31
T30939
hemocyanin G-type chain - giant octopus (fragment)
C:Species: Octopus dofleini (giant octopus)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30939
R:Miller, K.I.; Culf, M.E.; Lang, W.F.; Varga-Weisz, P.; Field, K.G.; van Holde, K.E.
J. Mol. Biol. 278, 827-841, 1998
A:Title: Sequence of the Octopus dofleini hemocyanin subunit: structural and evolutionary
A:Reference number: Z20940; MUID:98277150; PMID:9614945
A:Accession: T30939
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2896 <MLI>
A:Cross-references: UNIPROT:O61363, EMBL:AF020548, NID:G3132879, PID:G3132880, PIDN:AA03

C:Genetics:
A:Note:Odhy
C:Superfamily: hemocyanin

Query Match 43.4%; Score 43; DB 2; Length 2896;
Best Local Similarity 53.8%; Pred. No. 4e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 TIREWLTSTRTPS 18
DB 1427 TIRSWTGRDPS 1439

RESULT 32
DEBSPA

pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain - Bacillus subtilis
N:Alternate names: pyruvate dehydrogenase complex, E1 component alpha chain
C:Species: Bacillus subtilis
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004

C:Accession: B36718; H68673
R:Hemila, H.; Palva, A.; Paulin, L.; Arvidson, S.; Palva, I.

J. Bacteriol. 172, 5052-5063, 1990

A:Title: Secretary S complex of Bacillus subtilis: sequence analysis and identity to pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain
A:Reference number: A36718; MUID:90368558; PMID:1697575

A:Accession: B36718
A:Molecule type: DNA

A:Residues: 1-371 <HEM>

A:Cross-references: UNIPROT:P21881; GB:M57435; GB:M31542; NID:g143375; PIDN:AAA62681.1;

R:Kunert, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berthel, C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Konigstein, G.; Krogh, S.; Kuno, M.; Kurita, K.; Lapidus, A.; Lardinois, A.;

Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Muesel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudeg, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli,

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon, A.;

Authors: Schleicher, S.; Schreier, R.; Scottone, P.; Sekiguchi, J.; Sekowska, A.; Seron, T.;

Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: H69673

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1178, 'A', 180-371 <KIN>

A:Cross-references: GB:299111; GB:AL009126; NID:g2633699; PIDN:CAM3331.1; PID:g2633829

A:Experimental source: strain 168

C:Genetics:

A:Gene: pdhA

C:Function:

A:Description: catalyzes the decarboxylation of pyruvate coupled with formation of S-ace

A:Pathway: glycolysis

A:Note: uses thiamine diphosphate as a cofactor

C:Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bi

C:Keywords: flavoprotein; glycolysis; oxidoreductase; phosphoprotein; thiamin pyrophosph

F:2-371/Product: pyruvate dehydrogenase (lipoamide) alpha chain #status predicted <MAT>

F:165-212/Domain: thiamin pyrophosphate-binding domain homology <TPB>

Query Match 43.4%; Score 42.5; DB 1; Length 371;
Best Local Similarity 64.7%; Pred. No. 49;
Matches 11; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 3 EGPTLRWLTSTR--TPHS 18
DB 259 EGPTLRTTFRGPHPT 275

RESULT 33

JC4742

transposase - Corynebacterium glutamicum

C:Species: Corynebacterium glutamicum

C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C:Accession: JC4742

R:Correia, A.; Pisabarro, A.; Castro, J.M.; Martin, J.F.

Gene 170, 91-94, 1996

A:Title: Cloning and characterization of an IS-like element present in the genome of Br

A:Reference number: JC4742; MUID:96200862; PMID:8621097

A:Accession: JC4742

A:Molecule type: DNA

A:Residues: 1-436 <COR>

A:Cross-references: UNIPROT:Q45293; EMBL:266534

A:Experimental source: ATCC 13869

A:Note: The authors translated the initiation codon TGT for residue 1 as Val

A:Note: The authors translated the codon ATT for residue 125 as Tyr

C:Genetics:

A:Gene: GTG

F:388-415/Domain: DNA binding #status predicted <DNA>

F:405-415/Region: helix-turn-helix

Query Match 43.4%; Score 42.5; DB 2; Length 436;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 9; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 2 IEG---PTLRWLTSTRTP 16
DB 206 VEGSRADALRTWLAATP 223

RESULT 34

B84271

glutamyl-tRNA synthetase [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: B84271

R:Mc, W.V.; Kennedy, S.P.; Mahatras, G.G.; Berguet, B.; Pan, M.; Shukla, H.D.; Lasky,

Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl,

Jung, K.H.; Alam, M.; Preltas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; L

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: B84271

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-586 <STO>

A:Cross-references: UNIPROT:Q9HQ11; GB:AB004437; NID:g10580690; PIDN:AA919534.1; GSPDB:

C:Genetics:

A:Gene: glts

C:Superfamily: glutamine-tRNA ligase; glutamine-tRNA ligase homology

Query Match 43.4%; Score 42.5; DB 2; Length 586;
Best Local Similarity 44.4%; Pred. No. 81;
Matches 8; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 3 EGPTLRWLTSTR--TPH 17
DB 259 KNPALRDWAFRWDTPH 276

RESULT 35

AH1884

hypothetical protein al10625 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AH1884

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Matanabe, A.; Iriuch

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AH1884

A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-236 <KUR>
 A:Cross-references: UNIPROT:Q8Y262, GB:BA000019, PIDN:BAB72583.1, PID:gl1129971, GSPDB:C
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all0625

Query Match 42.9%; Score 42; DB 2; Length 236;
 Best Local Similarity 58.3%; Pred. No. 35;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 PTLEWLTSTPT 16
 ||:||||:|
 60 PYLGEMLTHTQP 71

RESULT 36

G87394
 hypothetical protein CCL171 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: G87394

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwim, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: G87394

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <STO>

A:Cross-references: UNIPROT:Q9A923, GB:AE005673, NID:gl3422493, PIDN:AAK23155.1; GSPDB:C

C:Genetics:

A:Gene: CCL171

C:Superfamily: HCCA isomerase/mitochondrial glutathione S-transferase

Query Match 42.9%; Score 42; DB 2; Length 253;
 Best Local Similarity 42.9%; Pred. No. 38;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 5 PTLEWLTSTPT 18
 ||:||||:|
 53 PTLEWLTSTPT 66

RESULT 37

D70601
 UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) galU [similarity] - Mycobacteri

C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: D70601

R:Col, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

.; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Ruter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: D70601

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-306 <COL>

A:Cross-references: UNIPROT:O05576, GB:Z94752, GB:AL123456, NID:g3261731, PIDN:CAB08153.

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: galU

C:Superfamily: Escherichia coli UTP-glucose-1-phosphate uridylyltransferase

C:Keywords: nucleotidyltransferase

Query Match 42.9%; Score 42; DB 2; Length 306;
 Best Local Similarity 63.6%; Pred. No. 47;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 4 GPTLEWLTST 14
 |||||:|
 DB 290 GPDRLRLVAR 300

RESULT 38

JL0119

Fc gamma (IgG) receptor IIb precursor - human

N:Alternate names: Fc gamma (IgG) receptor II (low affinity) beta; surface glycoprotein

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: JL0119; A43543; A60568; A45877; S00478

R:Brooks, D.G.; Qiu, W.O.; Luster, A.D.; Ravetch, J.V.

J. Exp. Med. 170, 1369-1385, 1989

A:Title: Structure and expression of human IgG FcR II (CD32): functional heterogeneity is

A:Reference number: JL0118; MUID:90010791; PMID:2529342

A:Accession: JL0119

A:Molecule type: mRNA

A:Residues: 1-310 <BRO>

A:Cross-references: UNIPROT:P31994

R:Engelhardt, W.; Geerdts, C.; Frey, J.

Eur. J. Immunol. 20, 1367-1377, 1990

A:Title: Distribution, inducibility and biological function of the cloned and expressed

A:Reference number: A43543; MUID:90316181; PMID:2142460

A:Accession: A43543

A:Molecule type: mRNA

A:Residues: 1-204, 'Y', 206-254, 274-310 <ENG>

A:Cross-references: GB:X52473; NID:g3928171; PIDN:CAA36713.1; PID:g29428

R:Engelhardt, W.; Geerdts, C.; Frey, J.

Mol. Immunol. 27, 379-382, 1990

A:Title: Organization of human FCRII and FCRII-like (betaFCRII) genes: structural homolo

A:Reference number: A60568; MUID:90294837; PMID:2141667

A:Accession: A60568

A:Molecule type: DNA

A:Residues: 1-38 <EN2>

R:Seki, T.

Immunogenetics 30, 5-12, 1989

A:Title: Identification of multiple isoforms of the low-affinity human IgG Fc receptor.

A:Reference number: A45877; MUID:89307398; PMID:2526077

A:Accession: A45877

A:Molecule type: preliminary

A>Status: preliminary

A:Residues: 1-74, 'O', '76-119, 'V', 121-204, 'Y', 206-231, 'T', 233-254, 274-310 <SEK>

A:Cross-references: GB:M28696; NID:gl84843; PIDN:AA36051.1; PID:g306929

A:Note: the authors translated the codon CAG for residue 75 as His

R:Stengelin, S.; Stamenkovic, I.; Seed, B.

EMBO J. 7, 1053-1059, 1988

A:Title: Isolation of cDNAs for two distinct human Fc receptors by ligand affinity clon

A:Reference number: S00477; MUID:88296409; PMID:3402431

A:Accession: S00478

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-35, 'S', '7-204, 'Y', 206-253, 'G', 255 <STZ>

A:Note: the authors suggest that the cDNA is derived from a precursor RNA that still con

C:Genetics:

A:Gene: GDB:FCGR2B; FCG2; FCGR2

A:Cross-references: GDB:18183; OMIM:146790

A:Map position: 1q23-1q23

A:Intron: 131/1

C:Superfamily: Fc gamma receptor III; immunoglobulin homology

C:Keywords: alternative splicing; glycoprotein; immunoglobulin, immunoglobulin receptor,

F1-4/Domain: signal sequence #status predicted <STG>

F1-4/Domain: signal sequence #status predicted <STG>

F1-4/Domain: signal sequence #status predicted <STG>

F1-4/Domain: signal sequence #status predicted <STG>

F1-4/Domain: signal sequence #status predicted <STG>

F1-4/Domain: signal sequence #status predicted <STG>

F1-4/Domain: signal sequence #status predicted <STG>

Best Local Similarity 63.6%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LREWLTSRTPH 17
| | | | |
Db 129 LSEWLVTQTPH 139

RESULT 39
JL0118
Fc gamma (IgG) receptor IIA precursor - human
N.Alternative names: Fc gamma (IgG) receptor II (low affinity) alpha; surface glycoprotein
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JL0118; A31932; S02297; S00477; S02296
R/Protein: D.G.; Qiu, W.Q.; Luster, A.D.; Ravetch, J.V.
J. Exp. Med. 170, 1369-1385, 1989
A/Title: Structure and expression of human IgG FcRII (CD32): functional heterogeneity is
A/Reference number: JL0118; MUID:90010791; PMID:2529342
A/Accession: A31932
A/Molecule type: mRNA
A/Residues: 1-317 <PRO>
A/Cross-references: UNIPROT:P12318; GB:M31932; NID:g182473; PIDN:AAA55827.1; PID:g182474
A/Note: It is uncertain whether Met-1, Met-3, or Met-7 is the initiator
R/Hibbs, M.L.; Bonadonna, L.; Scott, B.M.; McKenzie, I.F.C.; Hogarch, P.M.
Proc. Natl. Acad. Sci. U.S.A. 85, 2240-2244, 1988
A/Title: Molecular cloning of a human immunoglobulin G Fc receptor.
A/Reference number: S02296; MUID:88176920; PMID:2965389
A/Accession: A31932
A/Molecule type: mRNA
A/Residues: 3-317 <HIB>
A/Cross-references: EMBL:J03619; NID:g183619; PIDN:AAA35932.1; PID:g306803
R/Stuart, S.G.; Trounstein, M.L.; Vaux, D.J.T.; Koch, T.; Martens, C.L.; Mellman, I.; Mc
J. Exp. Med. 166, 1668-1684, 1987
A/Title: Isolation and expression of cDNA clones encoding a human receptor for IgG (Fc-gamma-1).
A/Reference number: S02297; MUID:88061079; PMID:2824655
A/Accession: S02297
A/Molecule type: mRNA
A/Residues: 1-'T', 3-317 <STU>
A/Cross-references: EMBL:Y00644; NID:g31335; PIDN:CAA6872.1; PID:g31336
A/Note: It is uncertain whether Met-1 or Met-7 is the initiator
R/Seki, T
Immunogenetics 30, 5-12, 1989
A/Title: Identification of multiple isoforms of the low-affinity human IgG Fc receptor.
A/Reference number: A45877; MUID:9307398; PMID:2526077
A/Accession: B45877
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 7-317 <SEK>
A/Cross-references: GB:M28697; NID:g184841; PIDN:AAA6050.1; PID:g306928
R/Stengel, S.; Stamenkovic, I.; Seed, B.
EMBO J. 7, 1053-1059, 1988
A/Title: Isolation of cDNAs for two distinct human Fc receptors by ligand affinity cloning.
A/Reference number: S00477; MUID:88296409; PMID:3402431
A/Accession: S00477
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 7-317 <STB>
C/Genetics:
A/Gene: GDB:FCGR2A
A/Cross-references: GDB:119903; OMIM:146790
A/Map position: 1q23-1q23
C/Superfamily: Fc gamma receptor III; immunoglobulin homology
C/Keywords: glycoprotein; immunoglobulin receptor; transmembrane protein
F/1-35/Domain: signal sequence #status predicted <SIG>
F/36-317/Product: IgG Fc receptor IIA #status predicted <REI>
F/36-216/Domain: extracellular #status predicted <EXT>
F/55-106/Domain: immunoglobulin homology <IMM1>
F/136-189/Domain: immunoglobulin homology <IMM2>
F/217-240/Domain: transmembrane #status predicted <TM>
F/241-317/Domain: intracellular #status predicted <INT>

F/97,178/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 42.9%; Score 42; DB 2; Length 317;
Best Local Similarity 63.6%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LREWLTSRTPH 17
| | | | |
Db 120 LSEWLVTQTPH 130

RESULT 40
S06946
Fc gamma (IgG) receptor - human
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C/Accession: S06946
R/Stuart, S.G.; Simister, N.E.; Clarkson, S.B.; Kacinski, B.M.; Shapiro, M.; Mellman, I
EMBO J. 8, 3657-3666, 1989
A/Title: Human IgG Fc receptor (FcRII; CD32) exists as multiple isoforms in macrophage
A/Reference number: S06946; MUID:90059965; PMID:2531080
A/Accession: S06946
A/Molecule type: mRNA
A/Residues: 1-323 <STU>
A/Cross-references: UNIPROT:P11995; EMBL:X17652; NID:g32073; PIDN:CAA35642.1; PID:g3207
C/Superfamily: Fc gamma receptor III; immunoglobulin homology
C/Keywords: immunoglobulin receptor; transmembrane protein
F/64-115/Domain: immunoglobulin homology <IMM>

Query Match 42.9%; Score 42; DB 2; Length 323;
Best Local Similarity 63.6%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LREWLTSRTPH 17
| | | | |
Db 129 LSEWLVTQTPH 139

RESULT 41
B82096
conserved hypothetical protein VC2278 [imported] - Vibrio cholerae (strain N16961 serog
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: B82096
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gaim, M.L.; Dodson, R.J.
Chadson, D.; Ermolova, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragol, I.; Sellers,
1, R.R.; Mekalanos, J.D.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: B82096
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-430 <HEI>
A/Cross-references: UNIPROT:Q9KPT4; GB:AE004299; GB:AE003852; NID:g9656835; PIDN:AAF954
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC2278
A/Map position: 1
C/Superfamily: conserved hypothetical protein HI0125

Query Match 42.9%; Score 42; DB 2; Length 430;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LREWLTSRTPH 18
| | | | |
Db 119 IREWLINSIPHS 130

RESULT 42
B45438
myosin I beta, MMI beta - mouse (fragment)

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C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B45438
R:Sherr, E.H.; Joyce, M.P.; Greene, L.A.
J: Cell Biol. 120, 1405-1416, 1993
A:Title: Mammalian myosin I alpha, I beta, and I gamma: new widely expressed genes of th
A:Reference number: A45438; MUID:93194946; PMID:8449986
A:Accession: B45438
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-448 <SHE>
A:Cross-references: UNIPROT:Q9WT17
A>Note: Sequence extracted from NCBI backbone (NCBI:P.131911)
C:Superfamily: brush border myosin heavy chain I; myosin motor domain homology
F.1-448/Domain: myosin motor domain homology (fragment) <MWOT>

Query Match          42.9%; Score 42; DB 2; Length 448;
Best Local Similarity 69.2%; Pred. No. 72;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 IEGPTLEWLTSTR 14
          |||||
          164 VEGTTLREALTHR 176

RESULT 43
T37934
Conserved hypothetical protein SPAC1952.06c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21755
A:Accession: T37934
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-564 <MCD>
A:Cross-references: UNIPROT:Q9UUK1; EMBL:AL109820; PIDN:CAB52570.1; GSPDB:GN00066; SPDB:
A:Experimental source: strain 972h-; cosmid c1952
C:Genetics:
A:Gene: SPDB:SPAC1952.06c
A:Map position: 1

Query Match          42.9%; Score 42; DB 2; Length 564;
Best Local Similarity 57.1%; Pred. No. 93;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IEGPTLEWLTSTR 15
          :|||
          238 VENTTLVEWLTSTRS 251

RESULT 44
A39707
erythrocyte membrane band 4.2 protein - human
N:Alternate names: pallidin
N:Contains: erythrocyte membrane band 4.2 protein, long splice form; erythrocyte membrane
C:Species: Homo sapiens (man)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: A39707; A34865; B34865; A34863
R:Korogren, C.; Cohen, C.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 4840-4844, 1991
A:Title: Organization of the gene for human erythrocyte membrane protein 4.2: structural
A:Reference number: A39707; MUID:91271288; PMID:2052563
A:Accession: A39707
A:Molecule type: DNA
A:Residues: 1-721 <KOR1>
A:Cross-references: UNIPROT:P16452; GB:I06519; NID:G306738; PIDN:AAA52385.1; PID:G306740
A:Experimental source: cell type erythrocyte; tissue type peripheral blood; tissue lib h
R:Sun, L.A.; Chien, S.; Chang, L.S.; Lambert, K.; Bliss, S.A.; Bouhasira, E.E.; Nagel,
Proc. Natl. Acad. Sci. U.S.A. 87, 955-959, 1990
A:Title: Molecular cloning of human protein 4.2: a major component of the erythrocyte me

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A:Reference number: A34865; MUID:90138995; PMID:1689063
A:Accession: A34865
A:Molecule type: mRNA
A:Residues: 1-364; 'KRGGPC', 371-379, 'H', 381-405, 'L', 407-721 <SUN1>
A:Cross-references: GB:M30647; NID:g189433; PIND:AAA36401.1; PID:g189434
A:Accession: B34865
A:Molecule type: mRNA
A:Residues: 1-3, 34-364, 'KRGGPC', 371-379, 'H', 381-405, 'L', 407-721 <SUN2>
A:Cross-references: GB:M30646; NID:g189435; PIND:AAA36402.1; PID:g189436
A:Experimental source: Isolate Sickie cell patient; cell type reticulocyte
A:Note: parts of this sequence were determined by protein sequencing
R.Korogren, C.; Landler, U.; Lambert, S.; Speicher, D.; Cohen, C.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 613-617, 1990
A:Title: Complete amino acid sequence and homologies of human erythrocyte membrane prote
A:Reference number: A34883; MUID:90138879; PMID:2300550
A:Accession: A34883
A:Molecule type: mRNA
A:Residues: 1-3, 34-721 <KOR2>
A:Cross-references: GB:M29399; NID:g182083; PIND:AAA35798.1; PID:g182084
A:Comment: This protein is a major constituent of the erythrocyte membrane. It apparently
C:Genetics:
A:Gene: GDB:EPB42; PA
A:Cross-references: GDB:127385; OMIM:177070
A:Map position: 15q45-15q15
C:Superfamily: protein-glutamine gamma-glutamyltransferase
C:Keywords: alternative splicing; blocked amino end; glycoprotein; lipoprotein; myristyl
F:2-721/Product: erythrocyte membrane band 4.2 protein, long splice form #status predicted
F:2-3, 34-721/Product: erythrocyte membrane band 4.2 protein, short splice form #status p
F:298-316/Domains: transmembrane #status predicted <TRM>
F:518-520/Region: cell attachment (R-G-D) motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:103,420,444,559,604,705/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:278/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predic

Query Match          42.9%; Score 42; DB 2; Length 721;
Best Local Similarity 70.0%; Pred. No. 1,28+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      5 PRLREWLTSR 14
      | ||| ||| |
Db      280 PRLRQLWTR 289

RESULT 45
H75634
myosin-1c - mouse (Fragment)
N:Alternate names: myosin-1 beta
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C:Accession: H75634
C:Crossref: F.; Amanoai, A.E.; Blanchard, S.; Lenoir, M.; Ripoll, C.; Vago, P.; Hamel, C.;
Genomics 40, 332-341, 1997
A:Title: Cloning of the genes encoding two murine and human cochlear unconventional type
A:Reference number: A59253; MUID:97237053; PMID:9119401
A:Accession: H75634
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-807 <CRO>
A:Cross-references: UNIPROT:Q9WT17; GB:X99638; NID:g1924960; PIND:CAA67956.1; PID:g19249
C:Genetics:
A:Experimental source: strain BALB/c; tissue type cochlea; dev stage adult
C:Genetics:
A:Gene: MGI:Myo1c
A:Cross-references: MGI:106612
A:Map position: 11:44.1
C:Superfamily: brush border myosin heavy chain I; myosin motor domain homology
F:14-683/Domains: myosin motor domain homology <MMO>

Query Match          42.9%; Score 42; DB 2; Length 807;
Best Local Similarity 69.2%; Pred. No. 1,48+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 ISGPTLRWLTSR 14
      : || || || || ||

```

Db 309 VEGTILREALTR 321

Search completed: September 1, 2005, 16:22:56
Job time : 15.7266 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:37 ; Search time 66.9496 Seconds
(without alignments)
137.677 Million cell updates/sec

Title: US-10-083-768-10

Perfect score: 98

Sequence: 1 SIEGPTLRWLTSTRTPHS 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54.5	55.6	332	2	08CP43
2	52.5	53.6	410	2	0629V1
3	52.5	53.6	410	2	063H26
4	51	52.0	753	2	09Y62
5	50	51.0	295	2	06DG77
6	49	50.0	466	2	089E08
7	49	50.0	576	2	08UND0
8	49	50.0	1049	2	09XBP6
9	48.5	49.5	410	1	ODBA_PSEPU
10	48.5	49.5	410	2	088E02
11	48.5	49.5	410	2	091IM2
12	48	49.0	150	2	09RV54
13	48	49.0	245	2	066272
14	48	49.0	249	2	082989
15	48	49.0	278	2	09XDV0
16	48	49.0	319	2	09RKM5
17	48	49.0	388	2	09KX10
18	48	49.0	481	2	08GAI0
19	48	49.0	632	2	0751T9
20	48	49.0	664	2	08NXL4
21	48	49.0	664	2	099UP8
22	48	49.0	664	2	07A5Z8
23	48	49.0	664	2	06G9Z3
24	48	49.0	664	2	06GHT5
25	47	48.0	91	2	08Y0T5
26	47	48.0	154	1	YD55_HABIN
27	47	48.0	245	2	066278
28	47	48.0	282	2	07QBP7
29	47	48.0	417	2	06JBD5
30	47	48.0	410	2	031703
31	47	48.0	667	2	08CSV9

32	47	48.0	818	2	Q7MWY0	Q7MWY0	alcaligenes
33	46.5	47.4	330	1	ODBA_BACSU	P37940	bacillus su
34	46.5	47.4	330	2	065HK8	P05hk8	bacillus 11
35	46.5	47.4	527	2	025564	025564	helicobacte
36	46	46.9	156	2	064K11	064K11	eleutheroda
37	46	46.9	156	2	064K12	064K12	eleutheroda
38	46	46.9	156	2	064K16	064K16	eleutheroda
39	46	46.9	156	2	064K24	064K24	eleutheroda
40	46	46.9	156	2	064K25	064K25	eleutheroda
41	46	46.9	377	2	082PX5	082PX5	streptomyce
42	46	46.9	559	2	Q745Z3	Q745Z3	thermus the
43	46	46.9	570	1	SYR_PYPAB	08zu33	pyrobaculum
44	46	46.9	664	2	09K9Z0	09K9Z0	bacillus ha
45	46	46.9	1028	1	MYIC_HUMAN	000159	homo sapien
46	46	46.9	1028	2	06NVJ7	06nvj7	homo sapien
47	46	46.9	1030	2	086Y95	086Y95	homo sapien
48	45.5	46.4	168	2	09V492	09V492	desulfohal
49	45.5	46.4	292	2	072E10	072E10	desulfovibr
50	45.5	46.4	328	2	097317	097317	plasmodium
51	45.5	46.4	331	2	08Y7B4	08Y7B4	listeria mo
52	45.5	46.4	331	2	092BX3	092BX3	listeria in
53	45.5	46.4	331	2	071EVO	071EVO	listeria mo
54	45.5	46.4	332	2	08GLC9	08GLC9	listeria mo
55	45	45.9	132	1	VE4_HPYZA	P25483	human papil
56	45	45.9	244	2	066Z69	066Z69	erythromicr
57	45	45.9	244	2	09R7K1	09R7K1	erythroba
58	45	45.9	245	2	082991	082991	erythroba
59	45	45.9	245	2	09ZM87	09ZM87	porphyrobac
60	45	45.9	246	2	066276	066276	porphyrobac
61	45	45.9	326	2	P95613	P95613	rhizobium g
62	45	45.9	444	2	08A250	08A250	infectious
63	45	45.9	444	2	08BDV4	08BDV4	infectious
64	45	45.9	450	2	09SLB9	09SLB9	arabidopsis
65	45	45.9	460	2	065854	065854	beet yellow
66	45	45.9	494	2	06NHQ1	06NHQ1	corynebacte
67	45	45.9	542	2	06APS4	06APS4	desulfocale
68	45	45.9	658	2	091AC1	091AC1	brachydanio
69	45	45.9	887	1	A4_DROME	P14599	drosofila
70	45	45.9	1036	1	AXO1_CHICK	P28655	gallus gall
71	45	45.9	2354	2	024135	024135	drosofila
72	45	45.9	2517	2	09VXG8	09VXG8	drosofila
73	44.5	45.4	342	2	072K49	072K49	thermus the
74	44.5	45.4	661	2	0962C0	0962C0	caenorhabdi
75	44.5	45.4	669	2	09NDH7	09NDH7	caenorhabdi
76	44.5	45.4	1009	2	07SEY7	07SEY7	neutrospora
77	44	44.9	191	2	0938S9	0938S9	uncultured
78	44	44.9	207	1	GTS3_CABEL	016116	caenorhabdi
79	44	44.9	245	2	082987	082987	erythroba
80	44	44.9	252	2	08XP09	08XP09	raletonia s
81	44	44.9	267	2	074FH6	074FH6	geobacter s
82	44	44.9	302	2	0742B3	0742B3	mycobacteri
83	44	44.9	309	2	073H24	073H24	wolbachia p
84	44	44.9	310	2	097Y70	097Y70	sulfolobus
85	44	44.9	354	2	082ZY5	082ZY5	pyrobaculum
86	44	44.9	375	2	07XBP6	07XBP6	oryza sativ
87	44	44.9	400	2	069568	069568	mycobacteri
88	44	44.9	492	1	Y193_COREF	08fp92	corynebacte
89	44	44.9	941	2	08OUJ6	08qu16	infectious
90	44	44.9	984	2	06MQ52	06mq52	bdellovibri
91	44	44.9	1028	2	028138	028138	bos taurus
92	44	44.9	1028	2	08X839	08X839	raletonia s
93	44	44.9	6889	2	08X840	08X840	raletonia s
94	43.5	44.4	216	2	09CK76	09CK76	m mus muscu
95	43.5	44.4	227	2	06A689	06A689	leiftsonia x
96	43.5	44.4	335	2	068334	068334	vibrio chol
97	43.5	44.4	327	2	09KTS1	09KTS1	vibrio chol
98	43.5	44.4	340	2	07XIL8	07XIL8	oryza sativ
99	43	43.9	118	2	07VB61	07VB61	prochloroco
100	43	43.9	157	2	Q9NMG3	Q9nmg3	homo sapien

ALIGNMENTS

```

RESULT 1
08CP43 ID 08CP43 PRELIMINARY; PRT; 332 AA.
AC 08CP43;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Branched-chain alpha-keto acid dehydrogenase E1.
GN OrderedlocusNames=SE1198;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950922;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
  Qin Z.-Q., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.,
  Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
  Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593(2003).
DR EMBL; AE016748; AA004797.1; -.
DR HSSP; P12694; 10LX.
DR GO; GO:0016624; F:oxidoreductase activity, acting on the alde. .; IEA.
DR GO; GO:0008152; P:metabolism, IEA.
DR InterPro; IPR001017; Dehydrogenase_E1.
DR Pfam; PF00676; E1_dh; 1.
DR Complete proteome.
SQ SEQUENCE 332 AA; 36682 MW; 0A9B4468EC96C975 CRC64;

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Query Match 55.6%; Score 54.5; DB 2; Length 332;
Best Local Similarity 76.5%; Pred. No. 2.5;
Matches 13; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
Db 234 EGPTLEWTLTSRT-TPHS 18
234 EGPTLEWTLTSRTTPHS 250

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RESULT 2
0629V1 ID 0629V1 PRELIMINARY; PRT; 410 AA.
AC 0629V1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 2-oxoisovalerate dehydrogenase, E1 component, alpha subunit (EC
  1.2.4.4).
GN ORFNames=BMAA2013;
OS Burkholderia mallei ATCC 23344.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
  Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=243160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 23344;
RX Nierman W.C., Deshaizer D., Kim H.S., Tettelin H., Nelson K.E.,
  Feldblum T., Ulrich R.L., Romling C.M., Brinkac L.M., Daugherty S.C.,
  Davidson T.D., Deboy R.T., Dmitrov G., Dodson R.J., Durkin A.S.,
  Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
  Mohammed Y., Nelson W.C., Radune D., Romero C.M., Sarrisa S.,
  Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafer N.,
  Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
DR EMBL; CP000011; ANI45601.1; -.
KW Oxidoreductase.
SQ SEQUENCE 410 AA; 45445 MW; 99DF85B96288CC2 CRC64;

```

```

Query Match 53.6%; Score 52.5; DB 2; Length 410;
Best Local Similarity 68.8%; Pred. No. 6.6;

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Matches 11; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 4 GPTLEWTLTSRT-TPHS 18
Db 298 GPTLEWTLTSRTTPHS 313

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RESULT 3
063H26 ID 063H26 PRELIMINARY; PRT; 410 AA.
AC 063H26;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 2-oxoisovalerate dehydrogenase alpha subunit (EC 1.2.4.4).
GN Name=bkdA1; ORFNames=BPS2273;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
  Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Tlball R.W., Peacock S.J., Cerdano-Tarraga A.M.,
  Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
  Bentley S.D., Sebahia M., Thomson N.R., Bacon N., Beacham I.R.,
  Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
  Chillingworth T., Cronin A., Crosset B., Davis P., Deshaizer D.,
  Felwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagers K.,
  Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
  Rabinowitch E., Rutherford K., Sanders M., Simmonds M.,
  Songisvial S., Stevens K., Tumapa S., Vesaratchavee M.,
  Whitehead S., Yeats C., Barrett B.G., Oyston P.C.F., Parthill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
  Burkholderia pseudomallei";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL; BX571966; CAH39759.1; -.
KW Oxidoreductase.
SQ SEQUENCE 410 AA; 45415 MW; 99C9C7DD52E88CC2 CRC64;

```

```

Query Match 53.6%; Score 52.5; DB 2; Length 410;
Best Local Similarity 68.8%; Pred. No. 6.6;
Matches 11; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
QY 4 GPTLEWTLTSRT-TPHS 18
Db 298 GPTLEWTLTSRTTPHS 313

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RESULT 4
09YE62 ID 09YE62 PRELIMINARY; PRT; 753 AA.
AC 09YE62;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 753aa long hypothetical aldehyde oxidoreductase.
GN OrderedlocusNames=APB0708;
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcals;
  Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KI;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
  Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anai A., Koeugi H.,
  Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
  Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
  Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kudota K.,
  Nakamura Y., Nomura N., Sako Y., Kikuchi H.;

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Query Match      50.0%; Score 49; DB 2; Length 576;
Best Local Similarity 72.7%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      8 REMLTSTRTPHS 18
      |||||
      158 REMLTSTRTPHT 168

RESULT 8
ID O9XBP6 PRELIMINARY; PRT; 1049 AA.
AC O9XBP6;
DT 01-NOV-1999 (TRMBLrel. 12, Created)
DT 01-NOV-1999 (TRMBLrel. 12, Last sequence update)
DE 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
DE Serine/threonine kinase PK08.
GN Name=pk08;
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DZF1;
RA Inouye S., Jain R., Ueki T., Nariya H., Xu C., Hsu M.,
RA Munoz-Dorado J., Farez-Vidal E., Inouye M.,
RA Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF159691; AAD42856.1; -.
DR HSSP; P71584; 106Y.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR CO; GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR008940; Prenyl_trans.
DR InterPro; IPR00719; TPR_kinase.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00515; TPR_1; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00028; TPR; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50005; TPR; 2.
DR PROSITE; PS50293; TPR_REGION; 1.
DR ATP-binding; Kinase; Repeat; TPR repeat.
DR KMW
SQ SEQUENCE 1049 AA; 114312 MW; 7752862DAA25338C CRC64;

Query Match      50.0%; Score 49; DB 2; Length 1049;
Best Local Similarity 53.3%; Pred. No. 68;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      2 IEGPTLEWLSTRTP 16
      |||||
      167 VEGTTLAEWMKERRP 181

RESULT 9
ID ODBA_PSEPU STANDARD; PRT; 410 AA.
AC P09060;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 2-oxoisovalerate dehydrogenase alpha subunit (EC 1.2.4.4) (Branched-
DE chain alpha-keto acid dehydrogenase E1 component alpha chain) (BCKDH
DE E1-alpha).
GN Name=bkdA1;
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G2;
RX MEDLINE=86329084; PubMed=3416875;
RA Burns G., Brown I., Hatter K., Idriss J., Sokatch J.R.;
RT "Similarity of the E1 subunits of branched-chain-oxoacid dehydrogenase
RT from Pseudomonas putida to the corresponding subunits of mammalian
RT branched-chain-oxoacid and pyruvate dehydrogenases.";
RL Eur. J. Biochem. 176:311-317(1988).
RN [2]
RP SEQUENCE OF 1-17 FROM N.A.
RC STRAIN=G2;
RX MEDLINE=91008935; PubMed=2211503;
RA Madhusudan K.T., Huang G., Burns G., Sokatch J.R.;
RT "Transcriptional analysis of the promoter region of the Pseudomonas
RT putida branched-chain keto acid dehydrogenase operon.";
RL J. Bacteriol. 172:5655-5663(1990).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=99356017; PubMed=10426958; DOI=10.1038/11563;
RA Aevermann A., Seger K., Turley S., Sokatch J.R., Hol W.G.J.;
RT "Crystal structure of 2-oxoisovalerate and dehydrogenase and the
RT architecture of 2-oxo acid dehydrogenase multienzyme complexes.";
RL Nat. Struct. Biol. 6:785-792(1999).
CC -1- FUNCTION: The branched-chain alpha-keto dehydrogenase complex
CC catalyzes the overall conversion of alpha-keto acids to acyl-CoA
CC and CO(2). It contains multiple copies of three enzymatic
CC components: branched-chain alpha-keto acid decarboxylase (E1),
CC lipamide acyltransferase (E2) and lipamide dehydrogenase (E3).
CC -1- CATALYTIC ACTIVITY: 3-methyl-2-oxobutanoate +
CC [dihydrolipoyl]lysine-residue (2-methylpropanoyl)transferase]
CC lipoyllysine = [dihydrolipoyl]lysine-residue (2-
CC methylpropanoyl)transferase] S-(2-
CC methylpropanoyl)dihydrolipoyllysine + CO(2).
CC -1- CORDACTR: Thiamine pyrophosphate.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; M57613; AAA65614.1; -.
DR PIR; S01317; DEPSXA.
DR PDB; 1Q50; X-ray; A=2-408.
DR InterPro; IPR001017; Dehydrogenase_E1.
DR Pfam; PF00676; E1_dh; 1.
DR 3D-structure; Flavoprotein; Oxidoreductase; Thiamine pyrophosphate.
KW 3D-structure; Flavoprotein; Oxidoreductase; Thiamine pyrophosphate.
FT TURN 18 19
FT HELIX 24 26
FT TURN 32 33
FT TURN 40 41
FT HELIX 44 47
FT HELIX 48 51
FT TURN 52 52
FT TURN 55 55
FT STRAND 58 58
FT STRAND 60 61
FT TURN 64 64
FT STRAND 67 69
FT HELIX 74 99
FT HELIX 100 101
FT TURN 110 112
FT HELIX 113 122
FT TURN 125 126
FT STRAND 128 130
FT STRAND 136 141
FT TURN 142 143
FT HELIX 146 154
FT TURN 155 155

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FT TURN 157 158
FT TURN 160 163
FT TURN 167 168
FT STRAND 172 172
FT HELIX 173 175
FT TURN 176 176
FT STRAND 177 177
FT HELIX 186 200
FT TURN 201 202
FT STRAND 207 212
FT TURN 213 213
FT HELIX 214 231
FT TURN 219 231
FT STRAND 232 232
FT STRAND 235 241
FT STRAND 244 245
FT TURN 246 247
FT STRAND 248 249
FT HELIX 250 253
FT TURN 254 257
FT TURN 261 261
FT HELIX 262 266
FT TURN 267 268
FT STRAND 270 275
FT TURN 276 277
FT HELIX 279 294
FT TURN 295 296
FT STRAND 300 305
FT TURN 314 315
FT HELIX 318 320
FT TURN 321 321
FT TURN 324 325
FT HELIX 326 329
FT TURN 331 332
FT HELIX 335 345
FT TURN 346 347
FT HELIX 351 373
FT TURN 374 375
FT HELIX 388 390
FT HELIX 399 406
FT TURN 407 407
SQ SEQUENCE 410 AA; 45268 MW; 0C998460CCFB9CF4 CRC64;

Query Match 49.5%; Score 48.5; DB 1; Length 410;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 4 GPTLRWLTSTRT-PHS 18
DB 298 GPTLRWLTSTRT-PHS 313

RESULT 10
Q88EQ2 PRELIMINARY; PRT; 410 AA.
AC Q88EQ2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 2-oxoisovalerate dehydrogenase, alpha subunit.
GN Name=bkd1; OrderedLocustNames=PP4401;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160468;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hildert H.,
RA Martins dos Santos V.A.P., Fouts D.B., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapfele B.K., Scanlan D., Tran K.,

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RA Moazzez A., Uteerback T.R., Rizzo M., Lee K., Kosack D., Moesti D.,
RA Medler H., Lauber J., Sejpandic D., Hohelsel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Frazer C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016790; AAN69979.1; -.
DR HSSP; P09060; I0S0.
DR TIGR; PP4401; -.
DR GO; GO:0016624; F:oxidoreductase activity, acting on the alde. .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001017; Dehydrogenase_E1.
DR Pfam; PF00676; El_dh; 1.
KW Complete proteome.
SQ SEQUENCE 410 AA; 45220 MW; B1AA98211D94A212 CRC64;

Query Match 49.5%; Score 48.5; DB 2; Length 410;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 4 GPTLRWLTSTRT-PHS 18
DB 298 GPTLRWLTSTRT-PHS 313

RESULT 11
Q91IM2 PRELIMINARY; PRT; 410 AA.
AC Q91IM2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 2-oxoisovalerate dehydrogenase (Alpha subunit).
GN Name=bkd1; OrderedLocustNames=PA2247;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Golty L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kae A., Laibig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL; AE004650; AAG05635.1; -.
DR PIR; C83365; C83365.
DR PIR; S05057; S05057.
DR HSSP; P09060; I0S0.
DR GO; GO:0016624; F:oxidoreductase activity, acting on the alde. .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001017; Dehydrogenase_E1.
DR Pfam; PF00676; El_dh; 1.
KW Complete proteome.
SQ SEQUENCE 410 AA; 45256 MW; BE3AF6FAB66F0F01 CRC64;

Query Match 49.5%; Score 48.5; DB 2; Length 410;
Best Local Similarity 62.5%; Pred. No. 29;
Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 4 GPTLRWLTSTRT-PHS 18
DB 298 GPTLRWLTSTRT-PHS 313

RESULT 12

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O9RV54
ID O9RV54 PRELIMINARY; PRT; 150 AA.
AC O9RV54;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein DR0948.
GN OrderedclustNames=DR0948;
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinetocaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577 (1999).
DR EMBL; AF001947; AAF10530.1; -.
DR FIC; C75456; C75456.
DR TIGR; DR0948; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 150 AA; 16891 MW; 69A7695F09BEF3FB CRC64;

Query Match 49.0%; Score 48; DB 2; Length 150;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 2 IEGLPTLRWLTSTRTP 17
Db 97 LDGSPAREMOTGTPH 112

RESULT 13
066272 PRELIMINARY; PRT; 245 AA.
AC O66272;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Photosynthetic reaction center L subunit (Fragment).
GN Name=pufl;
OS Erythrobacter litoralis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=39960;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAM14332;
RX MEDLINE=21622632; PubMed=11832943; DOI=10.1038/415630a;
RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
RA Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;
RT "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633 (2002).
DR EMBL; AB010981; BAA25791.1; -.
DR HSSP; P02954; 1QOV.
DR GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte. . .; IEA.
DR GO; GO:0045156; P:electron transporter, transferring electron. . .; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019684; P:photosynthesis, light reaction; IEA.
DR InterPro; IPR005871; Photo_L.
DR InterPro; IPR000484; Photo_RC.
DR Pfam; PF00124; Photo_RC; 1.
DR PRINTS; PRO0256; REACTNCENTRE.
DR TIGRFAMs; TIGR01157; pufl; 1.
RP SEQUENCE FROM N.A.
TIGRFAMs; TIGR01157; pufl; 1.

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DR PROSITE; PS00244; REACTION_CENTER; 1.
FT NON_TER 1
SQ SEQUENCE 245 AA; 27214 MW; 52B268713E199ABD CRC64;

Query Match 49.0%; Score 48; DB 2; Length 245;
Best Local Similarity 56.2%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 SIEGPTLRWLTSTRTP 16
Db 25 AIEGPTLRWLTSTRTP 40

RESULT 14
082989 PRELIMINARY; PRT; 249 AA.
AC 082989;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Photosynthetic reaction center L subunit (Fragment).
GN Name=pufl;
OS Erythrobacter sp.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=1042;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MBIC3019;
RX MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
RA Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;
RT "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633 (2002).
DR EMBL; AB015708; BAA32995.1; -.
DR HSSP; P02954; 1YST.
DR GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte. . .; IEA.
DR GO; GO:0045156; P:electron transporter, transferring electron. . .; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019684; P:photosynthesis, light reaction; IEA.
DR InterPro; IPR005871; Photo_L.
DR InterPro; IPR000484; Photo_RC.
DR Pfam; PF00124; Photo_RC; 1.
DR PRINTS; PRO0256; REACTNCENTRE.
DR TIGRFAMs; TIGR01157; pufl; 1.
DR PROSITE; PS00244; REACTION_CENTER; 1.
FT NON_TER 1
SQ SEQUENCE 249 AA; 27702 MW; 4D68EDC82B7166AD CRC64;

Query Match 49.0%; Score 48; DB 2; Length 249;
Best Local Similarity 56.2%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 SIEGPTLRWLTSTRTP 16
Db 25 AIEGPTLRWLTSTRTP 40

RESULT 15
09XDVO PRELIMINARY; PRT; 278 AA.
AC 09XDVO;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Photosynthetic reaction center L subunit.
GN Name=pufl;
OS Erythrobacter sp. MBIC3960.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=94771;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=MBIC3960;
 RX MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
 RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
 Hamada T., Eisen J.A., Frazer C.M., DeJong E.F.;
 RT "Unexpected diversity among marine aerobic anoxygenic phototrophs";
 RL Nature 415:630-633(2002).
 DR EMBL, AB027515; BAA78672.1; -.
 DR HSSP, P02954; 1YST.
 DR GO, GO:0030077; C:light-harvesting complex (sensu Proteobacte. . .; IEA.
 DR GO, GO:0045156; F:electron transporter, transferring electron. . .; IEA.
 DR GO, GO:0006118; P:electron transport; IEA.
 DR GO, GO:0019684; P:photosynthesis, light reaction; IEA.
 DR InterPro: IPR005871; Photo_L.
 DR InterPro: IPR000484; Photo_RC.
 DR Pfam, PF00124; Photo_RC; 1.
 DR PRINTS; PRO0256; REACTCENTRE.
 DR TIGRPFAM; TIGR01157; pufl; 1.
 DR PROSITE; PS00244; REACTION_CENTER; 1.
 SQ SEQUENCE 278 AA; 30735 MW; 0BE61864B3C54FB CRC64;

Query Match 49.0%; Score 48; DB 2; Length 278;
 Best Local Similarity 56.2%; Pred. No. 23;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 SEPTLRWMLSRTP 16
 :|||||
 DB 54 AIEGPTLNPMLIDIP 69

RESULT 16

Q9RKM5 PRELIMINARY; PRT; 319 AA.

AC Q9RKM5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative MerR family transcriptional regulator.
 GN ORFNames=SCD17.06c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 NC NCB1_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 Cronin A., Frazer A., Godle A., Hidalgo J., Hornsby T., Howarth S.,
 Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 Rabbinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)";
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: Contains 1 HTH merR-type DNA-binding domain.
 DR EMBL, AL939118; CAB56383.1; -.
 DR GO, GO:0005622; C:intracellular; IEA.
 DR GO, GO:0003700; F:transcription factor activity; IEA.
 DR GO, GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR000551; HTH_MerR.
 DR InterPro: IPR009061; Putativ_DNA_bind.
 DR Pfam, PF00376; MerR; 1.
 DR PRINTS; PRO0040; HTHMER.
 DR SMART; SM00422; HTH_MER_1;
 DR PROSITE; PS50937; HTH_MER_2; 1.
 SQ Complete proteome; DNA-binding.
 OS SEQUENCE 319 AA; 34841 MW; 1F51905A8BA5365B CRC64;

Query Match 49.0%; Score 48; DB 2; Length 319;

Best Local Similarity 66.7%; Pred. No. 27;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 SEPTLRWMLSRTP 14
 :|||||
 DB 258 DSEPLEWLAGR 269

RESULT 17

Q9KX10 PRELIMINARY; PRT; 388 AA.

AC Q9KX10;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Protein kinase.
 GN Name=pxnB; Synonyms=ORF388;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NC NCB1_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COL;
 RX MEDLINE=20031141; PubMed=10566865;
 RA de Lencastre H., Wu S.W., Pinho M.G., Ludovico A.M., Filipe S.,
 Gardete S., Sobral R., Gill S., Chung M., Tomasz A.;
 RT "Antibiotic resistance as a stress response: complete sequencing of a
 large number of chromosomal loci in Staphylococcus aureus strain COL
 that impact on the expression of resistance to methicillin";
 RL Microb. Drug Resist. 5:163-175(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COL;
 RA Wu S.;
 RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL, Y13639; CAA73979.1; -.
 DR HSSP, P71584; 106Y.
 DR GO, GO:0005524; F:ATP binding; IEA.
 DR GO, GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO, GO:0016740; F:transferase activity; IEA.
 DR GO, GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011009; Kinase_like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR InterPro: IPR008271; Ser_Thr_pkin_AS.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-Binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 388 AA; 43764 MW; 0582809E06379580 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 388;
 Best Local Similarity 58.8%; Pred. No. 33;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IEPTLRWMLSRTPS 18
 :|||||
 DB 90 IEPTLRWMLSRTPS 106

RESULT 18

Q8GA10 PRELIMINARY; PRT; 481 AA.

AC Q8GA10;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative amino acid permease.
 DR Arthrobacter nicotovorans.
 OG Plasmid PAOI.

OC Bacteria: Actinobacteria: Actinobacteridae: Actinomycetales;
OC Micrococciaceae; Micrococcaceae; Arthrobacter.
OK NCBI_TaxID=29320;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95115562; PubMed=7815950;
RA Greher-Beck S., Igloi G.L., Pust S., Schilz R., Decker K.,
RA Brandesch R.;
RT "Structural analysis and molybdenum-dependent expression of the PAO1-
RT encoded nicotine dehydrogenase genes of Arthrobacter nicotianovorus.",
RL Mol. Microbiol. 13:929-936(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96172783; PubMed=8588735;
RA Wenzel C., Igloi G., Hemminger H., Brandesch R.;
RT "A PAO1-encoded molybdopterin cofactor gene (moa) of Arthrobacter
RT nicotianovorus: characterization and site-directed mutagenesis of the
RT encoded protein.",
RL Arch. Microbiol. 164:142-151(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98088982; PubMed=9428706;
RA Menendez C., Otto A., Igloi G., Nick P., Brandesch R., Schubach B.,
RA Botcher B., Brandesch R.;
RT "Molybdate-uptake genes and molybdopterin-biosynthesis genes on a
RT bacterial plasmid. Characterization of MoaA as a filament-forming
RT protein with adenosinetriphosphatase activity.",
RL Eur. J. Biochem. 250:524-531(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=9906870; PubMed=9878353; DOI=10.1006/jmbi.1998.2227;
RA Schenk S., Hoelz A., Kraus B., Decker K.;
RT "Gene structure and properties of enzymes of the plasmid-encoded
RT nicotine catabolism of Arthrobacter nicotianovorus.",
RL J. Mol. Biol. 284:1323-1339(1998).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97230479; PubMed=9073580; DOI=10.1006/plas.1996.1272;
RA Menendez C., Igloi G.L., Brandesch R.;
RT "IS1473, a putative insertion sequence identified in the plasmid PAO1
RT from Arthrobacter nicotianovorus: isolation, characterisation and
RT distribution among Arthrobacter species.",
RL Plasmid 37:35-41(1997).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=21405725; PubMed=11514508;
DOI=10.1128/JB.183.18.5262-5267.2001;
RA Batsch D., Sandu C., Brandesch R., Igloi G.L.;
RT "A gene cluster on pAO1 of Arthrobacter nicotianovorus involved in the
RT degradation of the plant alkaloid nicotine: cloning, purification and
RT characterization of 2,6-dihydroxypyridine 3-hydroxylase.",
RL J. Bacteriol. 183:5262-5267(2001).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=22505657; PubMed=12618462;
DOI=10.1128/JB.185.6.1976-1986.2003;
RA Igloi G.L., Brandesch R.;
RT "Sequence of the 16S-Ribosome catabolic plasmid PAO1 from Arthrobacter
RT nicotianovorus and identification of a PAO1-dependent nicotine uptake
RT system.",
RL J. Bacteriol. 185:1976-1986(2003).
RN [8]
RP EMBL, AJ507836; CAD47924.1; -;
DR GO, GO:0016021; C: integral to membrane; IEA.
DR GO, GO:0005279; F: amino acid-polyamine transporter activity; IEA.
DR GO, GO:0006865; P: amino acid transport; IEA.
DR GO, GO:0006810; P: transport; IEA.
DR InterPro, IPR002293; AA/perl_permease1.
DR InterPro, IPR004841; Permease_region.
DR Pfam, PF00324; AA_permease; I.
KM Plasmid; Transmembrane; Transport.
SQ SEQUENCE 481 AA; 49782 MW; 4EA9FB3BB876B64 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 481;

Best Local Similarity 56.2%; Pred. No. 42;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 SIEGPTLRWLTSTRP 16
Db 366 SLVGPVWMLWLSSTP 381
RESULT 19
ID 0751J9 PRELIMINARY; PRT; 632 AA.
AC 0751J9;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein B1130610.3 (Hypothetical protein
DE P0022D06.17).
GN Name=B1130610.3; Synonym=P0022D06.17;
OS Oryza sativa [japonica cultivar-group].
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrharioideae; Oryzaceae; Oryza.
OK NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Heing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Lee P.-F., Chang S.-J., Chen H.-C., Chen S.-K.,
RA Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y.,
RA Hsiao S.-H., Hsiung J.-N., Hsu C.-H., Kau P.-I., Lee M.-C.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Heing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL "Oryza sativa PAC P0022D06 genomic sequence."
RT Submitted (Sep-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL, AC130603; AAT01306.1; -;
DR EMBL, AC132485; AAU03115.1; -;
DR InterPro, IPR009105; Colicin_E3_cat.
KM Hypothetical protein.
SQ SEQUENCE 632 AA; 69035 MW; 8EBDE6377EB5BD0F CRC64;
Query Match 49.0%; Score 48; DB 2; Length 632;
Best Local Similarity 60.0%; Pred. No. 56;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 IEGPTLRWLTSTRP 16
Db 400 LEGESLREWLFPDTP 414
RESULT 20
ID 08NX14 PRELIMINARY; PRT; 664 AA.
AC 08NX14;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE MW1103 protein.
GN OrderedLocustNames=MW1103;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OK NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;

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RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RU Lancet 359:1819-1827(2002).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF004826; BAB94968.1; -.
DR HSP; P71584; 106Y.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008658; F:penicillin binding; IEA.
DR GO; GO:0006674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF03793; PASTA; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00740; PASTA; 3.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Complete proteome; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 664 AA; 74363 MW; 26F1386C5DB61828 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 664;
Best Local Similarity 58.8%; Pred. No. 59;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IEGPTLRWLTSTRTPHS 18
ID ||||| |::| |
DB 90 IEGPTLSEYIESHGPLS 106

RESULT 21
O99UP8 PRELIMINARY; PRT; 664 AA.
AC O99UP8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protein kinase.
GN OrderedLocustNames=SAV1220;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RU Lancet 357:1225-1240(2001).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF003361; BAB57382.1; -.
DR PIR; G89894; G89894.
DR HSP; P71584; 106Y.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008658; F:penicillin binding; IEA.
DR GO; GO:0006474; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.

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DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR005543; PASTA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF03793; PASTA; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00740; PASTA; 3.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Complete proteome; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 664 AA; 74377 MW; 3461386C5DB61828 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 664;
Best Local Similarity 58.8%; Pred. No. 59;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IEGPTLRWLTSTRTPHS 18
ID ||||| |::| |
DB 90 IEGPTLSEYIESHGPLS 106

RESULT 22
O7A5Z8 PRELIMINARY; PRT; 664 AA.
AC O7A5Z8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Protein kinase.
GN OrderedLocustNames=SA1063;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; Pubmed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RU Lancet 357:1225-1240(2001).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF003361; BAB42315.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008658; F:penicillin binding; IEA.
DR GO; GO:0006474; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006473; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR005543; PASTA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF03793; PASTA; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00740; PASTA; 3.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; TYR_KC; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00106; PROTEIN_KINASE_ST; 1.

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KW ATP-binding: Complete proteome; Kinase;
 KM Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 664 AA; 74377 MW; 3461386C5DB61828 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 664;
 Best Local Similarity 58.8%; Pred. No. 59;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IEPTLRWLTSTRTPHS 18
 |||||::|
 Db 90 IEPTLRSEYIESHGPLS 106

RESULT 23

ID Q6G9Z3 PRELIMINARY; PRT; 664 AA.

AC Q6G9Z3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Serine/threonine-protein kinase (EC 2.7.1.1-).
 GN OrderedLocustNames=SA51154;
 OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RN [1]

RA Spratt B.G., Parkhill J.;

RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1 SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; BX571857; CAG42931.1; -.
 DR GO; GO:0006524; F:ATP binding; IEA.
 DR GO; GO:0006674; F:penicillin binding; IEA.
 DR GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0006468; P:protein kinase activity; IEA.
 DR InterPro: IPR011009; Kinase_like.
 DR InterPro: IPR005543; PASTA.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam; PF03793; PASTA; 2.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00740; PASTA; 3.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding: Complete proteome; Kinase;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 664 AA; 74363 MW; 26F1386C5DB61828 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 664;
 Best Local Similarity 58.8%; Pred. No. 59;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IEPTLRWLTSTRTPHS 18
 |||||::|

Db 90 IEPTLRSEYIESHGPLS 106

RESULT 24

ID Q6GHL5 PRELIMINARY; PRT; 664 AA.

AC Q6GHL5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Serine/threonine-protein kinase (EC 2.7.1.1-).
 GN Name=PKMB; OrderedLocustNames=SA41196;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RN [1]

RA Spratt B.G., Parkhill J.;

RT "Complete genomes of two clinical Staphylococcus aureus strains:
 evidence for the rapid evolution of virulence and drug resistance.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 CC -1 SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; BX571855; CAG40198.1; -.
 DR GO; GO:0006524; F:ATP binding; IEA.
 DR GO; GO:0006674; F:penicillin binding; IEA.
 DR GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011009; Kinase_like.
 DR InterPro: IPR005543; PASTA.
 DR InterPro: IPR002290; Prot_kinase.
 DR InterPro: IPR008271; Ser_thr_kinase.
 DR InterPro: IPR001245; Ser_thr_pkinase.
 DR Pfam; PF03793; PASTA; 2.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00740; PASTA; 3.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding: Complete proteome; Kinase;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 664 AA; 74363 MW; 26F1386C5DB61828 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 664;
 Best Local Similarity 58.8%; Pred. No. 59;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 IEPTLRWLTSTRTPHS 18
 |||||::|
 Db 90 IEPTLRSEYIESHGPLS 106

RESULT 25

ID Q8Y015 PRELIMINARY; PRT; 91 AA.

AC Q8Y015;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein RSC1059.

```

GN Name=RS04149; OrderedLocNames=RS01059;
OS Ralstonia solanacearum (pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
ON NCB1_TaxId=305;
RX SEQUENCE FROM N.A.
RC STRAIN=GM11000; PubMed=11823852; DOI=10.1038/415497a;
RX MEDLINE=21681879;
RA Salanoubat M., Genin S., Artiguenave F., Gouy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Catolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguer P., Thebaud P., Whalen M., Winkler P., Levy M.,
RA Weisenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502 (2002).
DR EMBL; AL646062; CAD14761.1; -.
KW Complete proteome.
SQ SEQUENCE 91 AA; 10321 MW; 2B4DFEB37A528AD CRC64;

Query Match
Best Local Similarity 48.0%; Score 47; DB 2; Length 91;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 EGGPTLRWLTSTRTP 16
Db 75 LDGPAVQAWLMAQTP 89

RESULT 26
ID YD55_HABIN STANDARD; PRT; 154 AA.
AC P44168;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical UPF0260 protein H11355.
GN OrderedLocNames=H11355;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
ON NCB1_TaxId=727;
RX SEQUENCE FROM N.A.
RC STRAIN=Rd / KM20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uitterback T.R., Hanna M.C., Nguyen D.T., Saudel D.M., Brandon R.C.,
RA Pine L.D., Fritchman J.A., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512 (1995).
CC -1- SIMILARITY: Belongs to the UPF0260 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U32814; AAC23002.1; -.
CC PIR; P64026; P64026.
CC TIGR; H11355; -.
DR HAMAP; MF_00676; -. 1.

```

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DR InterPro; IPR008228; UCP006173.
DR Pfam; PF05779; DUF838; 1.
DR PIRSF; PIRSF006173; UCP006173; 1.
DR PRODom; PD021710; UCP006173; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 154 AA; 18163 MW; 886CE6D467E8AB55 CRC64;

Query Match
Best Local Similarity 48.0%; Score 47; DB 1; Length 154;
Matches 11; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 3 EGGPTLRWLTSTRTPHS 18
Db 105 EGGPTLRWLTSTRTPHS 122

RESULT 27
ID O66278 PRELIMINARY; PRT; 245 AA.
AC O66278;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Photosynthetic reaction center L subunit (Fragment).
GN Name=pufl;
OS Agrobacterium sanguineum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae.
ON NCB1_TaxId=73269;
RX SEQUENCE FROM N.A.
RC STRAIN=JAM12620;
RX MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
RA Hamada T., Eisen J.A., Fraser C.M., Delong E.F.;
RT "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633 (2002).
DR EMBL; AB011074; BAA25722.1; -.
DR HSSP; P02954; IQOV;
DR GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte. . . IEA.
DR GO; GO:0045156; P:electron transporter, transferring electron. . . IEA.
DR GO; GO:006118; P:electron transport; IEA.
DR GO; GO:0019684; P:photosynthesis, light reaction; IEA.
DR InterPro; IPR005871; Photo_L.
DR InterPro; IPR000484; Photo_RC.
DR Pfam; PF00124; Photo_RC; 1.
DR PRINTS; PR00256; REACTNCENTRE.
DR TIGRPFAM; TIGR01157; pufl; 1.
DR PROSITE; PS00244; REACTION_CENTER; 1.
FT NON_TER 1
SQ SEQUENCE 245 AA; 26840 MW; DBACDB4DA050DB80 CRC64;

Query Match
Best Local Similarity 48.0%; Score 47; DB 2; Length 245;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 EGGPTLRWLTSTRTPHS 18
Db 27 EGGPTLRWLTSTRTPHS 42

RESULT 28
ID Q70BP7 PRELIMINARY; PRT; 282 AA.
AC Q70BP7;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE AgCP2340 (Fragment).
GN Name=agCG44337; ORFNames=ENSGANG0000014770;
OS Anopheles gambiae str. PE8T.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematoceera; Culicoidae; Anopheles.

```

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OX NCBI_TaxID=180454;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data
DR EMBL; AAAB0100878; EAA08303.1; -.
DR InterPro; IPR008042; Retrotrans_Pao.
DR Pfam; PF05380; Peptidase_A17; 1.
FT NON_TER 1
FT NON_TER 282
SQ SEQUENCE 282 AA, 31558 MW, 8154BA517F1FD32A CRC64;

Query Match
Best Local Similarity 48.0%; Score 47; DB 2; Length 282;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 STEGPTLRWLTSTRT 15
DB 31 SLEGEQLQEWLQFRT 45

RESULT 29
ID Q6J6D5 PRELIMINARY; PRT; 417 AA.
AC Q6J6D5;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Carboxypeptidase A (EC 3.4.17.1).
Name=CPA-VI;
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RC SEQUENCE FROM N.A.
RA Iseo J., Amenezes A., Wells M.A.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY590492; AAT36730.1; -.
DR HSSP; P00730; IAPM.
DR GO; GO:0004182; F:carboxypeptidase A activity; IEA.
DR GO; GO:0004180; F:carboxypeptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000834; Peptidase_M14.
DR InterPro; IPR003146; Prot_inh_M14A.
DR InterPro; IPR009020; Prot_inh_propept.
DR Pfam; PF00246; Peptidase_M14; 1.
DR Pfam; PF02244; Propep_M14; 1.
DR PRINTS; PR00765; CRBOXYPRTASEA.
DR SMART; SM00631; Zn_pept; 1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
DR Carboxypeptidase; Hydrolase.
SQ SEQUENCE 417 AA, 47505 MW, E599DB6DA4A1B97B CRC64;

Query Match
Best Local Similarity 48.0%; Score 47; DB 2; Length 417;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 TLREWLTSRTPHS 18
DB 226 TNRQWKRTTTPHS 228

RESULT 30
ID Q31703 PRELIMINARY; PRT; 430 AA.
AC Q31703; Q7BVS3;

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DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Molybdopterin biosynthesis protein MoeA.
GN Name=moeA; OrderedLocustNames=BSU14280;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bortero M.G., Bessieres P., Bolotin A., Borcherdt S.,
RA Borriss R., Boursier L., Brans A., Braun M., Briggell S.C., Bron S.,
RA Broillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Distenhof A., Ehrlich S.D., Emerson P.T.,
RA Eutlian K.-D., Errington J., Fabret C., Ferrati E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Kleier-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Maasda S., Mauel C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Potworlik S.,
RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivoita C., Rocha E., Roche B.,
RA Rose M., Sadate Y., Sato T., Scantlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Serr S.J., Serron P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takegi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Yamakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA Vassarotti A., Viari A., Wambut R., Wedler E., Wedler E.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=1168;
RX MEDLINE=90368558; PubMed=1697575;
RA Hemila H., Palva A., Paulin L., Arvidson S., Palva I.,
RT "Secretory S complex of Bacillus subtilis: sequence analysis and
RT identity to pyruvate dehydrogenase."
RL J. Bacteriol. 172:5052-5063(1990).
RN [3]
RC SEQUENCE FROM N.A.
RC STRAIN=1168;
RX MEDLINE=97144523; PubMed=8990290;
RA Henriques A.O., Bryan E.M., Beall B.W., Moran C.P., Jr.;
RT "cseI, cseE, and cseK2 are new members of mother-cell-specific
RT sporulation regulons in Bacillus subtilis."
RL J. Bacteriol. 179:389-398(1997).
RN [4]
RC SEQUENCE FROM N.A.
RC STRAIN=168;
RA Calwell R.M., Ferrati E.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99111; CAB13301.1; -.
DR EMBL; AF012285; AAC24902.1; -.
DR PIR; B69659; B69659.
DR HSSP; P12281; 1GBL.
DR GO; GO:0006777; P:Molybdopterin cofactor biosynthesis; IEA.
DR InterPro; IPR001453; MoeF_biosynth.
DR InterPro; IPR005110; MoeA_N.
DR InterPro; IPR005110; MoeA_N.

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DR Pfam: PR00994; MOCF_biosynth; 1.
 DR Pfam: PF03454; MOCF_C; 1.
 DR Pfam: PF03453; MOCF_N; 1.
 DR ProDom: PD002460; MOCF_biosynth; 1.
 DR TIGRFam: TIGR00177; molyb_syn; 1.
 KW Complete proteome.
 SQ SEQUENCE 430 AA; 46619 MW; DBECC5FB9F542388 CRC64;

Query Match 48.0%; Score 47; DB 2; Length 430;
 Best Local Similarity 50.0%; Pred. No. 53;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PRLREWLTSRTPS 18
 Db 323 PRLREWLTSRTPS 336

RESULT 31
 Q8CSV9 PRELIMINARY; PRT; 667 AA.
 ID Q8CSV9; 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DE 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 GN OrderedLocustNames=SE0895;
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RX PubMed=12950922;
 RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
 Qiu Z.-Q., Zhao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
 Yuan Z.-H., Zhao G.-P., Gu D., Danchin A., Wen Y.-M.;
 RT "Genome-based analysis of virulence genes in a non-biofilm-forming
 Staphylococcus epidermidis strain (ATCC 12228).";
 RL Mol. Microbiol. 49:1577-1593(2003).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AE016746; AAC04492.1; -.
 DR HSSP: P71584; 106Y
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:000658; F:penicillin binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011008; Kinase_like.
 DR InterPro: IPR005543; PASTA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR Pfam: PF03793; PASTA; 2.
 DR Pfam: PF00069; Kinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00740; PASTA; 3.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PSS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PSS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Complete proteome; Kinase;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 667 AA; 75411 MW; 479877B4531CDD97 CRC64;

Query Match 48.0%; Score 47; DB 2; Length 667;
 Best Local Similarity 58.8%; Pred. No. 86;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IEQPTLREWLTSRTPS 18
 Db 90 IEQPTLREWLTSRTPS 106

RESULT 32
 Q7MWY0 PRELIMINARY; PRT; 818 AA.
 ID Q7MWY0; 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DE 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 GN Name=trbE; ORFNames=PHG362;
 OS Alkaligenes eutrophus (Ralstonia eutropha).
 OG Plasmid megaplasmid pHG1.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Wauteria.
 OX NCBI_TaxID=510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H16;
 RX MEDLINE=22830147; PubMed=12948488; DOI=10.1016/S0022-2036(03)00894-5;
 RA Schwartz E., Henne A., Cramm R., Bittinger T., Friedrich B.,
 RA Gottschalk G.;
 RT "Complete Nucleotide Sequence of pHG1: A Ralstonia eutropha H16
 Megaplasmid Encoding Key Enzymes of H₂-based Lithoautotrophy and
 Anaerobiosis.";
 RL J. Mol. Biol. 332:369-383(2003).
 DR EMBL: AY305378; AAP8611.1; -.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR InterPro: IPR004346; CAGE_TtBE_VtTB.
 DR Pfam: PF03135; CAGE_TtBE_VtTB; 1.
 KW Plasmid.
 SQ SEQUENCE 818 AA; 92392 MW; AFD46E761EDC99B CRC64;

Query Match 48.0%; Score 47; DB 2; Length 818;
 Best Local Similarity 50.0%; Pred. No. 11e+02;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IEQPTLREWLTSRT 15
 Db 426 IEQPTLREWLTSRT 439

RESULT 33
 ODBA_BACSU STANDARD; PRT; 330 AA.
 ID ODBA_BACSU; 01-OCT-1994 (Rel. 30, Created)
 AC P37940;
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 2-oxoisovalerate dehydrogenase alpha subunit (EC 1.2.4.4) (Branched-
 chain alpha-keto acid dehydrogenase E1 component alpha chain) (BCMDH
 DE E1-alpha).
 GN Name=bfmbA; Synonyms=bfmbA; OrderedLocustNames=BS024050;
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-22.
 RC STRAIN=168;
 RX MEDLINE=93279308; PubMed=8504804;
 RA Wang G.-F., Kuriki T., Roy K.L., Kaneda T.;
 RT "The primary structure of branched-chain alpha-oxo acid dehydrogenase
 from Bacillus subtilis and its similarity to other alpha-oxo acid
 dehydrogenases.";
 RT Eur. J. Biochem. 213:1091-1099(1993).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / JH642;
 RX MEDLINE=97124195; PubMed=8969508;
 RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
 Kobayashi Y.;
 RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
 the Bacillus subtilis genome containing the skin element and many
 RT sporulation genes.";
 RL Microbiology 142:3103-3111(1996).

[3]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=93843577; DOI=10.1038/36786;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero L.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier M., Brans A., Braun M., Brigelli S.C., Bron S.,
RA Brouillet S., Brunsch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Enright S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabrit C., Ferrati E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleron N.,
RA Ghim S.-Y., Glaser P., Goffeau A., Goltightly E.J., Grandi G.,
RA Giuseppe G., Guy B.-J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holteppel S., Hosono S., Hulo M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata B., Kaascheta T., Klaer-Biancard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kuanuo M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lees S.M., Levine A., Liu H., Maeda S., Mauel C.,
RA Medigne C., Medina N., Mellado R.P., Mizuno M., Moesil D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro V., Pohl T.M., Portetelle D., Potwollik S.,
RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rooba E., Roche B.,
RA Rose M., Sadiet Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serro P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Yamakoshi A., Tanaka T., Terpetra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandemol M., Vanlier F.,
RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Wetzsteiger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E.,
RA Yoshikawa H., Danchin A.,
RT "the complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*,"
RL Nature 390:249-256(1997).
CC -1- FUNCTION: The branched-chain alpha-keto dehydrogenase complex catalyzes the overall conversion of alpha-keto acids to acyl-CoA and CO(2). It contains multiple copies of three enzymatic components: branched-chain alpha-keto acid decarboxylase (E1), lipamide acyltransferase (E2) and lipamide dehydrogenase (E3).
CC -1- CATALYTIC ACTIVITY: 3-methyl-2-oxobutanoate + [dihydrolipoyllysine-residue (2-methylpropanoyl)]transferase [lipoyllysine = (dihydrolipoyllysine-residue (2-methylpropanoyl)]transferase [S-(2-methylpropanoyl)]dihydrolipoyllysine + CO(2).
CC -1- COFACTOR: Thiamine pyrophosphate.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -----
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CC -----
DR EMBL, M97391, AAA22278.1; -
DR EMBL, D84432, BAA12598.1; -
DR EMBL, Z99116, CAA14336.1; -
DR PIR, C69593; C69593.
DR HSSP, P12694; 1DTM.
DR Subtilast; BG10307; bfmBA.
DR InterPro; IPR001017; Dehydrogenase_E1.
DR Pfam; PF00676; E1_dh; 1.
KW Complete proteome; Direct protein sequencing; Flavoprotein; Oxidoreductase; Thiamine pyrophosphate.
SQ SEQUENCE 330 AA; 36334 MW; 39584D3FA363B656 CRC64;

```

Qy      3  EGPTRLREWLTSR-TPHS 18
      ||||| : : ||||
Db      237 EGPTRLTETISYRLTPHS 253

RESULT 34
065HK8
ID 065HK8 PRELIMINARY; PRT; 330 AA.
AC 065HK8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE BkdA (Branched-chain alpha-keto acid dehydrogenase E1 subunit) (2-oxoisovalerate dehydrogenase alpha subunit).
GN Name=bkdA; ORFNames=BL01504, BL102582;
OS Bacteria; licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCHI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 13;
RX PubMed=15383718;
RA Velth M., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenreich P., Baumeister S., Henne A., Liesegang H., Merkl R., Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an Organism with Great Industrial Potential.";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J., Tang M., de Leon A.L., Xiang H., Gueti V., Clausen I.G., Olsen P.B., Raemussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D., Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; AE017333; AAU41456.1; -.
DR EMBL; CP000002; AAU24096.1; -.
SQ SEQUENCE 330 AA; 36463 MW; BE314979P9065C9B CRC64;

Query Match 47.4%; Score 46.5; DB 2; Length 330;
Best Local Similarity 64.7%; Pred. No. 48;
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy      3  EGPTRLREWLTSR-TPHS 18
      ||||| : : ||||
Db      237 EGPTRLTETISYRLTPHS 253

RESULT 35
025564
ID 025564 PRELIMINARY; PRT; 527 AA.
AC 025564;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein HP0906;
GN OrderedLocustNames=HP0906;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCHI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S.R., Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,

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OS Eleutherodactylus augusti (barking frog).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Telmatobiinae; Eleutherodactylus.
OK NCBI_TaxId=228429;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Huachucamets AZ, Santaritamets AZ, and Huachucamets17_AZ;
RA Goldberg C.S., Sullivan B.K., Malone J.H., Schwalbe C.R.;
RT "Divergence among barking frogs (Eleutherodactylus augusti) in the
RT southwestern United States.";
RL Herpetologica 60:312-320(2004).
DR EMBL; AY442941; AAS49133.1; -.
DR EMBL; AY442948; AAS49140.1; -.
DR EMBL; AY442938; AAS49130.1; -.
KM Mitochondrion.
FT NON TER
SQ SEQUENCE 156 AA; 16791 MW; DC21B329322A77EB CRC64;

Query Match 46.9%; Score 46; DB 2; Length 156;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 EMLTSRTPHS 18
DB 77 EMLISSTPHS 86

RESULT 40
064K25 PRELIMINARY; PRT; 156 AA.
AC 064K25;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
DE NADH dehydrogenase subunit II (Fragment).
GN Name=ND2;
OS Eleutherodactylus augusti (barking frog).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
OC Telmatobiinae; Eleutherodactylus.
OX NCBI_TaxId=228429;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Huachucamets30_AZ;
RA Goldberg C.S., Sullivan B.K., Malone J.H., Schwalbe C.R.;
RT "Divergence among barking frogs (Eleutherodactylus augusti) in the
RT southwestern United States.";
RL Herpetologica 60:312-320(2004).
DR EMBL; AY442940; AAS49132.1; -.
KM Mitochondrion.
FT NON TER
SQ SEQUENCE 156 AA; 16830 MW; DC21B329322A60DB CRC64;

Query Match 46.9%; Score 46; DB 2; Length 156;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 EMLTSRTPHS 18
DB 77 EMLISSTPHS 86

RESULT 41
082PX5 PRELIMINARY; PRT; 377 AA.
AC 082PX5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DR Hypoetical protein.

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GN OrderedLocustNames=SAV747;
OS Streptomyces avermectilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.
OK NCBI_TaxId=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermectilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermectilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005023; BAC68457.1; -.
KM Complete proteome; Hypoetical protein.
SQ SEQUENCE 377 AA; 41307 MW; 0253176AAAB62F3 CRC64;

Query Match 46.9%; Score 46; DB 2; Length 377;
Best Local Similarity 61.5%; Pred. No. 67;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IEPTLRWLTNR 14
DB 168 MEGPDLRAWLPKR 180

RESULT 42
0745Z3 PRELIMINARY; PRT; 559 AA.
AC 0745Z3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Ribonucleoside-diphosphate reductase alpha chain.
GN OrderedLocustNames=TRP0162;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OG Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OC NCBI_TaxId=262724;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15064768;
RA Henne A., Brueggemann H., Raasch C., Wietzer A., Hartsch T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenzcek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
RT "The genome sequence of the extreme thermophile Thermus
RT thermophilus.";
RL Nat. Biotechnol. 22:547-553(2004).
DR EMBL; AE017222; AAS82492.1; -.
DR GO; GO:0005971; Cytridonucleoside-diphosphate reductase complex; IEA.
DR GO; GO:0004748; P-ribonucleoside-diphosphate reductase activity; IEA.
DR GO; GO:0006260; P-DNA replication; IEA.
DR InterPro; IPR000788; Ribonucleo_red.
DR InterPro; IPR010994; Ruva_2_like.
DR InterPro; IPR005829; Sug_transporter.
DR Pfam; PF02867; Ribonuc_red_1gc; 1.
DR PRINTS; PR01183; RIBORDTASEM1.
DR PROSITE; PS00216; SUAR_TRANSPORT_1; UNKNOWN_1.
KM Complete proteome.

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SEQ SEQUENCE 559 AA; 63800 MW; E3980D88A831A8FB CRC64;

Query Match 46.9%; Score 46; DB 2; Length 559;
Best Local Similarity 47.1%; Pred. No. 1e+02;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IEQPTLRWLTSTRTPS 18
Db 168 VEPDLEWLSIQREHS 184

RESULT 43

SYE_PYRAE STANDARD; PRT; 570 AA.

ID SYE_PYRAE STANDARD; PRT; 570 AA.
AC Q8Z0J3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
DE (Gluts).
GN Name=glx; OrderedLocNames=PAE2969;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_Taxid=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
aerophilum.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AE009904; AAL64575.1; -.
DR HSSP; P00962; INYL.
DR HAMAP; MF 00022; -; 1.
DR InterPro; IPR004526; Glx arch.
DR InterPro; IPR000924; Glu tRNA-synt 1c.
DR InterPro; IPR011035; Ribosomal_L25rel.
DR InterPro; IPR001412; tRNA-synt 1.
DR Pfam; PF00749; tRNA-synt 1c; 1.
DR Pfam; PF03950; tRNA-synt 1c; 1.
DR PRINTS; PR00987; TRNASYNTHLU.
DR TIGRAME; TIGR00463; glx arch; 1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
KW Protein biosynthesis.
FT SITE 107 117 "HIGH" region.
SQ SEQUENCE 570 AA; 65837 MW; 767FCEB29A3064C CRC64;

Query Match 46.9%; Score 46; DB 1; Length 570;
Best Local Similarity 42.1%; Pred. No. 1.1e+02;
Matches 8; Conservative 5; Mismatches 0; Indels 6; Gaps 1;

Qy 5 PTLREWL-----TSRTPH 17
Db 258 PSYRDWVAFRITDTSKTPH 276

RESULT 44

Q9K9Z0 PRELIMINARY; PRT; 664 AA.

ID Q9K9Z0 PRELIMINARY; PRT; 664 AA.
AC Q9K9Z0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Serine/threonine protein kinase.
GN OrderedLocNames=BH2504;
OC Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_Taxid=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
RT Nucleic Acids Res. 28:4317-4331(2000).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AP001515; BAB06223.1; -.
DR PIR; H83962; H83962.
DR HSSP; P71584; 106Y.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008658; F:penicillin binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR005543; PASTA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF03793; PASTA; 3.
DR Pfam; PF00069; PKinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00740; PASTA; 3.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Complete proteome; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 664 AA; 73719 MW; E2FP225DCC6BE52 CRC64;

Query Match 46.9%; Score 46; DB 2; Length 664;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IEQPTLRWLTSTRTP 16
Db 90 VEPDLEWLSIQREHP 104

RESULT 45

MYIC_HUMAN STANDARD; PRT; 1028 AA.

ID MYIC_HUMAN STANDARD; PRT; 1028 AA.
AC O00159;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Myosin Ic (Myosin I beta) (MMI-beta) (MMIB).
GN Name=MYOIC;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.

```

RC TISUE=Kidney;
RX MEDLINE:97237053; PubMed:9119401; DOI:10.1006/geno.1996.4526;
RA Crozet F., Amraoui A.E., Blanchard S., Lenoir M., Ripoll C., Vago P.,
RA Hamel C., Fizes C., Levi-Acobas F., Depetris D., Mattei M.-G.,
RA Weil D., Pujol R., Petit C.;
RT "Cloning of the genes encoding two murine and human cochlear
RT unconventional type I myosins.";
CC Genomics 40:332-341(1997).
CC -I- FUNCTION: Myosins are actin-based motor molecules with ATPase
CC activity. Unconventional myosins serve in intracellular movements.
CC Their highly divergent tails are presumed to bind to membranous
CC compartments, which would be moved relative to actin filaments (By
CC similarity).
CC -I- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X98507; CAA67131.1; -.
DR PIR: A59253; A59253.
DR HSR: P08799; 1MND.
DR Genew: HGNC:7597; MYO1C.
DR MIM: 606538; -.
DR GO: GO:0016461; C:unconventional myosin; TAS.
DR GO: GO:0009592; P:detection of sound; TAS.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; Myosin_head.
DR InterPro: IPR010926; Myosin_tail_2.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00612; IQ; 3.
DR Pfam: PF00612; Myosin_head; 1.
DR Pfam: PF06017; Myosin_tail_2; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR PRODOM: PD000355; Myosin_head; 1.
DR SMART: SM00015; IQ; 2.
DR SMART: SM00015; Myosin_head; 1.
DR PROSITE: PS50096; IQ; 2.
DR Actin-binding; ATP-binding; Calmodulin-binding; Multigene family;
KW Myosin; Repeat.
KV
FT DOMAIN 1 683 Myosin head-like.
FT DOMAIN 699 722 IQ 1.
FT DOMAIN 723 751 IQ 2.
FT NP BIND 105 112 ATP (potential).
SQ SEQUENCE 1028 AA; 11803 MW; 0B9C3680527F85C6 CRC64;

Query Match 46.9%; Score 46; DB 1; Length 1028;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

Search completed: September 1, 2005, 16:21:10
 Job time : 70.9496 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 1, 2005, 15:48:02 ; Search time 87.3453 Seconds
(without alignments)
84.131 Million cell updates/sec

Title: US-10-083-768-11

Perfect score: 106
Sequence: 1 LAIEGPTLRQWLHGNGRDT 19Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	100.0	19	2	AAW09494
2	106	100.0	19	2	AAW09461
3	106	100.0	19	2	AAW36645
4	106	100.0	19	3	AAAB17022
5	106	100.0	19	4	AAU25864
6	106	100.0	19	4	AAU25825
7	106	100.0	19	5	ABB72908
8	106	100.0	19	7	ADU73060
9	106	100.0	19	8	ADU52695
10	106	100.0	19	8	ADU51656
11	101	95.3	19	2	AAW33028
12	63	59.4	135	6	ABG71749
13	62	58.5	15	2	AAW67721
14	60.5	57.1	40	3	AAAB17302
15	60	56.6	28	3	AAAB17285
16	60	56.6	29	7	ADU73011
17	60	56.6	29	7	ADU73007
18	60	56.6	29	7	ADU73006
19	60	56.6	29	8	ADU52642
20	60	56.6	29	8	ADU52646
21	60	56.6	29	8	ADU52641
22	60	56.6	29	8	ADU51603
23	60	56.6	29	8	ADU51602
24	60	56.6	29	8	ADU51607
25	60	56.6	31	7	ADU73009

26	60	56.6	31	7	ADU73010
27	60	56.6	31	8	ADU52644
28	60	56.6	31	8	ADU52645
29	60	56.6	31	8	ADU51606
30	60	56.6	31	8	ADU51605
31	59.5	56.1	18	7	ADN59659
32	59.5	56.1	22	7	ADN59826
33	59.5	56.1	25	7	ADN59700
34	59.5	56.1	36	3	AAU96526
35	59.5	56.1	36	3	AAAB17306
36	59	55.7	18	5	ABP51688
37	59	55.7	18	5	ABP51677
38	59	55.7	18	5	ABP51675
39	59	55.7	18	8	ADQ16641
40	59	55.7	18	8	ADQ16646
41	59	55.7	18	8	ADQ16647
42	59	55.7	22	7	ADN59819
43	59	55.7	128	8	ADQ16705
44	59	55.7	225	5	ABP51695
45	59	55.7	472	5	ADQ16647
46	59	55.7	472	8	ADQ16647
47	58	54.7	18	5	ABP51687
48	58	54.7	18	5	ABP51693
49	58	54.7	18	8	ADQ16617
50	58	54.7	18	8	ADQ16629
51	58	54.7	60	3	AAAB17311
52	58	54.7	60	3	ABP51685
53	58	54.7	247	5	ABP51691
54	58	54.7	247	5	ABP51690
55	58	54.7	269	3	AAAB16960
56	58	54.7	269	3	ADQ16705
57	57	54.2	22	8	ADQ16708
58	57	53.8	18	5	ABP51686
59	57	53.8	18	5	ABP51685
60	57	53.8	18	7	ADN59663
61	57	53.8	18	8	ADQ16615
62	57	53.8	18	8	ADQ16613
63	57	53.8	22	7	ADN59830
64	57	53.8	25	7	ADN59708
65	57	53.8	43	7	ADN59759
66	56.5	53.3	36	3	AAU96523
67	56.5	53.3	36	3	AAAB17301
68	56.5	53.3	39	3	AAAB17304
69	56	52.8	12	2	AAW36781
70	56	52.8	13	2	AAW36779
71	56	52.8	13	4	AAU26018
72	56	52.8	13	4	AAU26008
73	56	52.8	13	4	AAU26035
74	56	52.8	13	4	AAU26035
75	56	52.8	13	8	ADU72489
76	56	52.8	13	8	ADU72488
77	56	52.8	13	8	ADU72489
78	56	52.8	14	2	AAW09463
79	56	52.8	14	2	AAW09468
80	56	52.8	14	2	AAW33030
81	56	52.8	14	2	AAW33034
82	56	52.8	14	2	AAW36782
83	56	52.8	14	2	AAW36774
84	56	52.8	14	2	AAW66715
85	56	52.8	14	2	AAW66730
86	56	52.8	14	2	AD124843
87	56	52.8	14	3	AAU96515
88	56	52.8	14	3	AAU96515
89	56	52.8	14	3	AAU96515
90	56	52.8	14	3	AAU96515
91	56	52.8	14	4	AAU26006
92	56	52.8	14	4	AAU26006
93	56	52.8	14	4	AAU26019
94	56	52.8	14	4	AAU26036
95	56	52.8	14	4	AAU26037
96	56	52.8	14	4	AAU26004
97	56	52.8	14	5	ABP72854
98	56	52.8	14	5	ABP72853

ADJ73010	TPO	mimet
ADJ52644	CHI	delet
ADJ52645	CHI	delet
ADJ51606	CHI	delet
ADJ51605	CHI	delet
ADN59659	Thrombopo	
ADN59826	TMP	pept1
ADN59700	Thrombopo	
AAU96526	Thrombopo	
AAAB17306	TPO	mimet
ABP51688	TPO	mimet
ABP51677	TPO	mimet
ABP51675	TPO	mimet
ADQ16641	TPO	mimet
ADQ16646	TPO	mimet
ADQ16647	TPO	mimet
ADN59819	TMP	pept1
ADQ16705	Modified	
ABP51695	SG1.1-TPO	
ADQ16647	Immunoglo	
ABP51687	TPO	mimet
ABP51693	TPO	mimet
ADQ16617	TPO	mimet
ADQ16629	TPO	mimet
AAAB17311	Synthetic	
ABP73405	TMP-TWP	G
AAAB16961	TMP-Fc	pr
AAAB16960	TMP-TWP-F	
ABP73413	TWP-TWP-F	
ADQ16708	Immunoglo	
ABP51686	TPO	mimet
ABP51685	TPO	mimet
ADN59663	Thrombopo	
ADQ16615	TPO	mimet
ADQ16613	TPO	mimet
ADN59830	TMP	pept1
ADN59708	Thrombopo	
ADN59759	Peptide-v	
AAU96523	Thrombopo	
AAAB17301	TPO	mimet
AAAB17304	TPO	mimet
AAW36781	Thrombopo	
AAW36779	Thrombopo	
AAU26018	Human	thr
AAU26008	Human	thr
AAU26035	Human	thr
ADU72525	TPO	mimet
ADU72488	TPO	mimet
ADU72489	TPO	mimet
ADU72489	TPO	mimet
AAW09463	Thrombopo	
AAW09468	Thrombopo	
AAW33030	Thrombopo	
AAW33034	Thrombopo	
AAW36782	Thrombopo	
AAW36774	Thrombopo	
AAW66715	Peptide C	
AAW66730	Peptide C	
AD124843	AF 12505	
AAU96515	Thrombopo	
AAU96515	TPO	mimet
AAU96515	TPO	mimet
AAU96515	TPO	mimet
AAU26006	Human	thr
AAU26006	Human	thr
AAU26019	Human	thr
AAU26036	Human	thr
AAU26037	Human	thr
AAU26004	Human	thr
ABP72854	TPO	mimet
ABP72853	TPO	mimet

99 56 52.8 14 5 ABP51669
100 56 52.8 14 5 AAE18011

Abp51669 Thrombopo
Aae18011 Human lig

ALIGNMENTS

RESULT 1
AAW09494
ID AAW09494 standard; protein; 19 AA.

AC AAW09494;

DT 10-SEP-1997 (first entry)

DE Thrombopoietin receptor binding peptide.

KW Haematology; thrombocytopenia; TPO; TR; proliferation;
bone marrow transfusion; chemotherapy; radiation therapy.

OS Synthetic.

PN WO9640189-A1.

PD 19-DEC-1996.

PF 05-JUN-1996; 96WO-US008998.

PR 07-JUN-1995; 95US-00472371.

PR 07-JUN-1995; 95US-00473604.

PR 07-JUN-1995; 95US-00476168.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00484090.

PR 07-JUN-1995; 95US-00485301.

XX (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
Matcheakls LC, Schatz PU, Wagstrom CR, Wrighton NC;

DR WPI; 1997-051883/05.

PT Thrombopoietin receptor-binding/activating peptide(s) and peptide
mimetic(s) - useful in treatment of haematological disorders, esp.
thrombocytopenia resulting from chemotherapy, etc.

PS Disclosure; Page 26; 106pp; English.

XX The present sequence is a peptide which binds to thrombopoietin (TPO)

CC receptor (TR). The compound can be used for treating patients suffering

CC from haematological disorders and thrombocytopenia resulting from

CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide

CC may also be used to maintain the proliferation and growth of TPO-

CC dependent cell lines and for use in biological research, for detecting

CC TPO receptors on living cells

XX Sequence 19 AA;

QY 1 LAIEGPTLRQWLHGNGRDT 19

DB 1 LAIEGPTLRQWLHGNGRDT 19

RESULT 2

AAW09461

ID AAW09461 standard; protein; 19 AA.

XX AAW09461;

DT 10-SEP-1997 (first entry)
XX Thrombopoietin receptor binding compound peptide.
DE Thrombopoietin receptor binding compound peptide.

KW Haematology; thrombocytopenia; TPO; TR; proliferation;
bone marrow transfusion; chemotherapy; radiation therapy.

OS Synthetic.

PN WO9640189-A1.

PD 19-DEC-1996.

PF 05-JUN-1996; 96WO-US008998.

PR 07-JUN-1995; 95US-00472371.

PR 07-JUN-1995; 95US-00473604.

PR 07-JUN-1995; 95US-00476168.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00484090.

PR 07-JUN-1995; 95US-00485301.

XX (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
Matcheakls LC, Schatz PU, Wagstrom CR, Wrighton NC;

DR WPI; 1997-051883/05.

PT Thrombopoietin receptor-binding/activating peptide(s) and peptide
mimetic(s) - useful in treatment of haematological disorders, esp.
thrombocytopenia resulting from chemotherapy, etc.

PS Claim 18; Page 89; 106pp; English.

XX The present sequence is a compound which binds to thrombopoietin (TPO)

CC receptor (TR). It has a molecular weight of < 8000 Da, and a binding

CC affinity to TR as expressed by an IC50 of no more than about 100 nM. The

CC compound (especially if modified, see features table) can be used for

CC treating patients suffering from haematological disorders and

CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone

CC marrow transfusions. The peptide may also be used to maintain the

CC proliferation and growth of TPO-dependent cell lines and for use in

CC biological research, for detecting TPO receptors on living cells

XX Sequence 19 AA;

QY 1 LAIEGPTLRQWLHGNGRDT 19

DB 1 LAIEGPTLRQWLHGNGRDT 19

RESULT 2

AAW09461

ID AAW09461 standard; protein; 19 AA.

XX AAW09461;

QY 1 LAIEGPTLRQWLHGNGRDT 19

Db 1 LAIEGPTLRQWLHNGRDT 19

RESULT 3
AAU36645 standard; peptide; 19 AA.

AAU36645;
11-MAR-1998 (first entry)
Thrombopoietin receptor binding peptide.
Thrombopoietin receptor; binding peptide; treatment; agonist;
haematological disorder; thrombocytopenia; chemotherapy;
radiation therapy; bone marrow transfusion; diagnosis;
signal transduction; receptor activation; cell culture.
Synthetic.
WO9640750-A1.
19-DEC-1996.
07-JUN-1996; 96WO-US009623.
07-JUN-1995; 95US-00478128.
07-JUN-1995; 95US-00485301.
(GLAXO) GLAXO GROUP LTD.
Dower WJ, Barrett RM, Cwikla SE, Duffin DJ, Gates CM, Johnson SS;
Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
WPI; 1997-052226/05.
Peptides and peptide mimetics which bind to and activate the
thrombopoietin receptor - useful in treatment of haematological
disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
Disclosure; Page 26; 106pp; English.
The present peptide, which binds the thrombopoietin receptor (TR), can be
used to treat disorders which are susceptible to treatment with a
thrombopoietin agonist, preferably haematological disorders and
thrombocytopenia resulting from chemotherapy, radiation therapy or bone
marrow transfusions. It can also be used diagnostically, e.g. to
investigate the mechanism of thrombopoietin signal transduction and
receptor activation, or to maintain the proliferation and growth of
thrombopoietin dependent cell lines

Query Match 100.0%; Score 106; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAIEGPTLRQWLHNGRDT 19
Db 1 LAIEGPTLRQWLHNGRDT 19

RESULT 4
AAB17022 standard; peptide; 19 AA.
AAB17022;
31-OCT-2000 (first entry)
TPO-mimetic peptide sequence SEQ ID NO:78.

Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
immunosuppressive; EPO, TPO, CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
vascular endothelial growth factor; matrix metalloproteinase; aschma;
thrombosis; pharmaceutical.

Synthetic.
WO200024782-A2.
04-MAY-2000.
25-OCT-1999; 99WO-US025044.
23-OCT-1998; 98US-0105371P.
22-OCT-1999; 99US-00428082.
(AMGEN-) AMGEN INC.
Feige U, Liu C, Cheetham J, Boone TC;
WPI; 2000-350702/30.
Novel composition of matter comprising an Fc domain and pharmacologically
active peptides, useful for treating cancer and autoimmune diseases.
Claim 19; Page 221; 608pp; English.
The present invention describes composition of matter (I) comprising an
Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
(X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
P3, and P4 = are each independently sequences of pharmacologically active
peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
c, d, e, and f = are each independently 0 or 1, provided that at least 1
of a and b is 1. The composition can have cytostatic, antiasthmatic,
thrombolytic and immunosuppressive activities. DNAs, vectors and host
cells from the present invention can be used for producing pharmaceutical
compositions. The compositions are useful for treating cancer, asthma,
thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
a Fab domain) can provide a longer half-life or incorporate functions
such as Fc receptor binding, protein A binding, complement fixation, and
possibly placental transfer. AA69443 to AA69526 and AAB1955 to
AAB19003 represent nucleotide and amino acid sequences used in the
exemplification of the present invention

Query Match 100.0%; Score 106; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAIEGPTLRQWLHNGRDT 19
Db 1 LAIEGPTLRQWLHNGRDT 19

RESULT 5
AAU25864 standard; peptide; 19 AA.
AAU25864;
17-DEC-2001 (first entry)
Human thrombopoietin receptor (TPO-R) activator peptide #50.
Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
haematologic; thrombocytopenia; chemotherapy; radiation therapy; EritrA;
bone marrow transplantation; haematological disorder; platelet disorder;

KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009622.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Poddaturi S;
 PI Yin Q;
 DR WPI; 2001-564142/63.
 XX
 PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 PS Disclosure; Col 20; 128pp; English.
 XX
 SQ Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent hematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX
 SQ Sequence 19 AA:
 XX
 Query Match 100.0%; Score 106; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAIEGPTLRQWLHGNGRDT 19
 DB 1 LAIEGPTLRQWLHGNGRDT 19
 XX
 RESULT 6
 AAU25825
 ID AAU25825 standard; peptide; 19 AA.
 XX
 AC AAU25825;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #11.
 XX
 KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;

KW bone marrow transplantation; hematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Poddaturi S;
 PI Yin Q;
 DR WPI; 2001-564142/63.
 XX
 PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 PS Disclosure; Col 67-68; 128pp; English.
 XX
 SQ Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent hematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX
 SQ Sequence 19 AA:
 XX
 Query Match 100.0%; Score 106; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAIEGPTLRQWLHGNGRDT 19
 DB 1 LAIEGPTLRQWLHGNGRDT 19
 XX
 RESULT 7
 ABB72908
 ID ABB72908 standard; peptide; 19 AA.
 XX
 AC ABB72908;
 XX
 DT 05-APR-2002 (first entry)
 XX
 DE TPO mimetic peptide SEQ ID NO:78.
 XX
 KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;

KM erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KM TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TGF-
 KM TPO mimetic peptide; EPO mimetic peptide; EGF; VEGF antagonist;
 KM MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KM cytostatic; antineoplastic; antiferility; haemostatic; dermatological;
 KM antianemic; anorectic; antiinflammatory; haemostatic; dermatological;
 KM neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KM cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KM sleep disorder; neurological degenerative disease; anaemia;
 KM thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KM Fanconi's syndrome.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS WO200183525-A2.
 PN
 PN WO200183525-A2.
 PD
 PD 08-NOV-2001.
 PF
 PF 02-MAY-2001; 2001WO-US014310.
 PR
 PR 03-MAY-2000; 2000US-00563286.
 XX
 XX (AMGEN) AMGEN INC.
 PI
 PI Feige U, Liu C, Cheetham JC, Boone TC, Gudae JM;
 DR
 DR WPI; 2002-130313/17.
 XX
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 XX
 PS Claim 39; Page 44; 176pp; English.
 XX
 XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antineoplastic, antidiabetic, opthalmological,
 CC antianemic, anorectic, antiinflammatory, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABB55655 to ABB57777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention
 XX
 XX Sequence 19 AA:
 SO
 Query Match 100.0%; Score 106; DB 5; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAIEGPTLRQWLHNGRDT 19
 DB 1 LAIEGPTLRQWLHNGRDT 19
 RESULT 8
 ADJ73060 standard; peptide; 19 AA.
 ID
 XX

AC ADJ73060;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX TPO mimetic peptide sequence SeqID 514.
 DE
 XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;
 KM mimetic; CDR mimetibody; gene therapy; transgenic; immune;
 KM cardiovascular; infectious; malignant; neurologic disease; anaemia;
 KM immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
 KM TPO.
 XX
 OS Synthetic.
 OS WO2003084477-A2.
 PN
 PN WO2003084477-A2.
 PD
 PD 16-OCT-2003.
 PF
 PF 24-MAR-2003; 2003WO-US009139.
 PR
 PR 29-MAR-2002; 2002US-0368791P.
 XX
 XX (CENZ) CENTOCOR INC.
 PA
 PA Heavner GA, Knight DM, Scallion BU, Ghayeb J;
 PI
 PI WPI; 2003-804237/75.
 DR
 DR WPI; 2003-804237/75.
 XX
 XX New CDR mimetibody comprising a portion of a heavy or light chain
 PT variable region comprising human framework or ligand binding region,
 PT useful for preparing a composition for treating e.g., immune,
 PT cardiovascular or neurologic disease.
 XX
 XX Disclosure; SEQ ID NO 514; 97pp; English.
 PS
 PS This invention relates to novel mammalian CDR mimetibodies, specific
 CC portions or variants thereof. Specifically, it refers to an antibody
 CC fragment where a protein has been inserted into, or replaces a portion
 CC of, one or more CDR regions, such that each CDR mimetibody comprises at
 CC least one portion of a heavy chain or light chain variable region, which
 CC itself comprises at least one human framework region and at least one
 CC ligand binding region (LBR). The present invention describes human
 CC mimetibodies, including modified immunoglobulins and cleavage products
 CC that can be useful in gene therapy and the generation of transgenic
 CC plants and animals. Furthermore, the CDR mimetibody is useful for
 CC preparing compositions for modulating, treating or reducing the symptoms
 CC of immune, cardiovascular, infectious, malignant and/or neurologic
 CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
 CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
 CC peptide sequence is a TPO mimetic peptide sequence used to make a
 CC mimetibody of the invention.
 CC
 XX
 XX Sequence 19 AA:
 SO
 Query Match 100.0%; Score 106; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAIEGPTLRQWLHNGRDT 19
 DB 1 LAIEGPTLRQWLHNGRDT 19
 RESULT 9
 ADJ52695 standard; peptide; 19 AA.
 ID
 XX
 XX ADJ52695;
 AC
 AC ADJ52695;
 DT
 DT 06-MAY-2004 (first entry)
 XX
 XX CH1 deleted mimetibody-related peptide SeqID514.
 DE
 XX CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
 KM

KW hypotensive; neuroprotective; nootropic; antibacterial; virucide;
 KW fungicide; gene therapy; immune disorder; cardiovascular disease;
 KW arrhythmia; hypertension; heart failure; neurodegenerative;
 KW multiple sclerosis; dementia; Alzheimer's disease; anaemia;
 KW cancerous condition; infectious disease; bacterial infection;
 KW viral infection; fungal infection.
 XX
 OS Unidentified.
 OS Synthetic.
 XX WO2004002417-A2.
 XX
 PD 08-JAN-2004.
 XX
 XX 27-JUN-2003; 2003WO-US020347.
 PF
 XX 28-JUN-2002; 2002US-0392431P.
 PR
 XX (CENZ) CENTOCOR INC.
 XX
 PA Heavenr GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
 PI Kutoleski KA;
 XX
 XX WPI; 2004-082870/08.
 DR
 XX
 PT New CHI-deleted mimetibody polypeptides and nucleic acids, useful for
 PT modulating, treating, alleviating, preventing an immune, cardiovascular,
 PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
 PT diseases.
 XX
 XX
 PS Claim 2; SEQ ID NO 514; 129pp; English.
 XX
 CC This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an immunosuppressive,
 CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
 CC antibacterial, virucide or fungicide activity. In addition, the disclosed
 CC sequences may prove useful for gene therapy. The CHI-deleted mimetibody
 CC is useful for diagnosing or treating a disease condition in a cell,
 CC tissue, organ or animal, specifically for modulating, treating,
 CC alleviating, preventing the incidence or reducing the symptoms of an
 CC immune, cardiovascular (for example arrhythmia, hypertension or heart
 CC failure), or neurodegenerative (for example multiple sclerosis, dementia
 CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
 CC conditions, or infectious diseases (for example bacterial, viral or
 CC fungal infection). The present sequence is that of a peptide which may be
 CC used during the creation of a mimetibody of the invention.
 CC
 CC
 SQ Sequence 19 AA:
 QY
 DB 1 LAIEGPTLRQWLHNGGRDT 19
 1 LAIEGPTLRQWLHNGGRDT 19
 RESULT 10
 ADJ51656
 ID ADJ51656 standard; peptide; 19 AA.
 XX
 AC ADJ51656;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 XX CHI deleted mimetibody-related peptide SegID514.
 DE
 XX CHI deleted mimetibody; osteopathic; cardiovascular-Gen;
 KW dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
 KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KW anti-allergic; muscular-Gen; cytostatic; anti-inflammatory; neuroleptic;

KW ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
 KW TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KW dental disorder; oral disorder; dermatological disorder; ear disorder;
 KW nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KW gastrointestinal disorder; gynaecological disorder; hepatic disorder;
 KW obstructive disorder; haematologic disorder; immunologic disorder;
 KW allergic disorder; infectious disorder; musculoskeletal disorder;
 KW oncological disorder; neurological disorder; nutritional disorder;
 KW ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KW renal disorder; pulmonary disorder.
 XX
 XX Unidentified.
 OS Synthetic.
 XX
 OS
 XX WO2004002424-A2.
 XX
 PD 08-JAN-2004.
 XX
 XX 30-JUN-2003; 2003WO-US020495.
 PF
 XX 28-JUN-2002; 2002US-0392431P.
 PR 19-SEP-2002; 2002US-0412144P.
 XX
 XX (CENZ) CENTOCOR INC.
 XX
 PA Heavenr GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
 PI Kutoleski KA;
 XX
 XX WPI; 2004-082872/08.
 DR
 XX
 PT New CHI deleted mimetibody polypeptide and nucleic acid, useful for
 PT diagnosing, preventing or treating cardiovascular, dermatologic,
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
 PT nutritional disorders.
 XX
 XX
 PS Claim 15; SEQ ID NO 514; 123pp; English.
 XX
 CC This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an osteopathic,
 CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
 CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
 CC immunomodulator, anti-allergic, muscular-Gen, cytostatic,
 CC anti-inflammatory, neuroleptic, ophthalmologic, nephrotropic or
 CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
 CC modulator or cytokine-agonist. The methods and compositions of the
 CC present invention are useful for the diagnosis, prevention and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the CHI deleted mimetibody, such as a bone or joint,
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
 CC endocrine, metabolic, gastrointestinal, gynaecological, allergic, infectious,
 CC obstructive, haematologic, immunologic, nutritional, ophthalmologic,
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
 CC pediatric, psychiatric, renal or pulmonary disorders. The present
 CC sequence is that of a peptide which may be used during the creation of a
 CC mimetibody of the invention.
 CC
 CC
 SQ Sequence 19 AA:
 QY
 DB 1 LAIEGPTLRQWLHNGGRDT 19
 1 LAIEGPTLRQWLHNGGRDT 19
 RESULT 11
 AAW33028
 ID AAW33028 standard; peptide; 19 AA.
 XX
 AC AAW33028;

XX	Peptide chain of compound which binds to the thrombopoietin receptor.
DE	thrombopoietin receptor; haematological disorder; screening; agonist;
KW	assay; megakaryocyte; blood disorder; thrombocytopaenia; TPO.
RN	
XX	Synthetic.
OS	
XX	
PH	Key
FT	Region
FT	Location/Qualifiers
FT	1..14
FT	/note= "thrombopoietin receptor agonist"
FT	Modified-site
FT	14
FT	/label= Megly
FT	/note= "Sarcosine"
FT	15
FT	/note= "Epsilon amino group of Lys, in its amide form, is attached to another peptide chain identical to the region (residues 1 to 14) of this peptide"
FN	
PN	WO9825965-A2.
XX	
PD	18-JUN-1998.
XX	
PF	09-DEC-1997; 97WO-EP006850.
XX	
PR	11-DEC-1996; 96US-00764640.
XX	
PA	(GLAXO) GLAXO GROUP LTD.
PI	Dower WJ, Barrett RM, Cwirla SE, Gates CM, Schatz PJ;
PI	Balsubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Poddaturi S;
PI	Yin Q;
DR	
XX	WPI, 1998-377261/32.
PT	New peptide compound(s) which can bind and activate thrombopoietin
PT	receptor - may be used in treating haematological disorders and in
PS	methods for screening for new thrombopoietin receptor agonists.
XX	
PS	Claim 2; Page 61; 78pp; English.
XX	
CC	The invention relates to peptide compounds composed of two peptide chains
CC	attached to each of the amino groups of a single lys in the amide form.
CC	The compounds are of formula (Pep1) (Pep2)(NH ₂), where Pep1 is of
CC	formula: X1-I-E-X2-P-T-L-X3-X4-X5-L-X6-X7-X8-X9-X10; and pep2 is of
CC	formula: X1-I-E-X2-P-T-L-X3-X4-X5-L-X6-X7-X8-X9'-X10'. X1 = H or acyl; X2
CC	= Gly or Sar (sarcosine); X3 = Arg, Ala, Nle (norleucine) or N-
CC	acetyllysine; X4 = Gln or Glu; X5 = Tyr, L-1-naphthylalanine or Phe; X6 =
CC	Ala, 5-amino-pentanoic acid or 2-aminobutyric acid; X7 = Ala,
CC	diphenylalanine, or is absent; X8 = Arg, p- amino-phenylalanine, N-
CC	acetyl-lysine, or is absent; X9, X9' = Ala, beta Ala, N-methyl-alanine,
CC	Sar, or is absent; X10, X10' = beta Ala or is absent. The new peptides
CC	are capable of binding to, and activating, the thrombopoietin (TPO)
CC	receptor. They may be used in vitro as tools for understanding the
CC	biological role of TPO. They may be used as competitive binders in assays/
CC	to screen for new TPO receptor agonists. They may be used as reagents for
CC	detecting TPO receptors in living cells, biological fluids, etc. They may
CC	be used to maintain growth and proliferation of TPO-dependent cells and
CC	for in vitro expansion of megakaryocytes. They may be used to activate
CC	TPO receptors in vivo, e.g., to treat blood disorders or
CC	thrombocytopaenia associated with bone marrow transusions, radiotherapy
CC	or chemotherapy. The present sequence represents a specific example of
CC	(Pep1)(K(NH ₂)
XX	
SQ	Sequence 15 AA;
XX	
QY	Query Match 58.5%; Score 62; DB 2; Length 15;
DB	Best Local Similarity 73.3%; Pred. No. 0.0097;
	Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0
	3 IEQGTTROWLHGNGR 17 : 1 IEQGTTROWLAARGK 15

RESULT 14

AAB17302 standard; peptide; 40 AA.

ID AAB17302
XX AC
XX AAB17302;
DT 31-OCT-2000 (first entry)
XX DE TPO-mimetic peptide sequence SEQ ID NO:358.
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumor necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW chromostats; pharmaceutical.
OS Synthetic.
XX PN WO200024782-A2.
PD 04-MAY-2000.
PF 25-OCT-1999; 99WO-US025044.
PR 23-OCT-1998; 98US-010537LP.
PR 22-OCT-1999; 99US-00428082.
XX PA (AMGE-) AMGEN INC.
PI Feige U, Liu C, Cheetham J, Boone TC;
DR WPI; 2000-350702/30.
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX Example 1; Page 322; 608pp; English.
XX PS The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-F3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNA's, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Rab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX SQ Sequence 40 AA;

Query Match 57.1%; Score 60.5; DB 3; Length 40;
Best Local Similarity 63.2%; Pred. No. 0.05;
Matches 12; Conservative 2; Mismatches 2; Indels 3; Gaps 1

3 IEGPTLRQWL--HGNGRD 18
|||||
DB 1 IEGPTLRQLAARAGGKRB 19

AA17285
 ID AA17285 standard; peptide; 28 AA.
 AC AA17285;
 DT 31-OCT-2000 (first entry)
 DE TPO-mimetic peptide sequence SEQ ID NO:341.
 XX
 XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 XX autoimmune disease; cytostatic; antineoplastic; thrombolytic; VEGF;
 XX immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 XX inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 XX cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 XX vascular endothelial growth factor; matrix metalloproteinase; asthma;
 XX thrombosis; pharmaceutical.
 OS Synthetic.
 XX
 XX WO200024782-A2.
 XX
 XX 04-MAY-2000.
 XX
 XX 25-OCT-1999; 99WO-US025044.
 XX
 XX 23-OCT-1998; 98US-0105371P.
 XX
 XX 22-OCT-1999; 99US-00428082.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Feige U, Liu C, Cheetham J, Boone TC;
 XX
 XX MPI; 2000-350702/30.
 XX
 XX Novel composition of matter comprising an Fc domain and pharmacologically
 XX active peptides, useful for treating cancer and autoimmune diseases.
 XX
 XX Example 1; Page 315; 608pp; English.
 XX
 XX The present invention describes composition of matter (I) comprising an
 XX Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 XX (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 XX independently selected from -(L1)-C-P1, -(L1)-C-P1-(L2)-d-P2, -(L1)-C-P1-
 XX (L2)-d-P2-(L3)-e-P3, or -(L1)-C-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,
 XX P3, and P4 = are each independently sequences of pharmacologically active
 XX peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 XX c, d, e, and f = are each independently 0 or 1, provided that at least 1
 XX of a and b is 1. The composition can have cytostatic, antineoplastic,
 XX thrombolytic and immunosuppressive activities, DNAs, vectors and host
 XX cells from the present invention can be used for producing pharmaceutical
 XX compositions. The compositions are useful for treating cancer, asthma,
 XX thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 XX a Fab domain) can provide a longer half-life or incorporate functions
 XX such as Fc receptor binding, protein A binding, complement fixation, and
 XX possibly placental transfer. AA69443 to AA69526 and AA69555 to
 XX AA69603 represent nucleotide and amino acid sequences used in the
 XX exemplification of the present invention
 XX
 XX Sequence 28 AA;
 XX
 XX Query Match 56.6%; Score 60; DB 3; Length 28;
 XX Best Local Similarity 100.0%; Pred. No. 0.04;
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 AIEGPTLRQWL 12
 XX |||||
 XX DB 14 AIEGPTLRQWL 24
 XX
 XX RESULT 16
 XX ID ADJ73011 standard; peptide; 29 AA.
 XX
 XX

AC ADJ73011;
 XX
 XX 06-MAY-2004 (first entry)
 XX
 XX TPO mimetic peptide sequence SeqID 465.
 XX
 XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;
 XX cardiovascular; infectious; malignant; neurologic disease; anaemia;
 XX immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
 XX TPO.
 XX
 XX OS Synthetic.
 XX
 XX PN WO2003084477-A2.
 XX
 XX PD 16-OCT-2003.
 XX
 XX PF 24-MAR-2003; 2003WO-US009139.
 XX
 XX PR 29-MAR-2002; 2002US-0368791P.
 XX
 XX (CENZ) CENTOCOR INC.
 XX
 XX Heaven GA, Knight DM, Scallion BJ, Ghayeb J;
 XX
 XX MPI; 2003-804237/75.
 XX
 XX New CDR mimetibody comprising a portion of a heavy or light chain
 XX variable region comprising human framework or ligand binding region,
 XX useful for preparing a composition for treating e.g., immune,
 XX cardiovascular or neurologic disease.
 XX
 XX PT disclosure; SEQ ID NO 465; 97pp; English.
 XX
 XX This invention relates to novel mammalian CDR mimetibodies, specific
 XX portions or variants thereof. Specifically, it refers to an antibody
 XX fragment where a protein has been inserted into, or replaces a portion
 XX of, one or more CDR regions, such that each CDR mimetibody comprises at
 XX least one portion of a heavy chain or light chain variable region, which
 XX itself comprises at least one human framework region and at least one
 XX CDR ligand binding region (LBR). The present invention describes human
 XX CDR mimetibodies, including modified immunoglobulins and cleavage products
 XX that can be useful in gene therapy and the generation of transgenic
 XX plants and animals. Furthermore, the CDR mimetibody is useful for
 XX preparing compositions for modulating, treating or reducing the symptoms
 XX of immune, cardiovascular, infectious, malignant and/or neurologic
 XX diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
 XX cardiant, antimicrobial, cytostatic and neuroprotective activities. This
 XX peptide sequence is a TPO mimetic peptide sequence used to make a
 XX CDR mimetibody of the invention.
 XX
 XX Sequence 29 AA;
 XX
 XX Query Match 56.6%; Score 60; DB 7; Length 29;
 XX Best Local Similarity 100.0%; Pred. No. 0.042;
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 AIEGPTLRQWL 12
 XX |||||
 XX DB 15 AIEGPTLRQWL 25
 XX
 XX RESULT 17
 XX ID ADJ73007 standard; peptide; 29 AA.
 XX
 XX AC ADJ73007;
 XX
 XX 06-MAY-2004 (first entry)
 XX
 XX TPO mimetic peptide sequence SeqID 461.
 XX
 XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;
 XX

PF 27-JUN-2003; 2003WO-US020347.
 XX
 XX 28-JUN-2002; 2002US-0392431P.
 XX
 XX (CENZ) CENTOCOR INC.
 PA
 XX Heavenr GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
 PI Kutoloski KA;
 XX
 XX WPI; 2004-082870/08.
 DR
 XX
 PT New CHI-deleted mimetibody polypeptides and nucleic acids, useful for
 PT modulating, treating, alleviating, preventing an immune, cardiovascular,
 PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
 PT diseases.
 PS
 XX
 PS Claim 2; SEQ ID NO 461; 129pp; English.
 CC This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an immunosuppressive,
 CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
 CC antibacterial, virucide or fungicide activity. In addition, the disclosed
 CC sequences may prove useful for gene therapy. The CHI-deleted mimetibody
 CC is useful for diagnosing or treating a disease condition in a cell,
 CC tissue, organ or animal, specifically for modulating, treating,
 CC alleviating, preventing the incidence or reducing the symptoms of an
 CC immune, cardiovascular (for example arrhythmia, hypertension or heart
 CC failure), or neurodegenerative (for example multiple sclerosis, dementia
 CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
 CC conditions, or infectious diseases (for example bacterial, viral or
 CC fungal infection). The present sequence is that of a peptide which may be
 CC used during the creation of a mimetibody of the invention.
 XX
 SO Sequence 29 AA;
 QY
 Query Match 56.6%; Score 60; DB 8; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 2 AIBGPTLRQWL 12
 15 AIBGPTLRQWL 25
 QY
 RESULT 20
 ADJ52646
 ID ADJ52646 standard; peptide; 29 AA.
 AC
 XX ADJ52646;
 XX
 DT 06-MAY-2004 (first entry)
 DE CHI deleted mimetibody-related peptide SeqID465.
 XX
 XX CHI deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
 KM hypotensive; neuroprotective; nootropic; antibacterial; virucide;
 KM fungicide; gene therapy; immune disorder; cardiovascular disease;
 KM arrhythmia; hypertension; heart failure; neurodegenerative;
 KM multiple sclerosis; dementia; Alzheimer's disease; anaemia;
 KM cancerous condition; infectious disease; bacterial infection;
 KM viral infection; fungal infection.
 XX
 OS Unidentified.
 OS Synthetic.
 XX
 PN WO2004002417-A2.
 XX
 PD 08-JAN-2004.
 XX
 PF 27-JUN-2003; 2003WO-US020347.
 XX
 XX 28-JUN-2002; 2002US-0392431P.
 PR

XX
 PA (CENZ) CENTOCOR INC.
 XX
 XX Heavenr GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
 PI Kutoloski KA;
 XX
 XX WPI; 2004-082870/08.
 DR
 XX
 PT New CHI-deleted mimetibody polypeptides and nucleic acids, useful for
 PT modulating, treating, alleviating, preventing an immune, cardiovascular,
 PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
 PT diseases.
 PS
 XX
 PS Claim 2; SEQ ID NO 465; 129pp; English.
 CC This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an immunosuppressive,
 CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
 CC antibacterial, virucide or fungicide activity. In addition, the disclosed
 CC sequences may prove useful for gene therapy. The CHI-deleted mimetibody
 CC is useful for diagnosing or treating a disease condition in a cell,
 CC tissue, organ or animal, specifically for modulating, treating,
 CC alleviating, preventing the incidence or reducing the symptoms of an
 CC immune, cardiovascular (for example arrhythmia, hypertension or heart
 CC failure), or neurodegenerative (for example multiple sclerosis, dementia
 CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
 CC conditions, or infectious diseases (for example bacterial, viral or
 CC fungal infection). The present sequence is that of a peptide which may be
 CC used during the creation of a mimetibody of the invention.
 XX
 SO Sequence 29 AA;
 QY
 Query Match 56.6%; Score 60; DB 8; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 2 AIBGPTLRQWL 12
 15 AIBGPTLRQWL 25
 QY
 RESULT 21
 ADJ52641
 ID ADJ52641 standard; peptide; 29 AA.
 AC
 XX ADJ52641;
 XX
 DT 06-MAY-2004 (first entry)
 DE CHI deleted mimetibody-related peptide SeqID460.
 XX
 XX CHI deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
 KM hypotensive; neuroprotective; nootropic; antibacterial; virucide;
 KM fungicide; gene therapy; immune disorder; cardiovascular disease;
 KM arrhythmia; hypertension; heart failure; neurodegenerative;
 KM multiple sclerosis; dementia; Alzheimer's disease; anaemia;
 KM cancerous condition; infectious disease; bacterial infection;
 KM viral infection; fungal infection.
 XX
 OS Unidentified.
 OS Synthetic.
 XX
 PN WO2004002417-A2.
 XX
 PD 08-JAN-2004.
 XX
 PF 27-JUN-2003; 2003WO-US020347.
 XX
 XX 28-JUN-2002; 2002US-0392431P.
 PA (CENZ) CENTOCOR INC.
 XX

PI Heavner GA, Knight DM, Ghrayeb J, Scallion BJ, Nesspor TC;
 PI Kutoolski KA;
 DR WPI; 2004-082870/08.
 XX
 XX
 PT New CHI deleted mimetibody polypeptides and nucleic acids, useful for
 PT modulating, treating, alleviating, preventing an immune, cardiovascular,
 PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
 PT disease.
 PS
 XX
 PS Claim 2; SEQ ID NO 460; 123pp; English.
 CC This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an immunosuppressive,
 CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
 CC antibacterial, virucide or fungicide activity. In addition, the disclosed
 CC sequences may prove useful for gene therapy. The CHI deleted mimetibody
 CC is useful for diagnosing or treating a disease condition in a cell,
 CC tissue, organ or animal, specifically for modulating, treating,
 CC alleviating, preventing the incidence or reducing the symptoms of an
 CC immune, cardiovascular (for example arrhythmia, hypertension or heart
 CC failure), or neurodegenerative (for example multiple sclerosis, dementia
 CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
 CC conditions, or infectious diseases (for example bacterial, viral or
 CC fungal infection). The present sequence is that of a peptide which may be
 CC used during the creation of a mimetibody of the invention.
 CC
 XX
 SQ Sequence 29 AA;
 Query Match 56.6%; Score 60; DB 8; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.042; 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0;
 QY 2 AIEGPTLRQWL 12
 |||||
 DB 15 AIEGPTLRQWL 25
 |||||
 RESULT 22
 ADJ51603
 ID ADJ51603 standard; peptide; 29 AA.
 AC ADJ51603;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE CHI deleted mimetibody-related peptide SeqID461.
 XX
 KW CHI deleted mimetibody; osteopathic; cardiovascular-Gen;
 KW dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
 KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KW antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
 KW ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
 KW TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KW dental disorder; oral disorder; dermatological disorder; ear disorder;
 KW nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KW gastrointestinal disorder; gynaecological disorder; hepatic disorder;
 KW obstetric disorder; haematological disorder; immunological disorder;
 KW allergic disorder; infectious disorder; musculoskeletal disorder;
 KW oncological disorder; neurological disorder; nutritional disorder;
 KW ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KW renal disorder; pulmonary disorder.
 XX
 OS Unidentified.
 OS Synthetic.
 XX
 PN WO2004002424-A2.
 PN 08-JAN-2004.
 PD
 XX
 PF 30-JUN-2003; 2003WO-US020495.
 XX

PR 28-JUN-2002; 2002US-0392431P.
 PR 19-SEP-2002; 2002US-0412144P.
 XX
 XX
 PA (CENZ) CENTOOR INC.
 XX
 XX
 PI Heavner GA, Knight DM, Ghrayeb J, Scallion BJ, Nesspor TC;
 PI Kutoolski KA;
 DR WPI; 2004-082872/08.
 XX
 XX
 PT New CHI deleted mimetibody polypeptide and nucleic acid, useful for
 PT diagnosing, preventing or treating cardiovascular, dermatologic, and
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
 PT nutritional disorders.
 PS
 XX
 PS Claim 14; SEQ ID NO 461; 123pp; English.
 CC This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an osteopathic,
 CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
 CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
 CC immunomodulator, antiallergic, muscular-Gen, cytostatic,
 CC antiinflammatory, neuroleptic, ophthalmological, nephrotropic or
 CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
 CC modulator or cytokine-agonist. The methods and compositions of the
 CC present invention are useful for the diagnosis, prevention and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the CHI deleted mimetibody, such as a bone or joint,
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
 CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
 CC obstetric, haematologic, immunological, allergic, infectious,
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
 CC pediatric, psychiatric, renal or pulmonary disorders. The present
 CC sequence is that of a peptide which may be used during the creation of a
 CC mimetibody of the invention.
 CC
 XX
 SQ Sequence 29 AA;
 Query Match 56.6%; Score 60; DB 8; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.042; 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0;
 QY 2 AIEGPTLRQWL 12
 |||||
 DB 15 AIEGPTLRQWL 25
 |||||
 RESULT 23
 ADJ51602
 ID ADJ51602 standard; peptide; 29 AA.
 AC ADJ51602;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE CHI deleted mimetibody-related peptide SeqID460.
 XX
 KW CHI deleted mimetibody; osteopathic; cardiovascular-Gen;
 KW dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
 KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KW antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
 KW ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
 KW TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KW dental disorder; oral disorder; dermatological disorder; ear disorder;
 KW nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KW gastrointestinal disorder; gynaecological disorder; hepatic disorder;
 KW obstetric disorder; haematological disorder; immunological disorder;
 KW allergic disorder; infectious disorder; musculoskeletal disorder;
 KW oncological disorder; neurological disorder; nutritional disorder;
 KW ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KW renal disorder; pulmonary disorder.
 XX

OS	Unidentified.
OS	Synthetic.
PN	WO2004002424-A2.
XX	
PD	08-JAN-2004.
XX	
PF	30-JUN-2003; 2003WO-US020495.
PR	28-JUN-2002; 2002US-0392431P.
FR	19-SEP-2002; 2002US-0412144P.
XX	
PA	(CENZ) CENTOCOR INC.
XX	
P1	Heavner GA, Knight DM, Ghareyb J, Scallion BJ, Nesspor TC;
P1	Kucolowski KA,
DR	WPI, 2004-082872/08.
XX	
PT	New CHI deleted mimetibody polypeptide and nucleic acid, useful for
PT	diagnosing, preventing or treating cardiovascular, dermatologic,
PT	endocrine, gastrointestinal, gynecologic, infectious, neurologic and
PT	nutritional disorders.
XX	
PS	Claim 14; SEQ ID NO 460; 123pp; English.
CC	
CC	This invention relates to CHI deleted mimetibodies (and the DNA sequences
CC	which encode them), compositions, methods and uses. The invention may be
CC	useful for the development of compounds with an osteopathic,
CC	cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
CC	gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
CC	immunomodulator, antiallergic, muscular-Gen, cystostatic,
CC	antiinflammatory, neuroleptic, ophthalmological, nephrotropic or
CC	respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
CC	modulatory or cytokine-agonist. The methods and compositions of the
CC	present invention are useful for the diagnosis, prevention and/or
CC	treatment of diseases or conditions associated with aberrant expression
CC	or activity of the CHI deleted mimetibody, such as a bone or joint,
CC	cardiovascular, dental or oral, dermatological, ear, nose or throat,
CC	endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
CC	obstetric, haematologic, immunological, allergic, infectious,
CC	musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
CC	pediatric, psychiatric, renal or pulmonary disorders. The present
CC	sequence is that of a peptide which may be used during the creation of a
CC	mimetibody of the invention.
XX	
SQ	Sequence 29 AA:
	Query Match 56.6%; Score 60; DB 8; Length 29;
	Best Local Similarity 100.0%; Pred. No. 0.042;
Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	2 AIEGPTLRQWL 12
DB	15 AIEGPTLRQWL 25
RESULT 24	
ADJ51607	
ID	ADJ51607 standard; peptide; 29 AA.
XX	
AC	ADJ51607;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	
XX	
CH1	deleted mimetibody-related peptide SeqID465.
XX	
CH1	deleted mimetibody; osteopathic; cardiovascular-Gen;
KW	dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
KW	gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
KW	antiallergic; muscular-Gen; cystostatic; antiinflammatory; neuroleptic;
KW	ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
KW	TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
KW	

KW	dental disorder; oral disorder; dermatological disorder; ear disorder;
KW	nose disorder; throat disorder; endocrine disorder; metabolic disorder;
KW	gastrointestinal disorder; gynaecological disorder; hepatic disorder;
KW	obstetric disorder; haematologic disorder; musculoskeletal disorder;
KW	allergic disorder; infectious disorder; neurological disorder;
KW	oncological disorder; nutritional disorder; nutritional disorder;
KW	ophthalmologic disorder; pediatric disorder; psychiatric disorder;
KW	renal disorder; pulmonary disorder.
XX	
OS	Unidentified.
OS	Synthetic.
XX	
PN	WO2004002424-A2.
XX	
PD	08-JAN-2004.
XX	
PP	30-JUN-2003; 2003MO-US020495.
XX	
PR	28-JUN-2002; 2002US-0392431P.
PR	19-SEP-2002; 2002US-0412144P.
XX	
PA	(CENZ) CENTOCOR INC.
XX	
P1	Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Neespor TC,
P1	Kutoloski KA;
XX	
DR	WPI; 2004-082872/08.
XX	
PT	New CHI deleted mimetibody polypeptide and nucleic acid, useful for
PT	diagnosing, preventing or treating cardiovascular, dermatologic,
PT	endocrine, gastrointestinal, gynecologic, infectious, neurologic and
PT	nutritional disorders.
XX	
PS	Claim 14; SEQ ID NO 465; 123pp; English.
XX	
CC	This invention relates to CHI deleted mimetibodies (and the DNA sequences
CC	which encode them), compositions, methods and uses. The invention may be
CC	useful for the development of compounds with an osteopathic,
CC	cardiovascular-gen, dermatological-gen, auditory, endocrine-gen,
CC	gastrointestinal-gen, gynaecological-gen, hepatotropic, haemostatic,
CC	immunomodulator, antiallergic, muscular-gen, cytostatic,
CC	antiinflammatory, neuroleptic, ophthalmological, nephrotropic or
CC	respiratory-gen activity acting as a tumour necrosis factor (TNF)-
CC	modulator or cytokine-agonist. The methods and compositions of the
CC	present invention are useful for the diagnosis, prevention and/or
CC	treatment of diseases or conditions associated with aberrant expression
CC	or activity of the CHI deleted mimetibody, such as a bone or joint,
CC	cardiovascular, dental or oral, dermatological, ear, nose or throat,
CC	endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
CC	obstetric, haematologic, immunological, allergic, infectious,
CC	musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
CC	pediatric, psychiatric, renal or pulmonary disorders. The present
CC	sequence is that of a peptide which may be used during the creation of a
CC	mimetibody of the invention.
XX	
XX	
SEQ	Sequence 29 AA;
XX	
QY	Query Match 56.6%; Score 60; DB 8; Length 29;
DB	Best Local Similarity 100.0%; Pred. NO. 0.042;
Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	2 AIEGPTLRQWL 12
DB	15 AIEGPTLRQWL 25
RESULT 25	
ADJ73009	
ID	ADJ73009 standard; peptide; 31 AA.
XX	
AC	ADJ73009;
XX	
DT	06-MAY-2004 (first entry)

FH Key Location/Qualifiers
 FT Misc-difference 16 /note="Residue is a BrAc residue"
 FT XX
 PN WO2004002417-A2.
 XX
 PD 08-JAN-2004.
 XX
 PF 27-JUN-2003; 2003WO-US020347.
 XX
 PR 28-JUN-2002; 2002US-0392431P.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Heavner GA, Knight DM, Ghrayeb J, Scallion BJ, Nesspor TC;
 PI Kutoloski KA;
 XX
 DR WPI; 2004-082870/08.
 XX
 PT New CH1-deleted mimetibody polypeptides and nucleic acids, useful for
 PT modulating, treating, alleviating, preventing an immune, cardiovascular,
 PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
 PT diseases.
 XX
 PS Claim 2; SEQ ID NO 463; 129pp; English.
 XX
 CC This invention relates to CH1 deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an immunosuppressive,
 CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
 CC antibacterial, virucide or fungicide activity. In addition, the disclosed
 CC sequences may prove useful for gene therapy. The CH1-deleted mimetibody
 CC is useful for diagnosing or treating a disease condition in a cell,
 CC tissue, organ or animal, specifically for modulating, treating,
 CC alleviating, preventing the incidence or reducing the symptoms of an
 CC immune, cardiovascular (for example arrhythmia, hypertension or heart
 CC failure), or neurodegenerative (for example multiple sclerosis, dementia
 CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
 CC conditions, or infectious diseases (for example bacterial, viral or
 CC fungal infection). The present sequence is that of a peptide which may be
 CC used during the creation of a mimetibody of the invention.
 XX
 SQ Sequence 31 AA;
 XX
 Query Match 56.6%; Score 60; DB 8; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AIEGPTLRQWL 12
 DB 17 AIEGPTLRQWL 27
 XX
 RESULT 28
 ADJ52645
 ID ADJ52645 standard; peptide; 31 AA.
 XX
 AC ADJ52645;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE CH1 deleted mimetibody-related peptide SeqID464.
 XX
 KM CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
 KM hypotensive; neuroprotective; nootropic; antibacterial; virucide;
 KM fungicide; gene therapy; immune disorder; cardiovascular disease;
 KM arrhythmia; hypertension; heart failure; neurodegenerative;
 KM multiple sclerosis; dementia; Alzheimer's disease; anaemia;
 KM cancerous condition; infectious disease; bacterial infection;
 KM viral infection; fungal infection.
 XX
 OS Undeidentified.
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 16 /note="Residue is a PEG residue"
 FT XX
 PN WO2004002417-A2.
 XX
 PD 08-JAN-2004.
 XX
 PF 27-JUN-2003; 2003WO-US020347.
 XX
 PR 28-JUN-2002; 2002US-0392431P.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Heavner GA, Knight DM, Ghrayeb J, Scallion BJ, Nesspor TC;
 PI Kutoloski KA;
 XX
 DR WPI; 2004-082870/08.
 XX
 PT New CH1-deleted mimetibody polypeptides and nucleic acids, useful for
 PT modulating, treating, alleviating, preventing an immune, cardiovascular,
 PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
 PT diseases.
 XX
 PS Claim 2; SEQ ID NO 464; 129pp; English.
 XX
 CC This invention relates to CH1 deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an immunosuppressive,
 CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
 CC antibacterial, virucide or fungicide activity. In addition, the disclosed
 CC sequences may prove useful for gene therapy. The CH1-deleted mimetibody
 CC is useful for diagnosing or treating a disease condition in a cell,
 CC tissue, organ or animal, specifically for modulating, treating,
 CC alleviating, preventing the incidence or reducing the symptoms of an
 CC immune, cardiovascular (for example arrhythmia, hypertension or heart
 CC failure), or neurodegenerative (for example multiple sclerosis, dementia
 CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
 CC conditions, or infectious diseases (for example bacterial, viral or
 CC fungal infection). The present sequence is that of a peptide which may be
 CC used during the creation of a mimetibody of the invention.
 XX
 SQ Sequence 31 AA;
 XX
 Query Match 56.6%; Score 60; DB 8; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AIEGPTLRQWL 12
 DB 17 AIEGPTLRQWL 27
 XX
 RESULT 29
 ADJ51606
 ID ADJ51606 standard; peptide; 31 AA.
 XX
 AC ADJ51606;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE CH1 deleted mimetibody-related peptide SeqID464.
 XX
 KM CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
 KM dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
 KM gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KM antiallergic; muscular-Gen; cytostatic; antiinflammatory; neurologic;
 KM ophthalmological; nephrotoxic; respiratory-Gen; tumour necrosis factor;
 KM TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KM dental disorder; oral disorder; dermatological disorder; ear disorder;
 KM nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KM gastrointestinal disorder; gynaecological disorder; hepatic disorder;

KM obstetric disorder; haematologic disorder; immunological disorder;
 KM allergic disorder; infectious disorder; musculoskeletal disorder;
 KM oncological disorder; neurological disorder; nutritional disorder;
 KM ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KM renal disorder; pulmonary disorder.
 XX
 OS Unidentified.
 OS Synthetic.
 FT Key Location/Qualifiers
 FT Misc-difference 16
 FT /note= "Residue is a PEG residue"
 XX
 XX WO2004002424-A2.
 XX
 XX 08-JAN-2004.
 PD
 PF 30-JUN-2003; 2003WO-US020495.
 XX
 PR 28-JUN-2002; 2002US-0392431P.
 PR 19-SEP-2002; 2002US-0412144P.
 XX
 XX (CENZ) CENTOCOR INC.
 PA
 XX Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
 PI Kutlooski KA;
 XX
 DR WPI; 2004-082872/08.
 XX
 XX New CHI deleted mimetibody polypeptide and nucleic acid, useful for
 PT diagnosing, preventing or treating cardiovascular, dermatologic,
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
 PT nutritional disorders.
 XX
 PS Claim 14; SEQ ID NO 464; 123pp; English.
 CC
 CC This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an osteopathic,
 CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
 CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
 CC immunomodulator, anti-allergic, muscular-Gen, cytosstatic,
 CC anti-inflammatory, neuroleptic, ophthalmological, nephrotropic or
 CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
 CC modulator or cytokine-agonist. The methods and compositions of the
 CC present invention are useful for the diagnosis, prevention and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the CHI deleted mimetibody, such as a bone or joint,
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
 CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
 CC obstetric, haematologic, immunological, allergic, infectious,
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
 CC pediatric, psychiatric, renal or pulmonary disorders. The present
 CC sequence is that of a peptide which may be used during the creation of a
 CC mimetibody of the invention.
 CC
 CC
 SQ Sequence 31 AA;
 Query Match 56.6%; Score 60; DB 8; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 AIBGPTLRQWL 12
 Db 17 AIBGPTLRQWL 27
 RESULT 30
 ADJ51605
 ID ADJ51605 standard; peptide; 31 AA.
 XX
 AC ADJ51605;
 XX

DT 06-MAY-2004 (first entry)
 XX
 DE CHI deleted mimetibody-related peptide Segid463.
 XX
 XX CHI deleted mimetibody; osteopathic; cardiovascular-Gen;
 KM dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
 KM gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KM anti-allergic; muscular-Gen; cytosstatic; anti-inflammatory; neuroleptic;
 KM ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
 KM TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KM dental disorder; oral disorder; dermatological disorder; ear disorder;
 KM nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KM gastrointestinal disorder; gynaecological disorder; hepatic disorder;
 KM obstetric disorder; haematologic disorder; immunological disorder;
 KM allergic disorder; infectious disorder; musculoskeletal disorder;
 KM oncological disorder; neurological disorder; nutritional disorder;
 KM ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KM renal disorder; pulmonary disorder.
 XX
 XX Unidentified.
 OS Synthetic.
 FT Key Location/Qualifiers
 FT Misc-difference 16
 FT /note= "Residue is a BrAc residue"
 XX
 XX WO2004002424-A2.
 XX
 XX 08-JAN-2004.
 PD
 PF 30-JUN-2003; 2003WO-US020495.
 XX
 XX 28-JUN-2002; 2002US-0392431P.
 PR 19-SEP-2002; 2002US-0412144P.
 XX
 XX (CENZ) CENTOCOR INC.
 PA
 XX Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
 PI Kutlooski KA;
 XX
 DR WPI; 2004-082872/08.
 XX
 XX New CHI deleted mimetibody polypeptide and nucleic acid, useful for
 PT diagnosing, preventing or treating cardiovascular, dermatologic,
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
 PT nutritional disorders.
 XX
 PS Claim 14; SEQ ID NO 463; 123pp; English.
 CC
 CC This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an osteopathic,
 CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
 CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
 CC immunomodulator, anti-allergic, muscular-Gen, cytosstatic,
 CC anti-inflammatory, neuroleptic, ophthalmological, nephrotropic or
 CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
 CC modulator or cytokine-agonist. The methods and compositions of the
 CC present invention are useful for the diagnosis, prevention and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the CHI deleted mimetibody, such as a bone or joint,
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
 CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
 CC obstetric, haematologic, immunological, allergic, infectious,
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
 CC pediatric, psychiatric, renal or pulmonary disorders. The present
 CC sequence is that of a peptide which may be used during the creation of a
 CC mimetibody of the invention.
 CC
 CC
 SQ Sequence 31 AA;
 Query Match 56.6%; Score 60; DB 8; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 QY 2 AIBGPTLRQWL 12
 Db 17 AIBGPTLRQWL 27
 RESULT 30
 ADJ51605
 ID ADJ51605 standard; peptide; 31 AA.
 XX
 AC ADJ51605;
 XX

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AIEGPTLRQWL 12
17 AIEGPTLRQWL 27

RESULT 31
ADN59659
ID ADN59659 standard; peptide; 18 AA.

AC ADN59659;

DT 01-JUL-2004 (first entry)

DE Thrombopoietin mimetic peptide (TMP8), seq id 8.

XX Haemostatic; antihaemic; immunosuppressive; platelet;

XX transmembrane signalling; mpl receptor; thrombopoietin mimetic peptide;

KW TMP; c-mpl receptor; platelet precursor; megakaryocyte;

KW thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;

KW autoimmune haemolytic anaemia; Hughes's syndrome;

XX lupoid thrombocytopenia.

OS Homo sapiens.

PN WO2003031589-A2.

PD 17-APR-2003.

PF 11-OCT-2002; 2002WO-US032552.

XX 11-OCT-2001; 2001US-0328666P.

PR 10-OCT-2002; 2002US-00269806.

XX (AMGE-) AMGEN INC.

PI Min H, Sitney KC, Hartley C;

XX MPI; 2003-403101/38.

DR Novel thrombopoietin mimetic peptides which bind to mpl receptor, and

XX which stimulate the production of platelets and/or the production of

PT platelet precursors, useful for treating thrombocytopenia.

PS Claim 6; SEQ ID NO 8; 126pp; English.

XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that

CC binds to the c-mpl (mpl) receptor, and which stimulates the production of

CC platelets and/or the production of platelet precursors, is new. Further

CC disclosed is a composition of matter (II) that binds to an mpl receptor,

CC and a pharmaceutical composition comprising (II) and a carrier. The

CC pharmacological composition of the invention is useful for treating

CC thrombocytopenia in an animal, and for increasing megakaryocytes or

CC platelets in a patient. The TMP of the invention is useful for treating

CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.,

CC disease conditions involving thrombocytopenia such as aplastic anaemia,

CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,

CC autoimmune haemolytic anaemia, Hughes's syndrome and lupoid

CC thrombocytopenia. The TMP of the invention is also useful for

CC maintaining the viability or storage life of platelets and/or

CC megakaryocytes and its derived cells. The compounds demonstrate an

CC improved ability to bind to and/or trigger transmembrane signal through,

CC i.e. activating, the mpl receptor the compounds have superior

CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in

CC vitro, the production of platelets and/or megakaryocytopenic activity,

CC i.e. the ability to stimulate, in vivo and in vitro, the production of,

CC platelet precursors. Further, certain of the compounds also exhibit

CC superior therapeutic properties, such as improved plasma half-life,

CC biological activity and in vivo circulation time. The current sequence

CC represents a preferred TMP of the invention.

XX Sequence 18 AA;

Query Match 56.1%; Score 59.5; DB 7; Length 18;
Best Local Similarity 73.3%; Pred. No. 0.029;
Matches 11; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 4 EGPTRLQWL-HNGNR 17
4 EGPTRLQWLHNGRQ 18

RESULT 32
ADN59826
ID ADN59826 standard; peptide; 22 AA.

AC ADN59826;

DT 01-JUL-2004 (first entry)

DE TMP peptide TMP8.

XX Haemostatic; antihaemic; immunosuppressive; platelet;

XX transmembrane signalling; mpl receptor; thrombopoietin mimetic peptide;

KW TMP; c-mpl receptor; platelet precursor; megakaryocyte;

KW thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;

KW autoimmune haemolytic anaemia; Hughes's syndrome;

XX lupoid thrombocytopenia; linker.

OS Homo sapiens.

PN WO2003031589-A2.

PD 17-APR-2003.

PF 11-OCT-2002; 2002WO-US032552.

XX 11-OCT-2001; 2001US-0328666P.

PR 10-OCT-2002; 2002US-00269806.

XX (AMGE-) AMGEN INC.

PI Min H, Sitney KC, Hartley C;

XX MPI; 2003-403101/38.

DR Novel thrombopoietin mimetic peptides which bind to mpl receptor, and

XX which stimulate the production of platelets and/or the production of

PT platelet precursors, useful for treating thrombocytopenia.

PS Example 6; Page 83; 126pp; English.

XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that

CC binds to the c-mpl (mpl) receptor, and which stimulates the production of

CC platelets and/or the production of platelet precursors, is new. Further

CC disclosed is a composition of matter (II) that binds to an mpl receptor,

CC and a pharmaceutical composition comprising (II) and a carrier. The

CC pharmacological composition of the invention is useful for treating

CC thrombocytopenia in an animal, and for increasing megakaryocytes or

CC platelets in a patient. The TMP of the invention is useful for treating

CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.,

CC disease conditions involving thrombocytopenia such as aplastic anaemia,

CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,

CC autoimmune haemolytic anaemia, Hughes's syndrome and lupoid

CC thrombocytopenia. The TMP of the invention is also useful for

CC maintaining the viability or storage life of platelets and/or

CC megakaryocytes and its derived cells. The compounds demonstrate an

CC improved ability to bind to and/or trigger transmembrane signal through,

CC i.e. activating, the mpl receptor the compounds have superior

CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in

CC vitro, the production of platelets and/or megakaryocytopenic activity,

CC i.e. the ability to stimulate, in vivo and in vitro, the production of

CC platelet precursors. Further, certain of the compounds also exhibit

CC superior therapeutic properties, such as improved plasma half-life,

CC biological activity and in vivo circulation time. The current sequence

CC represents a preferred TMP of the invention.

XX Sequence 18 AA;

CC represents a TMP peptide of the invention to which a two amino acid "cap"
 CC has been added to the carboxy terminal to increase peptide affinity.
 XX
 XX
 SQ Sequence 22 AA;

Query Match 56.1%; Score 59.5; DB 7; Length 22;

Best Local Similarity 73.3%; Pred. No. 0.037;

Matches 11; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 4 EGGTLRQWL-HGNGR 17
 |||||:|||||:
 Db 6 EGGTLKQWLPHGRGQ 20

RESULT 33

ADNS9700
 ID ADNS9700 standard; peptide; 25 AA.

AC ADNS9700;

XX 01-JUL-2004 (first entry)

DT Thrombopoietin mimetic peptide TMP8, seq id 49.

DE Haemostatic; antianaemic; immunosuppressive; platelet;

XX transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;

KW TMP; c-mpl receptor; platelet precursor; megakaryocyte;

KW thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;

KW autoimmune haemolytic anaemia; Hughes's syndrome;

XX lupoid thrombocytopenia.

OS Homo sapiens.

XX WO2003031589-A2.

PN 17-APR-2003.

XX 11-OCT-2002; 2002WO-US032552.

PF 11-OCT-2001; 2001US-0328666P.

PR 10-OCT-2002; 2002US-00269806.

XX (AMGB-) AMGEN INC.

PA Min H, Sicney KC, Hartley C;

PI WPI; 2003-403101/38.

XX N-PSDB; ADNS96999.

DR Novel thrombopoietin mimetic peptides which bind to mpl receptor, and

XX which stimulate the production of platelets and/or the production of

PT platelet precursors, useful for treating thrombocytopenia.

PS Disclosure; SEQ ID NO 49; 126pp; English.

XX The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that

CC binds to the c-mpl (mpl) receptor, and which stimulates the production of

CC platelets and/or the production of platelet precursors, is new. Further

XX disclosed is a composition of matter (II) that binds to an mpl receptor,

CC and a pharmaceutical composition comprising (II) and a carrier. The

XX pharmaceutical composition of the invention is useful for treating

XX thrombocytopenia in an animal, and for increasing megakaryocytes or

XX platelets in a patient. The TMP of the invention is useful for treating

XX conditions involving a megakaryocyte and/or platelet deficiency, e.g.

XX disease conditions involving thrombocytopenia such as aplastic anaemia,

XX autoimmune thrombocytopenia, drug induced immune thrombocytopenia,

XX autoimmune haemolytic anaemia, Hughes's syndrome and lupoid

XX thrombocytopenia. The TMP of the invention is also useful for

XX maintaining the viability or storage life of platelets and/or

XX megakaryocytes and its derived cells. The compounds demonstrate an

XX improved ability to bind to and/or trigger transmembrane signal through,

XX i.e. activating, the mpl receptor the compounds have superior

XX thrombopoietic activity, i.e. the ability to stimulate, in vivo and in

CC vitro, the production of platelets and/or megakaryocytopenic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a TMP fragment.
 XX

Sequence 25 AA;

Query Match 56.1%; Score 59.5; DB 7; Length 25;

Best Local Similarity 73.3%; Pred. No. 0.042;

Matches 11; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 4 EGGTLRQWL-HGNGR 17
 |||||:|||||:
 Db 7 EGGTLKQWLPHGRGQ 21

RESULT 34

AA96526
 ID AA96526 standard; peptide; 36 AA.

XX AA96526;

XX 04-SEP-2000 (first entry)

DT Thrombopoietin mimetic peptide compound 7.

DE Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production;

KW anti-human immunodeficiency virus; anti-HIV; anti-anaemic; dermatological;

KW immunosuppressive; anti-inflammatory; linker.

XX Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..14

XX Modified-site 1 /note= "optionally linked to an Fc molecule"

XX Peptide 15..18 /label= linker

XX Peptide 19..32 /label= TMP_2

XX WO200024770-A2.

XX 04-MAY-2000.

XX 22-OCT-1999; 99WO-US024834.

XX 23-OCT-1998; 98US-0105348P.

XX (AMGB-) AMGEN INC.

XX Liu C, Feige U, Cheetham J;

XX WPI; 2000-365108/31.

XX Thrombopoietic peptides which activate mpl receptors and increase the

XX production of platelets or platelet precursors, useful for treatment of

XX diseases which involve thrombocytopenia.

XX Claim 16; Page 62; 91pp; English.

XX A compound which binds to an mpl receptor comprising a thrombopoietin

XX mimetic peptide (TMP) dimer joined by a linker (TMP_1-(L_1) TMP_2), is

XX new. TMP 1 and TMP 2 are amino acid sequences varying from at least 10 to

XX 14 residues in length comprising X-2-X-1-0, X-2-X-1-1, X-2-X-1-2, X-2-

XX X-1-3, X-2-X-1-4, X-1-X-1-0, X-1-X-1-1, X-1-X-1-2, X-1-X-1-3, and X-1-

XX X-1-4. X-1 = I, A, V, L, S or R; X-2 = E, D, K or V; X-3 = G or A; X-4 =

XX F; X-5 = T or S; X-6 = L, I, V, A, F, M, or K; X-1-1 = A, I, V, L, F,

XX X-9 = W, Y or F; X-1-0 = L, I, V, A, F, M, or K; X-1-1 = A, I, V, L, F,

XX S, T, K, H, or E; X-1-2 = A, I, V, L, F, G, S, or Q; X-1-3 = R, K, T, V,

CC N, Q or G; X₁₋₄ = A, I, V, L, F, T, R, E, or G; L₁ = linker comprising
 CC 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate
 CC the c-Mpl receptor which mediates the activity of endogenous
 CC thrombopoietin. The TMs are useful for increasing the production of
 CC platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which
 CC is useful for treatment of diseases which involve thrombocytopenia, e.g.
 CC aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
 CC virus associated ITP, and systemic lupus erythematosus

XX Sequence 36 AA;

Query Match 56.1%; Score 59.5; DB 3; Length 36;

Best Local Similarity 68.4%; Pred. No. 0.064; 1; Indels 5; Gaps 1;

Matches 13; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

3 IEGPTLRQWL-----HGNG 16
 |||||
 1 IEGPTLRQWLAAAGGNG 19

Db

RESULT 35

AAAB17306 standard; peptide; 36 AA.

AAAB17306;

31-OCT-2000 (first entry)

TPO-mimetic peptide sequence SEQ ID NO:362.

Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 autoimmunity; disease; cytotoxic; antineoplastic; thrombolytic; VEGF;
 immunosuppressive; EPO; TPO; CTAP4; mimetic; IL-1; TNF; antagonist; MMP;
 inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 vascular endothelial growth factor; matrix metalloproteinase; aschma;
 thrombosis; pharmaceutical.

Synthetic.

WO200024782-A2.

04-MAY-2000.

25-OCT-1999; 99WO-US025044.

23-OCT-1998; 98US-0105371P.

22-OCT-1999; 99US-00428082.

(AMGE-) AMGEN INC.

Peige U, Liu C, Cheetham J, Boone TC,

WPI; 2000-350702/30.

Novel composition of matter comprising an Fc domain and pharmacologically
 active peptides, useful for treating cancer and autoimmune diseases.

Example 1; Page 324; 608pp; English.

The present invention describes composition of matter (I) comprising an
 Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 (X1)-a-F1-(X2)-b, where: F1 = an Fc domain; X1 and X2 = are each
 independently selected from -(L1)-c-P1, -(L1)-c-P1-(L2)-d-P2, -(L1)-c-P1-
 (L2)-d-P2-(L3)-e-P3, or -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,
 P3, and P4 = are each independently sequences of pharmacologically active
 peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 c, d, e, and f = are each independently 0 or 1, provided that at least 1
 of a and b is 1. The composition can have cytostatic, antineoplastic,
 thrombolytic and immunosuppressive activities. DNAs, vectors and host
 cells from the present invention can be used for producing pharmaceutical
 compositions. The compositions are useful for treating cancer, asthma,
 thrombosis, or autoimmune diseases. The use of an Fc domain (rather than

CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AA63943 to AA639526 and AA616955 to
 CC AA618003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention

XX Sequence 36 AA;

Query Match 56.1%; Score 59.5; DB 3; Length 36;

Best Local Similarity 68.4%; Pred. No. 0.064; 1; Indels 5; Gaps 1;

Matches 13; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

3 IEGPTLRQWL-----HGNG 16
 |||||
 1 IEGPTLRQWLAAAGGNG 19

Db

RESULT 36

ABP51688 standard; peptide; 18 AA.

ABP51688;

01-OCT-2002 (first entry)

TPO mimetic peptide SEQ ID NO:39.

TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 complementarity determining region; immunoglobulin; anti-anaemic;
 haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

Homo sapiens.

Synthetic.

WO200246238-A2.

13-JUN-2002.

05-DEC-2001; 2001WO-US047656.

05-DEC-2000; 2000US-0251448P.

04-MAY-2001; 2001US-0288889P.

29-MAY-2001; 2001US-0294068P.

(ALEX-) ALEXION PHARM INC.

Bowdish KS, Barbas-Frederickson S, Renshaw M;

WPI; 2002-566610/60.

N-PSDB; AB073366.

A novel immunogen molecule comprising a region in which amino acid
 residues corresponding to at least a portion of the complementary
 determining region are replaced or fused with an erythropoietin or
 thrombopoietin mimetic.

Claim 20; Fig 5; 113pp; English.

The present invention describes an immunoglobulin molecule or its fragment
 (I) comprising a region where amino acid residues corresponding to at
 least a portion of the complementary determining region (CDR) are
 replaced or fused with biologically active peptides e.g. a peptide
 mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 that is flanked with proline at its carboxy terminus. (I) has
 anti-anaemic, haemostatic and nephrotropic activities, and can be used as
 a stimulator of proliferation, differentiation and maturation of
 haematopoietic cells; and a stimulator of haematopoiesis. (I) is useful
 for stimulating proliferation, differentiation or growth of
 promegakaryocytes or megakaryocytes, where (I) is contacted with
 promegakaryocytes or megakaryocytes, which results in increased platelet
 production. (I) with a region where amino acid residues corresponding to
 a portion of CDR is replaced with an EPO mimetic, or which has one or
 more of its CDRs fused to an EPO mimetic, is useful for increasing the

CC production of red blood cells, where (I) is contacted with haematopoietic
 CC stem cells or their progenitors. (I) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC AB073288 to AB073377 and ABP51669 to ABP51696 represent sequences used in
 CC the exemplification of the present invention

XX Sequence 18 AA;

Query Match 55.7%; Score 59; DB 5; Length 18;
 Best Local Similarity 91.7%; Pred. No. 0.035;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAIEGPTLRQWL 12
 | | | | | | | | | |
 DB 1 LPIEGPTLRQWL 12

RESULT 37

ABP51677
 ID ABP51677 standard; peptide; 18 AA.

XX ABP51677;

DT 01-OCT-2002 (first entry)

XX TPO mimetic peptide SEQ ID NO:61.

DE TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;

XX complementarity determining region; immunoglobulin; antianaemic;

KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX Homo sapiens.

OS Synthetic.

XX WO200246238-A2.

PN 13-JUN-2002.

XX 05-DEC-2001; 2001WO-US047656.

PF 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

XX (ALEX-) ALEXION PHARM INC.

PA Bowdish KS, Barbas-Frederickson S, Renshaw M;

PI WPI; 2002-566610/60.

DR A novel immunogen molecule comprising a region in which amino acid

XX residues corresponding to at least a portion of the complementary

PT determining region are replaced or fused with an erythropoietin or

XX thrombopoietin mimetic.

XX Claim 91; Page 57; 113pp; English.

CC The present invention describes an immunoglobulin molecule or its fragment
 CC (I) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (I) has
 CC antianaemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (I) is contacted with
 CC production. (I) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or

CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (I) is contacted with haematopoietic
 CC stem cells or their progenitors. (I) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC AB073288 to AB073377 and ABP51669 to ABP51696 represent sequences used in
 CC the exemplification of the present invention

XX Sequence 18 AA;

Query Match 55.7%; Score 59; DB 5; Length 18;
 Best Local Similarity 73.3%; Pred. No. 0.035;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 IEGPTLRQWLHNGR 17
 | | | | | | | | | |
 DB 3 IEGPTLRQWLARAR 17

RESULT 38

ABP51675
 ID ABP51675 standard; peptide; 18 AA.

XX ABP51675;

DT 01-OCT-2002 (first entry)

XX TPO mimetic antibody related peptide graft SEQ ID NO:66.

DE TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;

XX complementarity determining region; immunoglobulin; antianaemic;

KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.

XX Homo sapiens.

OS Synthetic.

XX WO200246238-A2.

PN 13-JUN-2002.

XX 05-DEC-2001; 2001WO-US047656.

PF 05-DEC-2000; 2000US-0251448P.

PR 04-MAY-2001; 2001US-0288889P.

PR 29-MAY-2001; 2001US-0294068P.

XX (ALEX-) ALEXION PHARM INC.

PA Bowdish KS, Barbas-Frederickson S, Renshaw M;

PI WPI; 2002-566610/60.

DR A novel immunogen molecule comprising a region in which amino acid

XX residues corresponding to at least a portion of the complementary

PT determining region are replaced or fused with an erythropoietin or

XX thrombopoietin mimetic.

XX Example 4; Page 55; 113pp; English.

CC The present invention describes an immunoglobulin molecule or its fragment
 CC (I) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (I) has
 CC antianaemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (I) is contacted with
 CC production. (I) with a region where amino acid residues corresponding to

CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (1) is contacted with haematopoietic
 CC stem cells or their progenitors. (1) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in
 CC the exemplification of the present invention

XX Sequence 18 AA;

Query Match 55.7%; Score 59; DB 5; Length 18;

Best Local Similarity 91.7%; Pred. No. 0.035; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAIEGPTLRQWL 12
 Db 1 LPLEGPTLRQWL 12

RESULT 39

ADQ16619 standard; peptide; 18 AA.

ADQ16619;

09-SBP-2004 (first entry)

TPO mimetic peptide with random flanking residues SEQ ID NO:39.

immunoglobulin; complementarity determining region; CDR; peptide mimetic;
 erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 immunotherapy; thrombocytopenia.

Unidentified.

WO2004050017-A2.

17-JUN-2004.

17-NOV-2003; 2003WO-US036894.

02-DEC-2002; 2002US-00307724.

(ALEX-) ALEXION PHARM INC.

Bowdish KS, Frederickson S, Renshaw M;

WPI; 2004-460973/43.

N-PSDB; ADQ16620.

New immunoglobulin molecule comprising a region, where two
 complementarity determining regions (CDRs) are replaced with EPO mimetic
 or a TPO mimetic, useful for treating thrombocytopenia.

Example 1; SEQ ID NO 39; 107pp; English.

The invention relates to a novel immunoglobulin molecule or its fragment
 comprising a region where amino acid residues corresponding to at least a
 portion of a two complementarity determining regions (CDRs) are replaced
 with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 invention has immunosuppressive activity, and may have a use in
 immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 treating thrombocytopenia as a result of chemotherapy, bone marrow
 transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 The present sequence represents a TPO mimetic peptide with flanking
 residues.

Sequence 18 AA;

Query Match 55.7%; Score 59; DB 8; Length 18;

Best Local Similarity 91.7%; Pred. No. 0.035; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAIEGPTLRQWL 12
 Db 1 LPLEGPTLRQWL 12

RESULT 40

ADQ16641 standard; peptide; 18 AA.

ADQ16641;

09-SBP-2004 (first entry)

TPO mimetic peptide with flanking amino acids SEQ ID NO:61.

immunoglobulin; complementarity determining region; CDR; peptide mimetic;
 erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 immunotherapy; thrombocytopenia.

Unidentified.

WO2004050017-A2.

17-JUN-2004.

17-NOV-2003; 2003WO-US036894.

02-DEC-2002; 2002US-00307724.

(ALEX-) ALEXION PHARM INC.

Bowdish KS, Frederickson S, Renshaw M;

WPI; 2004-460973/43.

New immunoglobulin molecule comprising a region, where two
 complementarity determining regions (CDRs) are replaced with EPO mimetic
 or a TPO mimetic, useful for treating thrombocytopenia.

Example 6; SEQ ID NO 61; 107pp; English.

The invention relates to a novel immunoglobulin molecule or its fragment
 comprising a region where amino acid residues corresponding to at least a
 portion of a two complementarity determining regions (CDRs) are replaced
 with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 invention has immunosuppressive activity, and may have a use in
 immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 treating thrombocytopenia as a result of chemotherapy, bone marrow
 transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 The present sequence represents a TPO mimetic peptide with flanking
 residues.

Sequence 18 AA;

Query Match 55.7%; Score 59; DB 8; Length 18;
 Best Local Similarity 73.3%; Pred. No. 0.035; Mismatches 4; Indels 0; Gaps 0;

QY 3 IEIGPTLRQWLHNGR 17
 Db 3 IEIGPTLRQWLHNGR 17

RESULT 41

ADQ16646 standard; peptide; 18 AA.

ADQ16646;

ADQ16646;

DT 09-SEP-2004 (first entry)
 XX
 DE TPO mimetic peptide SEQ ID NO:65.
 XX
 KW immunoglobulin; complementarity determining region; CDR; peptide mimetic;
 KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 XX immunotherapy; thrombocytopenia.
 XX
 OS Unidentified.
 XX
 PN WO2004050017-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 17-NOV-2003; 2003WO-US036894.
 XX
 PR 02-DEC-2002; 2002US-00307724.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Bowdish KS, Frederickson S, Renshaw M;
 XX
 DR MPI; 2004-460973/43.
 DR N-PSDB; ADQ16645.
 XX
 PT New immunoglobulin molecule comprising a region, where two
 PT complementarity determining regions (CDRs) are replaced with EPO mimetic
 PT or a TPO mimetic, useful for treating thrombocytopenia.
 XX
 PS Example 4; SEQ ID NO 66; 107pp; English.
 XX
 CC The invention relates to a novel immunoglobulin molecule or its fragment
 CC comprising a region where amino acid residues corresponding to at least a
 CC portion of a two complementarity determining regions (CDRs) are replaced
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 CC invention has immunosuppressive activity, and may have a use in
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow
 CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide of the invention.
 XX
 SQ Sequence 18 AA;
 CC
 Query Match 55.7%; Score 59; DB 8; Length 18;
 Best Local Similarity 91.7%; Pred. No. 0.035; 1; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 LAIEGPTLRQWL 12
 | | | | | | | | | | | | | |
 Db 1 LPIEGPTLRQWL 12

RESULT 42
 ID ADNS9819 standard; peptide; 22 AA.
 AC ADNS9819;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE TWP peptide TWP1.
 XX
 KW Haemostatic; antihaemic; immunosuppressive; platelet;
 KW transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 KW TWP; c-mpl receptor; platelet precursor; megakaryocyte;
 KW thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
 KW autoimmune haemolytic anaemia; Hughes' syndrome;
 XX lupoid thrombocytopenia; linker.
 OS Homo sapiens.
 XX
 PN WO2003031589-A2.

XX
 PD 17-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032552.
 XX
 PR 11-OCT-2001; 2001US-0328666P.
 PR 10-OCT-2002; 2002US-00269806.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Min H, Sitney KC, Hartley C;
 XX
 DR MPI; 2003-403101/38.
 XX
 PT Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
 PT which stimulate the production of platelets and/or the production of
 PT platelet precursors, useful for treating thrombocytopenia.
 XX
 PS Example 6; Page 83; 126pp; English.
 XX
 CC The invention relates to a thrombopoietin mimetic peptide (TWP) (I) that
 CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
 CC platelets and/or the production of platelet precursors, is new. Further
 CC disclosed is a composition of matter (II) that binds to an mpl receptor,
 CC and a pharmaceutical composition comprising (II) and a carrier. The
 CC pharmaceutical composition of the invention is useful for treating
 CC thrombocytopenia in an animal, and for increasing megakaryocytes or
 CC platelets in a patient. The TWP of the invention is useful for treating
 CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.,
 CC disease conditions involving thrombocytopenia such as aplastic anaemia,
 CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,
 CC autoimmune haemolytic anaemia, Hughes' syndrome and lupoid
 CC thrombocytopenia. The TWP of the invention is also useful for
 CC maintaining the viability or storage life of platelets and/or
 CC megakaryocytes and its derived cells. The compounds demonstrate an
 CC improved ability to bind to and/or trigger transmembrane signal through,
 CC i.e. activating, the mpl receptor the compounds have superior
 CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
 CC vitro, the production of platelets and/or megakaryocytic activity,
 CC i.e. the ability to stimulate, in vivo and in vitro, the production of
 CC platelet precursors. Further, certain of the compounds also exhibit
 CC superior therapeutic properties, such as improved plasma half-life,
 CC biological activity and in vivo circulation time. The current sequence
 CC represents a TWP peptide of the invention to which a two amino acid "cap"
 CC has been added to the carboxy terminal to increase peptide affinity.
 XX
 SQ Sequence 22 AA;
 CC
 Query Match 55.7%; Score 59; DB 7; Length 22;
 Best Local Similarity 64.7%; Pred. No. 0.044; 5; Indels 0; Gaps 0;
 Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 OY 3 IEGPTLRQWLHNGRDT 19
 | | | | | | | | | | | | | | | | | |
 Db 5 IEGPTLRQWLARALET 21

RESULT 43
 ID ADQ16705 standard; protein; 128 AA.
 AC ADQ16705;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Modified immunoglobulin clone 116 HC variable region SEQ ID NO:125.
 XX
 KW immunoglobulin; complementarity determining region; CDR; peptide mimetic;
 KW erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 KW immunotherapy; thrombocytopenia.
 XX
 OS Synthetic.
 XX
 PN

PT	New immunoglobulin molecule comprising a region, where two complementary determining regions (CDRs) are replaced with EPO mimetic or a TPO mimetic, useful for treating thrombocytopenia.
PS	
XX	Example 8; SEQ ID NO 124; 107bp; English.
CC	The invention relates to a novel immunoglobulin molecule or its fragment comprising a region where amino acid residues corresponding to at least a portion of a two complementarity determining regions (CDRs) are replaced with a peptide mimetic selected from an erythropoietin (EPO) mimetic and a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the invention has immunosuppressive activity, and may have a use in immunotherapy. The immunoglobulin molecule is useful for diagnosing or treating thrombocytopenia as a result of chemotherapy, bone marrow transplantation, or chronic diseases such as idiopathic thrombocytopenia. The present sequence represents immunoglobulin clone 116 heavy chain.
CC	
CC	
CC	
CC	
SO	Sequence 225 AA;
Query Match	55.7%; Score 59; DB 8; Length 225;
Best Local Similarity	91.7%; Pred. No. 0.59; Indels 0; Gaps 0
Matches 11; Conservative	0; Mismatches 1;
Cy	1 LAIRGPTLRQWL 12 100 LPIRGPTLRQWL 111
Dd	
RESULT 45	
ABP51695	
ID	ABP51695 standard; protein; 472 AA.
XX	
AC	ABP51695;
XX	
DT	01-OCT-2002 (first entry)
XX	
DE	SGI.1-TPO heavy chain amino acid sequence SEQ ID NO:67.
KX	TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region; complementarity determining region; immunogloblin; antianaemic; haemostatic; nephrotropic; haematopoietic cell; haematopoeisis.
KW	
KW	
OS	Homo sapiens.
OS	Synthetic.
PN	WO200246238-A2.
PD	13-JUN-2002.
XX	
PF	05-DEC-2001; 2001WO-US047656.
XX	
PR	05-DEC-2000; 2000US-0251448P.
PR	04-MAY-2001; 2001US-0288889P.
PPR	29-MAY-2001; 2001US-0294068P.
PA	(ALEX-) ALEXION PHARM INC.
XX	
XX	Bowdish KS, Barbados-Frederickson S, Renshaw M;
PI	
XX	
DR	MPJ; 2002-566610/60.
N-P8DB; ABQ73374.	
XX	
XX	A novel immunogen molecule comprising a region in which amino acid residues corresponding to at least a portion of the complementary determining region are replaced or fused with an erythropoietin or thrombopoetin mimetic.
PT	
XX	
PS	Example 4; Fig 13A; 113bp; English.
CC	The present invention describes an immunogloblin molecule or its fragment (I) comprising a region where amino acid residues corresponding to at least a portion of the complementary determining region (CDR) are replaced or fused with biologically active peptides e.g. a peptide

CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (I) has
 CC anti-nausea, haemostatic and nephroprotective activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (I) is contacted with
 CC promegakaryocytes or megakaryocytes, which results in increased platelet
 CC production. (I) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (I) is contacted with haematopoietic
 CC stem cells or their progenitors. (I) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease.
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABQ73288 to ABQ73377 and ABP5169 to ABP51696 represent sequences used in
 CC the exemplification of the present invention
 XX

Sequence 472 AA;

Query Match 55.7%; Score 59; DB 5; Length 472;
 Best Local Similarity 91.7%; Pred. No. 1.3;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAIGPPTLRQWL 12
 | |||||
 Db 118 LPIGPPTLRQWL 129

Search completed: September 1, 2005, 16:12:13
 Job time : 88.3453 secs

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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:57:33 ; Search time 14.4892 Seconds
(without alignments)
126.171 Million cell updates/sec

Title: US-10-083-768-11

Perfect score: 106
Sequence: 1 LAIEGPTLRQMLHNGRDT 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : PIR 79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	50	47.2	691	2 A54741	erythrocyte membra
2	50	47.2	721	2 A39707	erythrocyte membra
3	50	47.2	973	2 AB2340	hypothetical prote
4	50	47.2	1774	2 S13178	6-methylsalicylic
5	49	46.2	419	1 ESECRM	erythromycin ester
6	47	44.3	349	2 B87251	molymphom cofacto
7	47	44.3	391	2 E83151	hypothetical prote
8	46.5	43.9	602	2 T45278	oligopeptide ABC t
9	46	43.4	434	2 T31313	glutamate-1-semial
10	45.5	42.9	333	2 A36925	transcription acti
11	45	42.5	235	2 C83822	hypothetical prote
12	45	42.5	302	2 JN0143	catechol 1,2-dioxy
13	45	42.5	304	2 C90453	hypothetical prote
14	45	42.5	492	2 T01086	probable serine/th
15	44	41.5	209	2 A13455	transcription regu
16	44	41.5	229	2 JC7219	nuclear protein SR
17	44	41.5	278	2 F84127	hypothetical prote
18	44	41.5	331	2 B48445	glyceraldhyde-3-P
19	44	41.5	344	2 AE3379	molymphom cofacto
20	44	41.5	496	2 S25091	cruciferin Bnc2 -
21	44	41.5	571	2 A10506	probable sulfatase
22	44	41.5	972	2 T49773	related to actin-i
23	44	41.5	1712	2 CGH028	collagen alpha 2(I
24	44	41.5	3430	1 GNMWV	genome polyprotein
25	44	41.5	3433	1 GNMWV	genome polyprotein
26	43.5	41.0	296	2 AG0147	probable membrane
27	43	40.6	218	2 H82539	protein-L-isoaspar
28	43	40.6	313	2 A45822	beta-lactamase (BC
29	43	40.6	352	2 B69901	fatty-acid desatur

30	43	40.6	481	2 T05270	probable serine/th
31	43	40.6	664	2 G89894	protein kinase [im
32	43	40.6	841	2 A43254	protein-tyrosine-P
33	43	40.6	1023	2 E71376	conserved hypothet
34	42	39.6	104	2 B82797	conserved hypothet
35	42	39.6	106	2 AC3086	sarcosine oxidase
36	42	39.6	106	2 F98200	sarcosine oxidase
37	42	39.6	218	2 D83161	hypothetical prote
38	42	39.6	273	2 T44657	protein GP80 (limp
39	42	39.6	335	2 B72053	glyceraldhyde 3-P
40	42	39.6	335	2 B86568	glyceraldhyde 3-P
41	42	39.6	335	2 S43339	glyceraldhyde 3-P
42	42	39.6	339	2 A30754	hypothetical prote
43	42	39.6	407	2 A86298	hypothetical prote
44	42	39.6	422	2 P66826	hypothetical prote
45	42	39.6	433	2 S51837	glyceraldhyde-3-P
46	42	39.6	433	2 S51836	glyceraldhyde-3-P
47	42	39.6	457	2 D70901	probable lmu prote
48	42	39.6	473	2 B84853	hypothetical prote
49	42	39.6	926	2 B84642	hypothetical prote
50	42	39.6	1019	2 T11560	pol polyprotein -
51	42	39.6	1022	2 T51257	calmodulin-binding
52	42	39.6	1022	2 T50928	calmodulin-binding
53	42	39.6	1075	2 D70568	hypothetical prote
54	42	39.6	2357	2 A59249	class VII unconven
55	42	39.6	2843	1 RBHUP	adenomatous polypo
56	42	39.6	2845	1 I48505	adenomatous polypo
57	42	39.6	4548	1 S00657	apoprotein(a) (EC
58	41.5	39.2	495	2 AG0103	hypothetical prote
59	41.5	39.2	521	2 H86298	hypothetical prote
60	41.5	39.2	732	2 T45429	polyposphatase kin
61	41.5	39.2	742	2 E70673	probable ppk prote
62	41	38.7	306	2 P97120	translation elonga
63	41	38.7	349	2 B97912	dtldglucose 4,6-de
64	41	38.7	417	2 S07286	hypothetical prote
65	41	38.7	428	2 F85849	probable integrase
66	41	38.7	428	2 E91005	probable integrase
67	41	38.7	450	2 T01711	probable serine/th
68	41	38.7	497	2 A86146	hypothetical prote
69	41	38.7	518	2 AD2315	hypothetical prote
70	41	38.7	525	2 C69794	glutamate synthase
71	41	38.7	549	2 G97614	ABC transporter (A
72	41	38.7	549	2 AE2837	hypothetical prote
73	41	38.7	555	2 S56946	probable membrane
74	41	38.7	584	2 AC3321	ABC transporter At
75	41	38.7	600	2 T00759	hypothetical prote
76	41	38.7	631	2 B87250	dnak protein (limp
77	41	38.7	703	2 AC2430	hypothetical prote
78	41	38.7	905	2 T02205	lu-ECAM-1 protein
79	41	38.7	1149	2 T16515	adenosinetriphosph
80	41	38.7	1149	2 T30869	probable adenosine
81	41	38.7	1452	1 S17669	protein-tyrosine-P
82	41	38.7	1452	1 S17670	protein-tyrosine-P
83	41	38.7	1478	2 C82689	helicase, ATP depe
84	41	38.7	1639	2 T14181	peptide synthetase
85	41	38.7	2569	2 T14164	peptide synthetase
86	40.5	38.2	98	2 A70301	ribosomal protein
87	40.5	38.2	110	2 G90584	50S ribosomal prot
88	40.5	38.2	124	2 D71355	probable ribosomal
89	40.5	38.2	345	2 H71358	conserved hypothet
90	40.5	38.2	447	2 G95068	cysteiny1-CRNA syn
91	40.5	38.2	447	2 G97936	cysteine-tRNA liga
92	40.5	38.2	469	2 T48458	8-amino-7-oxononan
93	40.5	38.2	1175	2 T46124	hypothetical prote
94	40.5	38.2	1387	2 A96771	hypothetical prote
95	40.5	38.2	1736	2 T00391	hypothetical prote
96	40.5	38.2	93	2 E70967	phosphotricin N
97	40	37.7	154	2 AE3299	hypothetical prote
98	40	37.7	175	2 F69745	hypothetical prote
99	40	37.7	211	2 B95041	hypothetical prote
100	40	37.7	215	2 E96533	hypothetical prote

A:Molecule type: DNA
 A:Residues: 1-1774 <BEC>
 A:Cross-references: UNIPROT:P22367; GB:X55776; NID:93211; PIDD:CAA39295.1; PID:g3212
 C:Superfamily: Streptomyces hygroscopicus probable polyketide synthase module 4; 3-oxoac
 homology; [acyl-carrier-protein] S-malonyltransferase homology
 C:Keywords: carrier protein
 F:54-455/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>
 F:567-844/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
 F:1412-1605/Domain: short-chain alcohol dehydrogenase homology <SAD2>
 F:1698-1768/Domain: acyl carrier protein homology <ACP2>

Query Match 47.2%; Score 50; DB 2; Length 1774;
 Best Local Similarity 44.4%; Pred. No. 25;
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LAEGPTLRQWLHGNGRD 18
 :||:|||||:
 Db 488 LALQAKTLADMTWTAEKQD 505

RESULT 5

BSECRM

erythromycin esterase (EC 3.1.1.-) type II [validated] - Escherichia coli
 C:Species: Escherichia coli
 C>Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
 C:Accession: A24381
 R:Arthur, M.; Autissier, D.; Courvalin, P.
 Nucleic Acids Res. 14, 4987-4999, 1986
 A>Title: Analysis of the nucleotide sequence of the ereB gene encoding the erythromycin
 A:Reference number: A24381; PMID:86259072; PMID:3523438
 A:Accession: A24381
 A:Molecule type: DNA
 A:Residues: 1-419 <ART>
 A:Cross-references: UNIPROT:P05789; GB:X03988; NID:941355; PIDD:CAA27626.1; PID:g41357
 C:Comment: This enzyme confers resistance to erythromycin through inactivation by hydroly
 C:Genetics:
 A:Gene: ereB
 A:Function:
 A:Description: erythromycin esterase [validated, PMID:86259072]
 C:Superfamily: erythromycin esterase, type II
 C:Keywords: antibiotic resistance; carboxylic ester hydrolase

Query Match 46.2%; Score 49; DB 1; Length 419;
 Best Local Similarity 46.7%; Pred. No. 7.5;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 4 EGPTLRQWLHGNGRD 18
 :||:|||||:
 Db 79 EGQIINMWHGQCTD 93

RESULT 6

B87251

molibdenum cofactor biosynthesis protein A [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 16-Aug-2004
 C:Accession: B87251
 R:Nierman, W.C.; Feildlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gilm, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolenko, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A>Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; PMID:21173698; PMID:11259647
 A:Accession: B87251
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-349 <STO>
 A:Cross-references: UNIPROT:Q9AC48; GB:AE005673; NID:913421106; PIDD:AAK22006.1; GSPDB:G
 C:Genetics:
 A:Gene: CC0018
 C:Superfamily: Molibdenum cofactor Molibdenum cofactor precursor Z biosynthesis protein

Query Match 44.3%; Score 47; DB 2; Length 349;

Best Local Similarity 60.0%; Pred. No. 13;
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4 EGPTLRQWLHGNGRD 18
 :||:|||||:
 Db 191 EEPALIQWAHGRCGD 205

RESULT 7

E83151

hypothetical protein PA3949 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: E83151
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; Llm,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; PMID:20437337; PMID:10984043
 A:Accession: E83151
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-391 <STO>
 A:Cross-references: UNIPROT:Q9HX67; GB:AE004813; GB:AE004091; NID:99950134; PIDD:AA0733
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA3949

Query Match 44.3%; Score 47; DB 2; Length 391;
 Best Local Similarity 50.0%; Pred. No. 14;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 4 EGPTLRQWLHGNGRD 19
 :||:|||||:
 Db 64 DADALRAWIHGIDT 79

RESULT 8

T45278

oligopeptide ABC transport protein bldKB [imported] - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T45278
 R:McDowell, J.; McGovern, K.; Losick, R.
 submitted to the EMBL Data Library, August 1996
 A:Description: An oligopeptide permease responsible for the import of an extracellular
 A:Reference number: Z22954
 A:Accession: T45278
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-602 <NOD>
 A:Cross-references: UNIPROT:P72407; EMBL:U68036; PIDD:AA09555.1
 A:Experimental source: strain M145
 C:Genetics:
 A:Note: bldKB
 C:Function:
 A:Description: involved in aerial mycelium formation
 C:Keywords: oligopeptide transport

Query Match 43.9%; Score 46.5; DB 2; Length 602;
 Best Local Similarity 64.3%; Pred. No. 27;
 Matches 9; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

Qy 4 EGPT-LRQWLHGNG 16
 :||:|||||:
 Db 174 DGPTYLQWLSDGD 187

RESULT 9

T31313

glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - Cenarchaeum symbiosum
 C:Species: Cenarchaeum symbiosum

C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C/Accession: TJ3133
 R/Schleper, C.; Delong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swenson, R.V.
 J. Bacteriol. 180, 5003-5009, 1998
 A>Title: Genomic analysis reveals chromosomal variation in natural populations of the *un*
 A/Reference number: Z20994; MUID:98422450; PMID:9748430
 A/Accession: TJ3133
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-434 <SCH>
 A/Cross-references: UNIPROT:O74061; EMBL:AF083072; NID:93599393; PID:93599399; PIDN:AA6
 C/Genetics:
 A/Note: gsat
 C/Function:
 A/Description: heme biosynthesis
 C/Superfamily: ornithine-oxo-acid aminotransferase
 C/Keywords: intramolecular transferase; isomerase

Query Match 43.4%; Score 46; DB 2; Length 434;
 Best Local Similarity 41.2%; Pred. No. 23;
 Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 AIEPTLRQWLHGNGRD 18
 :||| :||| :
 Db 81 AVEGQLRGWIGTANE 97

RESULT 10
 A36925
 transcription activator LysR-type Cbdr - Xanthobacter flavus
 C/Species: Xanthobacter flavus
 C/Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
 C/Accession: A36925; S13578; S35408
 R/Van den Bergh, E.R.E.; Dijkhuizen, L.; Meijer, W.G.
 J. Bacteriol. 175, 6097-6104, 1993
 A>Title: Cbdr, a LysR-type transcriptional activator, is required for expression of the
 A/Reference number: A36925; MUID:94012468; PMID:8407781
 A/Accession: A36925
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-333 <VAN>
 A/Cross-references: UNIPROT:P2545; EMBL:Z22705; NID:9297851; PIDN:CAA80406.1; PID:95818
 R/Meijer, W.G.; Arneberg, A.C.; Enequist, H.G.; Terpstra, P.; Lidstrom, M.E.; Dijkhuizen,
 M.O. Gen. Genet. 225, 320-330, 1991
 A>Title: Identification and organization of carbon dioxide fixation genes in Xanthobacte
 A/Reference number: S13573; MUID:91171233; PMID:1500916
 A/Accession: S13578
 A/Molecule type: DNA
 A/Residues: 1-150 <MEI>
 A/Cross-references: EMBL:X17252
 C/Genetics:
 A/Gene: cbdr
 A/Start codon: GTG
 C/Superfamily: transcription activator LysR-type
 C/Keywords: DNA binding; transcription regulation

Query Match 42.9%; Score 45.5; DB 2; Length 333;
 Best Local Similarity 52.6%; Pred. No. 20;
 Matches 10; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 LATEG-PTLRQWLHGNGRD 18
 :||| :||| :|||
 Db 262 LEVEGLPVRQWLAVRARD 280

RESULT 11
 C83822
 hypothetical protein BH1379 [imported] - Bacillus halodurans (strain C-125)
 C/Species: Bacillus halodurans
 C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C/Accession: C83822
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000

A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A/Reference number: A83650; MUID:20512582; PMID:11058132
 A/Accession: C83822
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-235 <STO>
 A/Cross-references: UNIPROT:Q9KD40; GB:AP001511; GB:BA000004; NID:910173727; PIDN:BA050
 A/Experimental source: strain C-125
 C/Genetics:
 A/Gene: BH1379

Query Match 42.5%; Score 45; DB 2; Length 235;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 IEPTLRQWLHGNG 16
 :||| :||| :|||
 Db 125 VHGKAIQWLSDNG 138

RESULT 12
 JN0143
 catechol 1,2-dioxygenase (EC 1.13.11.1) - Pseudomonas sp. plasmid EST1001
 C/Species: Pseudomonas sp.
 C/Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 09-Jul-2004
 C/Accession: JN0143
 R/Kivisaar, M.; Kasak, L.; Nurk, A.
 Gene 98, 15-20, 1991
 A>Title: Sequence of the plasmid-encoded catechol 1,2-dioxygenase-expressing gene, pheB,
 A/Reference number: JN0143; MUID:91192610; PMID:2013408
 A/Accession: JN0143
 A/Molecule type: DNA
 A/Residues: 1-302 <KIV>
 A/Cross-references: UNIPROT:P31019; GB:M57500; NID:9145127; PIDN:AA64900.1; PID:9145129
 C/Genetics:
 A/Gene: pheB
 A/Genome: plasmid
 C/Superfamily: catechol 1,2-dioxygenase
 C/Keywords: aromatic hydrocarbon catabolism; oxidoreductase

Query Match 42.5%; Score 45; DB 2; Length 302;
 Best Local Similarity 56.2%; Pred. No. 22;
 Matches 9; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 4 BGPTRQWLHGNGRDT 19
 :||| :||| :|||
 Db 130 DGETW--WLGQVRDT 143

RESULT 13
 C90453
 hypothetical protein hpcF-2 [imported] - *Sulfolobus solfataricus*
 C/Species: *Sulfolobus solfataricus*
 C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C/Accession: C90453
 R/She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyaz, M.J.; Chan-
 jong, I.; Jeffries, A.C.; Kozera, C.U.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
 submitted to Genbank, April 2001
 A/Description: *Sulfolobus solfataricus* complete genome.
 A/Reference number: A99139
 A/Accession: C90453
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-304 <KUN>
 A/Cross-references: UNIPROT:Q97V63; GB:AE006641; NID:913816109; PIDN:AAK42882.1; GSPDB:G
 C/Genetics:
 A/Gene: hpcF-2

Query Match 42.5%; Score 45; DB 2; Length 304;
 Best Local Similarity 50.0%; Pred. No. 22;
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 185 VDPSTKDMRGRCG 198

RESULT 19

AE3379
molybdenum cofactor biosynthesis protein A [imported] - Brucella melitensis (strain 16M)
C/Species: Brucella melitensis
C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 16-Aug-2004
C/Accession: AE3379
R/DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goldsman, R.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A/Reference number: AD3252; PMID:11756688
A/Accession: AE3379
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-344 <KUR>
A/Cross-references: UNIPROT:Q8YGY6; GB:AE008917; PIDN:AA152200.1; PID:g17982982; GSPDB:G
A/Experimental source: strain 16M
C/Genetics:
A/Gene: BME11019
A/Map position: 1
C/Superfamily: Molybdenum cofactor Molybdenum cofactor precursor Z biosynthesis protein

Query Match 41.5%; Score 44; DB 2; Length 344;
Best Local Similarity 53.3%; Pred. No. 36;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 EGPTRLRWLHGNGRD 18
Db 184 EIEPLTRMAGRGMD 198

RESULT 20

S25091
cruciferin Bnc2 - rape
C/Species: Brassica napus (rape)
C/Date: 04-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C/Accession: S25091
R/Breen, J.P.; Crouch, M.L.
Plant Mol. Biol. 19, 1049-1055, 1992
A/Title: Molecular analysis of a cruciferin storage protein gene family of Brassica napus
A/Reference number: S25090; MUID:92379259; PMID:1511129
A/Accession: S25091
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-496 <BRE>
A/Cross-references: UNIPROT:P33524; EMBL:X59295; NID:g17791; PIDN:CAA41985.1; PID:g76292
C/Genetics:
A/Gene: Bnc2
A/Intons: 95/1; 222/2; 362/3
C/Superfamily: glycinin
C/Keywords: seed; storage protein

Query Match 41.5%; Score 44; DB 2; Length 496;
Best Local Similarity 47.1%; Pred. No. 54;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 LATEPTLRWHLGNGR 17
Db 226 LAGKNPQGSWHLGRGQ 242

RESULT 21

AI0506
probable sulfatase [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AI0506
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AI0506
A/Status: preliminary
A/Molecule type: DNA

A/Residues: 1-571 <PAR>
A/Cross-references: GB:AU513382; PIDN:CAD01193.1; PID:g16501322; GSPDB:GN00176
C/Genetics:
A/Gene: STY0046

Query Match 41.5%; Score 44; DB 2; Length 571;
Best Local Similarity 58.3%; Pred. No. 63;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 EGPTRLRWLHGN 15
Db 308 EDPYKDWLHIN 319

RESULT 22

T49773
related to actin-interacting protein AIP3 [imported] - Neurospora crassa
N/Alternate names: protein B9J10.100
C/Species: Neurospora crassa
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C/Accession: T49773
R/Schulte, U.; Aign, V.; Hohsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A/Reference number: Z25022
A/Accession: T49773
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-972 <SCH>
A/Cross-references: UNIPROT:Q9P571; EMBL:AL356324; GSPDB:GN00116; NCSP:B9J10.100
A/Experimental source: BAC clone B9J10; strain OR74A
C/Genetics:
A/Gene: NCSP:B9J10.100
A/Map position: 6
A/Intons: 29/3; 161/1; 329/1

Query Match 41.5%; Score 44; DB 2; Length 972;
Best Local Similarity 61.5%; Pred. No. 1,1e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 TLRLWHLGNGRDT 19
Db 59 TLTQWSRGVATDT 71

RESULT 23

CGH02B
collagen alpha 2(IV) chain precursor - human
N/Alternate names: procollagen alpha 2(IV) chain
C/Species: Homo sapiens (man)
C/Date: 07-Jun-1990 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C/Accession: A13024; S00007; S02624; S00246; S17678; S16911; B32117; S16877; S00165; S39
R/Hosikaka, S.L.; Tryggvason, K.
J. Biol. Chem. 263, 19488-19493, 1988
A/Title: The complete primary structure of the alpha2 chain of human type IV collagen an
A/Reference number: A13024; MUID:89066769; PMID:3198637
A/Accession: A13024
A/Molecule type: mRNA
A/Residues: 1-1712 <HOS1>
A/Cross-references: UNIPROT:P08572; EMBL:U04210; EMBL:X05610; GB:M20753; NID:g29550; PID
R/Hosikaka, S.L.; Kurkinen, M.; Tryggvason, K.
FEBS Lett. 216, 281-286, 1987
A/Title: Nucleotide sequence coding for the human type IV collagen alpha-2 chain cDNA re
ated region.
A/Reference number: S00007; MUID:87219158; PMID:3582677

A:Accession: S00007
A:Molecule type: mRNA
A:Residues: 1254-1398, 'V', 1400-1712 <HOS2>
A:Cross-references: EMBL:J04210; EMBL:X05610; GB:M20753; NID:g29550; PIDN:CAA29098.1; PI
A:Note: 1399-1116 was also found
R:Hostikka, S.L.; Trygvaeson, K.
FEBS Lett. 224, 297-305, 1987
A:Title: Extensive structural differences between genes for the alpha(1) and alpha(2) ch
A:Reference number: S026244; MUID:88083553; PMID:2826228
A:Accession: S02624
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1347-1350, 1377-1383, 1426-1432, 1465-1471, 1529-1535, 1625-1630 <HOS3>
A:Note: complete nucleotide sequence not shown
R:Brazel, D.; Pollner, R.; Oberbauer, I.; Kuehn, K.
Eur. J. Biochem. 172, 35-42, 1988
A:Title: Human basement membrane collagen (type IV): the amino acid sequence of the alph
A:Reference number: S00246; MUID:8815198; PMID:3345760
A:Accession: S00246
A:Molecule type: mRNA
A:Residues: 1-682, 'G', 684-1043 <BRA>
A:Cross-references: EMBL:X05562; NID:g30075; PIDN:CAA29076.1; PID:g30076
R:Oberbauer, I.
Submitted to the EMBL Data Library, June 1987
A:Reference number: S17678
A:Accession: S17678
A:Molecule type: mRNA
A:Residues: 1-470, 'P', 472-682, 'G', 684-1043 <OBE>
A:Cross-references: EMBL:X05562; NID:g30075; PIDN:CAA29076.1; PID:g30076
R:Poesschl, E.; Pollner, R.; Kuehn, K.
EMBO J. 7, 2687-2695, 1988
A:Title: The genes for the alpha(IV) and alpha2(IV) chains of human basement membrane c
A:Reference number: S02738; MUID:89030632; PMID:2846280
A:Accession: S16911
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-133 <POB>
A:Cross-references: EMBL:X12784; GB:M36963; NID:g30072; PIDN:CAA31275.1; PID:g30073
R:Siominen, R.; Huotari, M.; Hostikka, S.L.; Prockop, D.J.; Trygvaeson, K.
J. Biol. Chem. 263, 17217-17220, 1988
A:Title: The structural genes for alpha1 and alpha2 chains of human type IV collagen are
A:Reference number: A92690; MUID:89034231; PMID:3182844
A:Accession: B32117
A:Molecule type: DNA
A:Residues: 1-133 <SOI2>
A:Cross-references: EMBL:J04217; EMBL:J05039; NID:g180759; PIDN:AA53097.1; PID:g553233
R:Siominen, R.; Huotari, M.; Ganguly, A.; Prockop, D.J.; Trygvaeson, K.
J. Biol. Chem. 264, 13565-13571, 1989
A:Title: Structural organization of the gene for the alpha-1 chain of human type IV coll
A:Reference number: S16876; MUID:89340433; PMID:2701944
A:Accession: S16877
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-133 <SOI2>
A:Cross-references: EMBL:J04217; NID:g180759; PIDN:AA53097.1; PID:g553233; EMBL:J05039
A:Note: this sequence was submitted to the EMBL Data Library, October 1988
R:Siominen, R.; Qian, R.O.; Glanville, R.W.; Hofmann, H.; Deutzmann, R.; Kuehn, K.
Eur. J. Biochem. 168, 569-575, 1987
A:Title: Construction of a model for the aggregation and cross-linking region (7S domain
is region.
A:Reference number: S00165; MUID:88029476; PMID:3117548
A:Accession: S00165
A:Molecule type: protein
A:Residues: 37-247 <SIR1>
A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 3 in having 175-Gly
R:Ebale, J.A.; Goldik, R.; Mann, K.; Kuehn, K.
EMBO J. 12, 4795-4802, 1993
A:Title: The alpha-1-beta-1 integrin recognition site of the basement membrane collagen
A:Reference number: S39614; MUID:94038963; PMID:8223488
A:Accession: S39615
A:Molecule type: protein
A:Residues: 407-570 <EBL>
R:MacVright, R.S.; Benson, V.A.; Lovell, K.T.; van der Reet, M.; Fietzek, P.P.

Biochemistry 22, 4940-4948, 1983
A>Title: Isolation and characterization of pepsin-solubilized human basement membrane (C
A:Reference number: S16910; MUID:84053346; PMID:6416291
A:Accession: S16912
A:Molecule type: protein
A:Residues: 490-492,'X',494-496;675-677,'G',679-680,'G',682,684-685,'P' <MAC>
A:Experimental source: Placenta
R:Glanville, R.W.; Rauter, A.
Hopper-Seyler's Z. Physiol. Chem. 362, 943-951, 1961
A>Title: Pepsin fragments of human placental basement-membrane collagen showing intern
A:Reference number: S16908; MUID:82005835; PMID:6792033
A:Accession: B58517
A:Molecule type: protein
A:Residues: 490-492,'X',494-501,'P',503-507;952-957,'X',959-966,'X',968,984-986,'X',988-
81-1185 <GLA>
R:Killen, P.D.; Francocomo, C.A.; Yamada, Y.; Modi, W.S.; O'Brien, S.J.
Hum. Genet. 77, 318-324, 1987
A>Title: Partial structure of the human alpha-2(IV) collagen chain and chromosomal local
A:Reference number: S01450; MUID:88085168; PMID:3692475
A:Accession: S01450
A:Molecule type: mRNA
A:Residues: 1040,'I',1042-1398,'V',1400-1418,'W',1420-1635,'V',1637-1712 <KIL>
A:Cross-references: EMBL:M24766; NID:G537328; PIDN:AA52043.1; PID:G5373229
R:Siebold, B.; Deutzmann, R.; Kuehn, K.
Eur. J. Biochem. 176, 617-624, 1988
A>Title: The arrangement of intra- and intermolecular disulfide bonds in the carboxyter
A:Reference number: S02550; MUID:89005112; PMID:2844531
A:Accession: S02550
A:Molecule type: protein
A:Residues: 1480-1535;1545-1614;1617-1662,'H',1664-1700,'G',1705-1708;1710-1712 <SIE2>
A:Note: the sequence form Fig. 7 is inconsistent with that shown in Fig. 11 in having 1
R:Myers, J.C.; Howard, P.S.; Jelen, A.M.; Dion, A.S.; Macarak, E.J.
J. Biol. Chem. 262, 9231-9238, 1987
A>Title: Duplication of type IV collagen COOH-terminal repeats and species-specific exp
A:Reference number: A27114; MUID:87250571; PMID:2439508
A:Accession: B27114
A:Molecule type: mRNA
A:Residues: 1486-1574,'I',1576-1712 <MYE>
A:Cross-references: EMBL:002760; NID:G180425; PIDN:AA58422.1; PID:G180426
C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C:Genetics:
A:Gene: GDB:COL4A2
A:Cross-references: GDB:119792; OMIM:120090
A:Map position: 13q34-13q34
A:Introns: 15/2, 33/3; 1347/1, 1380/1; 1429/1; 1468/1; 1532/1, 1527/3 #status incomple
A:Note: the alpha 1(IV) and alpha 2(IV) chain genes are encoded on opposite strands wit
C:Complex: Type IV collagen is a heterotrimer of two alpha 1(IV) chains (see PIR:CGHUB
domains (with disulfide and desmosine cross-links), dimeric associations among trimer c
rupted helical domain (with disulfide and desmosine cross-links).
C:Function:
A:Description: structural component of basement membrane
C:Superfamily: collagen alpha 1(IV) chain
C:Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycop
P.1-28/Domain: signal sequence #status predicted <SIG>
P.29-1712/Product: collagen alpha 2(IV) chain #status predicted <MAT>
P.29-57/Domain: amino-terminal nonhelical, NHL <NHL>
F.58-1485/Region: interrupted helical
F.562-364/Region: cell attachment (R-G-D) motif
F.784-786/Region: cell attachment (R-G-D) motif
F.868-870/Region: cell attachment (R-G-D) motif
F.889-891/Region: cell attachment (R-G-D) motif
F.970-972/Region: cell attachment (R-G-D) motif
F.1069-1071/Region: cell attachment (R-G-D) motif
F.1128-1230/Region: cell attachment (R-G-D) motif
F.1452-1454/Region: cell attachment (R-G-D) motif
F.1486-1712/Domain: carboxyl-terminal nonhelical, NCI <NCI>
F.1495-1593/Domain: collagen IV carboxyl-terminal repeat <CT1>
F.1603-1708/Domain: collagen IV carboxyl-terminal repeat <CT2>
F.1622-1751/Region: collagen IV carboxyl-terminal repeat <CT3>
F.157,87,90,102,165,168,225,239,242/Binding site: carbohydrate (Lys) (covalent) #status
F.563,75,96,114,120,123,132,150,159,166,189 #status atypical
F.157,75,96,114,120,123,132,150,159,166,189 #status atypical

F:87, 90, 102, 165, 168, 225, 239, 242/Modified site: 5-hydroxylysine (Lys) #status experimental
 F:138/Binding site: carbohydrate (Aan) (covalent) #status experimental
 F:209/Modified site: 4-hydroxyproline (Pro) #status atypical
 F:161-681/Disulfide bonds: #status predicted
 F:1275/Binding site: carbohydrate (Aan) (covalent) #status predicted
 F:1504-1590, 1537-1593/Disulfide bonds: (or 1504-1593, 1537-1590) #status experimental
 F:1549-1555, 1658-1665/Disulfide bonds: #status experimental
 F:1612-1705, 1646-1708/Disulfide bonds: (or 1612-1708, 1646-1705) #status experimental

Query Match 41.5%; Score 44; DB 1; Length 1712;
 Best Local Similarity 63.6%; Pred. No. 2.1e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 AIEGPTLRQWL 12
 : : : : :
 DB 7 AVAGPALRRL 17

RESULT 24
 GNMWV
 genome polypeptide - West Nile virus
 N:contains: core protein V2; membrane-associated glycoprotein NV2 precursor; membrane-associated; nonstructural protein NV5
 C:Species: West Nile virus
 C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
 C:Accession: A25256
 R:Castle, E.; Leidner, U.; Nowak, T.; Wengler, G.; Wengler, G.
 Virology 149, 10-26, 1986
 A:Title: Primary structure of the West Nile flavivirus genome region coding for all nonstructural proteins
 A:Reference number: A25256; PMID:86124703; PMID:3753811
 A:Accession: A25256
 A:Molecule type: genomic RNA
 A:Residues: 1-3430 <CDS>
 A:Cross-references: UNIPROT:P06935; GB:M10103; GB:M12294; NID:G336167; PIDD:AAA48498.1;
 A:Note: Parts of this sequence, including the amino ends of the mature proteins, were determined from a yellow fever virus genome polypeptide
 C:Keywords: ATP; core protein; glycoprotein; membrane-associated protein; nucleotide binding site; product: core protein V2 #status predicted <CV2>
 F:1-92/Product: core protein V2 #status predicted <CV2>
 F:105-233/Product: membrane-associated glycoprotein NV2 precursor #status predicted <NV2>
 F:105-123/Domain: nonterminal signal sequence #status predicted <SS>
 F:124-233/Product: membrane-associated glycoprotein NV2 #status predicted <NV2>
 F:125-233/Product: membrane-associated nonglycosylated protein VI #status predicted <NV1>
 F:275-787/Product: membrane-associated glycoprotein V3 precursor #status predicted <NV3>
 F:275-290/Domain: nonterminal signal sequence #status predicted <SS>
 F:291-787/Product: membrane-associated glycoprotein V3 #status predicted <NV3>
 F:788-2109/Product: nonstructural protein NV4 #status predicted <NV4>
 F:1782-1787/Region: nucleotide-binding motif A (P-loop)
 F:1786-1789/Region: nucleotide-binding motif B
 F:2580-3427/Product: nonstructural protein NV5 #status predicted <NV5>
 F:138, 917, 962, 994, 1289, 1659, 1966, 2353, 2459, 2489, 2573, 2739, 2759, 2864, 2902/Binding site: C

Query Match 41.5%; Score 44; DB 1; Length 3430;
 Best Local Similarity 46.7%; Pred. No. 4.5e+02;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 EGGTLRQWLHNGRD 18
 : : : : :
 DB 3169 KGPVKTWLSNGEE 3183

RESULT 25
 GNMWV
 genome polypeptide - Kunjin virus (strain KEM61C)
 N:contains: capsid protein C; envelope protein E; membrane protein M; nonstructural protein NS4; nonstructural protein NS4b; nonstructural protein NS5
 C:Species: Kunjin virus
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
 C:Accession: A28697
 R:Coia, G.; Parker, M.D.; Speight, G.; Byrne, M.E.; Westaway, E.G.
 J. Gen. Virol. 69, 1-21, 1988
 A:Title: Nucleotide and complete amino acid sequences of Kunjin virus: definitive gene C
 A:Reference number: A28697; PMID:88089524; PMID:2826659

A:Accession: A28697
 A:Molecule type: genomic RNA
 A:Residues: 1-3433 <CDS>
 A:Cross-references: UNIPROT:P14335; GB:D00246; NID:G221966; PIDD:BAA00176.1; PID:G221967
 C:Keywords: ATP; capsid protein; envelope protein; membrane protein; nonstructural protein
 F:12-123/Product: capsid protein C #status predicted <CPC>
 F:124-290/Product: membrane protein M precursor #status predicted <MPP>
 F:124-215/Domain: nonterminal signal sequence #status predicted <SIG>
 F:216-290/Product: membrane protein M #status predicted <MPP>
 F:291-791/Product: envelope protein E #status predicted <EPE>
 F:1792-1143/Product: nonstructural protein NS1 #status predicted <NS1>
 F:1144-1374/Product: nonstructural protein NS2a #status predicted <NS2a>
 F:1375-1505/Product: nonstructural protein NS2b #status predicted <NS2b>
 F:1506-2124/Product: nonstructural protein NS3 #status predicted <NS3>
 F:1699-1706/Region: nucleotide-binding motif A (P-loop)
 F:1786-1791/Region: nucleotide-binding motif B
 F:1790-1793/Region: DEAH motif
 F:2125-2273/Product: nonstructural protein NS4a #status predicted <NS4a>
 F:2274-2528/Product: nonstructural protein NS4b #status predicted <NS4b>
 F:2529-3433/Product: nonstructural protein NS5 #status predicted <NS5>

Query Match 41.5%; Score 44; DB 1; Length 3433;
 Best Local Similarity 46.7%; Pred. No. 4.5e+02;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 EGGTLRQWLHNGRD 18
 : : : : :
 DB 3172 KGPVKTWLSNGEE 3186

RESULT 26
 AG0147
 probable membrane protein YPO1203 [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AG0147
 R:Parhill, J.; Wren, B.W.; Thomson, N.R.; Tilball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Harrigan, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; PMID:21470413; PMID:11586360
 A:Accession: AG0147
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-296 <KUN>
 A:Cross-references: UNIPROT:Q8ZGS7; GB:AL590842; PIDD:CAC90042.1; PID:G15979263; GSPDB:C
 A:Genes: YPO1203

Query Match 41.0%; Score 43.5; DB 2; Length 296;
 Best Local Similarity 71.4%; Pred. No. 37;
 Matches 10; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 LAIEG---PTLRQW 11
 ||| ||| ||| ||| |||
 DB 58 LAIRGHALPTLRQW 71

RESULT 27
 H82539
 protein-L-isoaspartate O-methyltransferase Xfz585 [imported] - Xylella fastidiosa (strain C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
 C:Accession: H82539
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: H82515; PMID:20365717; PMID:10910347
 A:Note: For a complete list of authors see reference number A59328 below
 A:Accession: H82539
 A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-218 <SIM>
A:Cross-references: UNIPROT:Q9PAD3; GB:AE004065; GB:AE003849; NID:99107795; PIND:AA6538
A:Experimental source: strain 9abc
A:Authors: A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A.
Brisson, M.A.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincanti, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laig
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XR2585
C:Superfamily: Escherichia coli protein-L-isoaspartate(D-aspartate) O-methyltransferase
Query Match 40.6%; Score 43; DB 2; Length 218;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 QWILHGNGR 17
Db 164 QWILHGNGR 171

RESULT 28
A:Accession: A45822
beta-lactamase (EC 3.5.2.6) precursor - Streptomyces badius
C:Species: Streptomyces badius
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-2004
C:Accession: A45822
R:Forman, M.; Haegsetroem, B.; Lindgren, L.; Jaurin, B.
J. Gen. Microbiol. 136, 589-598, 1990
A:Title: Molecular analysis of beta-lactamases from four species of Streptomyces: compar
A:Reference number: A45822; MUID:90362045; PMID:2391494
A:Accession: A45822
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <FOR>
A:Cross-references: UNIPROT:P35391; GB:M34178; NID:g153182; PIND:AAA26707.1; PID:g153183
C:Superfamily: Beta-lactamase I
C:Keywords: hydrolase
F:93/Active site: Ser #status predicted

Query Match 40.6%; Score 43; DB 2; Length 313;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 EGPTLRQWIMHGNGRDT 19
Db 187 EBPGLSRWVPGKXKDT 202

RESULT 29
B69901
fatty-acid desaturase homolog yocE - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C:Accession: B69901
R:Kunze, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Beret
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cht
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier
tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsreid, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauesl

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schlaich, S.; Schoefer, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sertor
akuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpers, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumeit, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: B69901
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-352 <KUN>
A:Cross-references: UNIPROT:Q34653; GB:Z99114; GB:AL009126; NID:g2634230; PIND:CA813810
A:Experimental source: strain 168
C:Genetics:
A:Gene: yocE
C:Superfamily: Fatty acid (acyl-CoA) desaturase
Query Match 40.6%; Score 43; DB 2; Length 352;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 10; Conservative 1; Mismatches 3; Indels 6; Gaps 1;

QY 2 AIEG-----PTLRQWIMHGNGR 15
Db 251 AVEGSSFFYLPTLRQWIMHGNGR 270

RESULT 30
T05270
probable serine/threonine-specific protein kinase (EC 2.7.1.-) T4L20.80 - Arabidopsis ti
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05270
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysheart, C.; Desseville, R.; De Clerck, R.; De
ews, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, September 1998
A:Reference number: Z15406
A:Accession: T05270
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-481 <BEV>
A:Cross-references: UNIPROT:Q65676; EMBL:AL023094
A:Experimental source: cultivar Columbia; BAC clone T4L20
C:Genetics:
A:Map position: 4
A:Insertions: 179/2; 216/2; 257/2; 314/2; 357/3
A:Note: T4L20.80
C:Keywords: phosphotransferase

Query Match 40.6%; Score 43; DB 2; Length 481;
Best Local Similarity 53.8%; Pred. No. 75;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 IEQPTLRQWIMHGNGR 15
Db 223 IDWGNLEQWIMHGNGR 235

RESULT 31
G89894
protein kinase [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89894
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89894
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-664 <KUR>

A:Cross-references: UNIPROT:Q99UP8; GB:BA000018; PID:g13701020; PIDN:BA842315.1; GSPDB:Q
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1063

Query Match 40.6%; Score 43; DB 2; Length 664;
Best Local Similarity 50.0%; Pred. No. 1,le+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 IEPTLRQWLHGNG 16
|||||
Db 90 IEPTLRSEYIESHG 103

RESULT 32
A43254
protein-tyrosine-phosphatase (EC 3.1.3.48) corkscrew - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A43254
R:Perkins, L.A.; Larsen, I.; Perrimon, N.
Cell 70, 225-236, 1992
A>Title: corkscrew encodes a putative protein tyrosine phosphatase that functions to tra
A:Reference number: A43254; PMID:92346711; PMID:1638629
A:Accession: A43254
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-841 <PER>
A:Cross-references: UNIPROT:P29349; GB:M94730; NID:g157144; PID:g157145
A:Experimental source: embryo
A>Note: sequence extracted from NCBI backbone (NCBIN:109964, NCBI:P109965)
C:Genetics:
A:Gene: FLYBase:cw
A:Superfamily: FLYBase:FBgn0000382
C:Cross-references: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:6-101/Domain: SH2 homology <SH2>
F:111-203/Domain: SH2 homology <SH2B>
F:552-634/Domain: protein-tyrosine-phosphatase homology <PTP>
F:583/Active site: Cys (phosphocysteine intermediate) #status predicted
F:589/Binding site: substrate phosphate (Arg) #status predicted

Query Match 40.6%; Score 43; DB 2; Length 841;
Best Local Similarity 60.0%; Pred. No. 1,4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 PTLRQWLHGNG 15
|||
Db 106 PTLRQWLHGNG 115

RESULT 33
E71376
conserved hypothetical protein TP0025 - syphilis spirochete
C:Species: *Treponema pallidum* subsp. *pallidum* (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: E71376
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, R.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khakh, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
rthy, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A>Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
A:Reference number: A71250; PMID:98332770; PMID:9665876
A:Accession: E71376
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1023 <COD>
A:Cross-references: UNIPROT:O83069; GB:AE001187; GB:AE000520; NID:g3322273; PIDN:AA6501
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0025

Query Match 40.6%; Score 43; DB 2; Length 1023;

Best Local Similarity 37.5%; Pred. No. 1,7e+02;
Matches 9; Conservative 4; Mismatches 3; Indels 8; Gaps 1;

QY 4 EGP-----TLRQWLHGNGRDT 19
|||
Db 396 DGPSLVLMORSRLRQWLHGNGAPES 419

RESULT 34
E82797
conserved hypothetical protein XF0501 [imported] - *Xylella fastidiosa* (strain 9a5c)
C:Species: *Xylella fastidiosa*
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: E82797
R:Anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A>Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A:Reference number: A82515; PMID:20365717; PMID:10910347
A>Note: for a complete list of authors see reference number A59328 below
A:Accession: E82797
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104 <SIM>
A:Cross-references: UNIPROT:Q9PG01; GB:AE003899; GB:AE003849; NID:g9105351; PIDN:AAF8331
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawaak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tanhaka, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Comments: annotation
C:Genetics:
A:Gene: XF0501

Query Match 39.6%; Score 42; DB 2; Length 104;
Best Local Similarity 42.9%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LAIEPTLRQWLHGNG 14
|||
Db 30 LGVSPVTNQCNG 43

RESULT 35
AC3086
sarcosine oxidase delta subunit [imported] - *Agrobacterium tumefaciens* (strain C58, Dupo
C:Species: *Agrobacterium tumefaciens*
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AC3086
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, L
erage, G.; Gillet, W.; Grant, J.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, W.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krepsan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; PMID:21608550; PMID:11743193
A:Accession: AC3086
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <KUR>
A:Cross-references: UNIPROT:O8U7Y8; GB:AE008689; PIDN:AA145105.1; PID:g17742774; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: soxH

A:Map position: linear chromosome
C:Superfamily: Corynebacterium sp. sarcosine oxidase delta chain

Query Match 39.6%; Score 42; DB 2; Length 106;

Best Local Similarity 47.1%; Pred. No. 20;

Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 3 IEPTLRQW-LHGNGR 17
::|||:|||||

Db 50 VKGPHFRWRHLHGCR 66

RESULT 36

P98200

sarcosine oxidase delta chain (sarcosine oxidase chain d) [imported] - Agrobacterium tum

C:Species: Agrobacterium tumefaciens

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C:Accession: F98200

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Marx, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; PMID:21608551; PMID:11743194

A:Accession: F98200

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-106 <RUR>

A:Cross-references: UNIPROT:Q8U7Y8; GB:AE007870; PIDN:AAK89128.1; PID:G15158936; GSPDB:Q

C:Genetics:

A:Gene: AGR_1105

A:Map position: linear chromosome

C:Superfamily: Corynebacterium sp. sarcosine oxidase delta chain

Query Match 39.6%; Score 42; DB 2; Length 106;

Best Local Similarity 47.1%; Pred. No. 20;

Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 3 IEPTLRQW-LHGNGR 17
::|||:|||||

Db 50 VKGPHFRWRHLHGCR 66

RESULT 37

D83161

hypothetical protein PA3885 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: D83161

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Broder, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; PMID:20437337; PMID:10984043

A:Accession: D83161

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-218 <STO>

A:Cross-references: UNIPROT:Q9HXG7; GB:AE004805; GB:AE004091; NID:99950055; PIDN:AA0727

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA3885

T44657

protein GP80 [imported] - bovine herpesvirus 4

C:Species: Bovine herpesvirus 4

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T44657

R:Komonte, P.; Van Santen, V.L.; Filie, P.; Lyaku, J.R.; Bublöt, M.; Pastoret, P.; Thiry

submitted to the EMBL Data Library, February 1997

A:Description: Identification and characterization of bovine herpesvirus 4 GP80: a new g

A:Reference number: Z22823

A:Accession: T44657

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-273 <LOW>

A:Cross-references: UNIPROT:P87519; EMBL:Z84818; PIDN:CA06616.1

C:Genetics:

A:introns: 177/1

Query Match 39.6%; Score 42; DB 2; Length 273;

Best Local Similarity 61.5%; Pred. No. 58;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 PTLRQWLNHGNGRD 18
|||:|||||

Db 210 PTRKNVILHGNGFD 222

RESULT 39

B72053

glyceralddehyde 3-phosphate dehydrogenase CP0123 [imported] - Chlamydia pneumoniae (

C:Species: Chlamydia pneumoniae

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: B72053; G81613

R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lamm, C.; Fan, J.; Olinger, L.; Grimwood, J.

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; PMID:99206606; PMID:10192388

A:Accession: B72053

A:Molecule type: DNA

A:Residues: 1-335 <ARN>

A:Cross-references: UNIPROT:Q9Z7T0; GB:AE001647; GB:AE001363; NID:94376920; PIDN:AA0187

A:Experimental source: strain CWD029

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

, C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis Morn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; PMID:20150255; PMID:10684935

A:Accession: G81613

A:Molecule type: DNA

A:Residues: 1-335 <REA>

A:Cross-references: GB:AE002173; GB:AE002161; NID:97189033; PIDN:AAF38006.1; PID:971890

A:Experimental source: strain AR39, HL cells

C:Genetics:

A:Gene: gAPA; CP0123

C:Superfamily: glyceralddehyde-3-phosphate dehydrogenase

Query Match 39.6%; Score 42; DB 2; Length 335;

Best Local Similarity 37.5%; Pred. No. 72;

Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LATEPTLRQWLNHGNG 16
::|||:|||||

Db 185 LVVDGSPSKDWRGGRG 200

RESULT 40

E86568

glyceralddehyde-3-P dehydrogenase [imported] - Chlamydia pneumoniae (strain J138)

C:Species: Chlamydia pneumoniae

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: E86568

R:Shirai, M.; Hiraoka, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.

RESULT 38

```

A:Reference number: AB6491; MUID:20330349; PMID:10671362
A:Accession: E86568
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-335 <STO>
A:Cross-references: UNIPROT:Q9Z7T0; GB:BA000008; NID:g8978996; PIDN:BAA98831.1; GSPDB:GN
A:Experimental source: strain UJ38
C:Genetics:
A:Gene: gapA
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match          39.6%; Score 42; DB 2; Length 335;
Best Local Similarity 37.5%; Pred. No. 72;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 LAIEPTLRQWLHNGG 16
      ||::||::|||
DB      185 LVVDPSKDWRGGRG 200

RESULT 41
S43339
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - red alga (Chn
C:Species: Chondrus crispus (carrageen)
C:Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S43339; S32692
C:Riand, M.F.; Valentín, C.; Brandt, U.; Bouget, F.Y.; Kloareg, B.; Cerff, R.
Plant Mol. Biol. 23, 981-994, 1993
A:Title: The GAPDH gene system of the red alga Chondrus crispus: promoter structures, inh
A:Reference number: S43339; MUID:94083567; PMID:8260635
A:Accession: S43339
A:Molecule type: DNA
A:Residues: 1-335 <LIN>
A:Cross-references: UNIPROT:P34920; EMBL:X73036; NID:g440394; PIDN:CAA51517.1; PID:g4403
Riand, M.F.; Valentín, C.; Martín, W.; Bouget, F.Y.; Kloareg, B.; Cerff, R.
submitted to the EMBL Data Library, April 1993
A:Description: The evolutionary origin of red algae as deduced from the nuclear genes en
A:Reference number: S32692
A:Accession: S32692
A:Molecule type: mRNA
A:Residues: 1-249, 'A', 251-335 <LIN>
A:Cross-references: EMBL:X73034; NID:g297453; PIDN:CAA51515.1; PID:g297454
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: gluconeogenesis; glycolysis; oxidoreductase

Query Match          39.6%; Score 42; DB 2; Length 335;
Best Local Similarity 40.0%; Pred. No. 72;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      3 IEPTLRQWLHNGR 17
      ::||::|||
DB      188 VDGPSKDWRGGRG 202

RESULT 42
A30754
hypothetical protein tera - Alcaligenes sp.
C:Species: Alcaligenes sp.
C:Date: 19-May-1988 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: J00361; A30754
R:Jobling, M.G.; Ritchie, D.A.
Gene 66, 245-258, 1988
A:Title: Nucleotide sequence of a plasmid determinant for resistance to tellurium anions
A:Reference number: J00361; MUID:89006266; PMID:3049247
A:Accession: J00361
A:Molecule type: DNA
A:Residues: 1-339 <UOL>
A:Cross-references: UNIPROT:Q44313
R:Jobling, M.G.
submitted to GenBank, September 1988
A:Reference number: A30754
A:Accession: A30754
A:Molecule type: DNA

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A;Residues: 1-224, 'M', 226-339 <J02>

Query Match      39.6%; Score 42; DB 2; Length 339;
Best Local Similarity 47.1%; Pred. No. 73;
Matches 8; Conservative 4; Mismatches 1; Indels 4; Gaps 1;

OY      2 AIEGPTLRQWLHGNGRD 18
      ||::|||::|
      234 ALDG-----EWHLINGRE 246

RESULT 43
A86298
Hypochemical protein F309.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86298
R;Thellogis: A.; Ecker, J.R.; Palm, C.J.; Federpietl, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huitzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F96826
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-422 <STO>
A;Cross-references: UNIPROT:Q9SAJ6; GB:AE005173; NID:94835756; PIDN:AAD340223.1; GSPDB:GN
C;Genetics:
A;Gene: TRK14.5
A;Map position: 1
C;Superfamily: glyceroldehyde-3-phosphate dehydrogenase

OY      3 IEGPTLRQWLHGNG 16
      ::||::|
      Db      257 VDGPSMKDWRCGRG 270

RESULT 44
F96826
Hypochemical protein TRK14.5 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F96826
R;Thellogis: A.; Ecker, J.R.; Palm, C.J.; Federpietl, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huitzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F96826
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-422 <STO>
A;Cross-references: UNIPROT:Q9SAJ6; GB:AE005173; NID:94835756; PIDN:AAD340223.1; GSPDB:GN
C;Genetics:
A;Gene: TRK14.5
A;Map position: 1
C;Superfamily: glyceroldehyde-3-phosphate dehydrogenase

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Query Match 39.6%; Score 42; DB 2; Length 422;
 Best Local Similarity 35.7%; Pred. No. 93;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 IEGPTLRQWLHGNG 16
 ::|||::|||
 DB 272 VDGPSMKDWRGGRG 285

RESULT 45

S51837
 glyceraldhyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) precursor - Scd
 N/Alternate names: PPSD17 protein
 C/Species: Pinus blyvestris (Scotch pine)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S51837
 R/Meyer-Gauen, G.; Scharrenberger, C.; Cerff, R.; Martin, W.
 Plant Mol. Biol. 26, 1155-1166, 1994
 A/Title: Molecular characterization of a novel, nuclear-encoded, NAD(+)-dependent glycer
 A/Reference number: S51836; MUID:95111098; PMID:7811973
 A/Accession: S51837
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-433 <MEY>
 A/Cross-references: UNIPROT:Q37264; EMBL:L32561; NID:G1100224; PTDN:AAD10214.1; PID:g110
 C/Genetics:
 A/Genome: nuclear
 C/Superfamily: glyceraldhyde-3-phosphate dehydrogenase
 C/Keywords: chloroplast; gluconeogenesis; glycolysis; oxidoreductase

Query Match 39.6%; Score 42; DB 2; Length 433;
 Best Local Similarity 35.7%; Pred. No. 95;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 IEGPTLRQWLHGNG 16
 ::|||::|||
 DB 283 VDGPSMKDWRGGRG 296

Search completed: September 1, 2005, 16:22:59
 Job time : 17.4892 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:37 ; Search time 70.6691 Seconds
(without alignments)
137.677 Million cell updates/sec

Title: US-10-083-768-11
Perfect score: 106
Sequence: 1 LAIBGPTLRQWHLHGNGRDT 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55.5	52.4	497	2	06LKY2 photobacter
2	51	48.1	71	2	076H55 salmonella
3	51	48.1	580	2	089RH2 bradyrhizob
4	51	48.1	667	2	08CSV9 o8csyv staphylococ
5	51	48.1	690	2	082RY5 streptomyce
6	50	47.2	326	2	069XG8 oryza sativ
7	50	47.2	407	2	08XYS6 ralsionia s
8	50	47.2	486	2	0877P6 pseudomonas
9	50	47.2	486	2	0877Q7 pseudomonas
10	50	47.2	690	2	0877V4 pseudomonas
11	50	47.2	690	1	BP42_HUMAN
12	50	47.2	690	1	BP42_MOUSE
13	50	47.2	691	2	06NXX8 mus musculu
14	50	47.2	973	2	08YPC5 anabaena sp
15	50	47.2	1774	1	MSAS_PENPA
16	49	46.2	245	2	066272 erythrobact
17	49	46.2	249	2	082989 erythrobact
18	49	46.2	278	2	09XDVO erythrobact
19	49	46.2	412	2	088D08 pseudomonas
20	49	46.2	419	1	EREB_ECOLI
21	49	46.2	547	2	07SFF9 o7sff9 neuropeptid
22	48.5	45.8	88	2	06YSI5 oryza sativ
23	48	45.3	154	2	082529 nitrosomona
24	48	45.3	168	2	09V492 drosophila
25	48	45.3	392	2	0688F0 oryza sativ
26	48	45.3	396	2	067UD0 oryza sativ
27	48	45.3	631	2	06LP74 photobacter
28	48	45.3	686	1	EP42_BOVIN
29	48	45.3	687	1	046509 bos taurus
30	48	45.3	1916	2	084PP9 myxococcus
31	47	44.3	182	2	075174 oryza sativ

32	47	44.3	344	2	055838	055838 yokose viru
33	47	44.3	349	1	MOA_CAUCR	09ac48 caulobacter
34	47	44.3	391	2	09HX67	09hx67 pseudomonas
35	47	44.3	483	2	0886U0	0886U0 oryza sativ
36	47	44.3	483	2	076676	076676 oryza sativ
37	47	44.3	3425	2	076918	076918 yokose viru
38	46.5	43.9	495	2	07MP20	07mp20 vibrio vuln
39	46.5	43.9	600	2	093IU2	093iu2 streptomyce
40	46.5	43.9	602	2	P72407	P72407 streptomyce
41	46	43.4	85	2	08RSL6	08rsl6 uncultured
42	46	43.4	256	2	09NBS3	09ndb3 tachypleus
43	46	43.4	279	2	06H5Y4	06h5y4 oryza sativ
44	46	43.4	349	1	MOA_RHIME	092db4 rhizobium m
45	46	43.4	434	2	074061	074061 cenarchaeum
46	46	43.4	451	2	087IX8	087ix8 vibrio para
47	46	43.4	495	2	08E9K7	08e9k7 shewanella
48	46	43.4	1044	2	08BDIH0	08bdih0 synecococc
49	46	43.4	1154	2	08NEN9	08nen9 homo sapien
50	46	43.4	4190	2	083Y48	083y48 pseudomonas
51	45.5	42.9	333	1	CBRR_XANFL	P25545 xanthobacte
52	45	42.5	81	2	09NDL7	09ndl7 hydra magni
53	45	42.5	139	2	09G5F9	09g5f9 hydra atten
54	45	42.5	194	2	086479	086479 streptococc
55	45	42.5	230	2	088H66	088h66 pseudomonas
56	45	42.5	235	2	09KD40	09kd40 bacillus ha
57	45	42.5	245	2	082987	082987 erythrobact
58	45	42.5	302	1	PHRB_PSEUE	P31019 pseudomonas
59	45	42.5	304	2	097V63	097v63 sulfolobus
60	45	42.5	346	2	08P199	08p199 streptococc
61	45	42.5	346	2	09A045	09a045 streptococc
62	45	42.5	346	2	07CNA2	07cna2 streptococc
63	45	42.5	348	1	RMUB_STRMU	P57580 streptococc
64	45	42.5	348	2	08GTF9	08gtf9 streptococc
65	45	42.5	348	2	08DZB1	08dzb1 streptococc
66	45	42.5	348	2	08E4X2	08e4x2 streptococc
67	45	42.5	349	2	07W0B9	07w0b9 bordetella
68	45	42.5	349	2	07W0C0	07w0c0 bordetella
69	45	42.5	349	2	07W0C4	07w0c4 bordetella
70	45	42.5	379	2	08PRC6	08prc6 xanthomonas
71	45	42.5	401	2	096C72	096c72 homo sapien
72	45	42.5	429	2	088NU2	088nu2 pseudomonas
73	45	42.5	433	2	07UTX3	07utx3 rhodospirell
74	45	42.5	467	2	08H846	08h846 oryza sativ
75	45	42.5	492	2	022764	022764 arabidopsis
76	45	42.5	577	2	08XYA0	08xya0 ralsionia s
77	45	42.5	639	1	P2B1_CRYNV	042773 cryptococcu
78	45	42.5	641	2	09Y879	09y879 cryptococcu
79	45	42.5	654	2	09AVL8	09av18 oryza sativ
80	45	42.5	656	2	06YZ49	06yz49 oryza sativ
81	45	42.5	794	2	09U353	09u353 caenorhabdt
82	45	42.5	821	2	0924E2	0924e2 apicomplexa
83	45	42.5	1082	2	063UG8	063ug8 burkholderia
84	45	42.5	1382	1	IF3A_HUMAN	014532 homo sapien
85	45	42.5	2042	2	09VUG3	09v193 drosophila
86	45	42.5	4163	2	09LAB6	09lae6 rhizobium 1
87	44.5	42.0	202	2	06AB11	06ab11 propionibac
88	44.5	42.0	244	2	07W0F8	07w0f8 bordetella
89	44.5	42.0	244	2	07WP46	07wp46 bordetella
90	44.5	42.0	319	2	09PRM5	09prms streptomyce
91	44.5	42.0	513	2	099044	099044 tarsius ban
92	44.5	42.0	513	2	08S759	08s759 tarsius ban
93	44.5	42.0	513	2	09B857	09b857 tarsius ban
94	44	41.5	81	2	09NDL5	09ndl5 tima formos
95	44	41.5	81	2	09NDL8	09ndl8 hydractinia
96	44	41.5	89	2	09NDL9	09ndl9 eirene sp.
97	44	41.5	109	2	09WUG8	09wug8 mus musculu
98	44	41.5	176	2	06AP30	06ap30 leifsonia x
99	44	41.5	192	2	0656A5	0656a5 oryza sativ
100	44	41.5	192	2	06U027	06u027 oryza sativ

ALIGNMENTS

```

RESULT 1
ID 06LKY2; PRELIMINARY; PRT; 497 AA.
AC 06LKY2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein YP00843.
GN Name=YP00843; OrderedlocusNames=PBPRB0156;
OS Photobacterium profundum (Photobacterium SP. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cesarro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations."
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR378675; CAG2029.1; -.
KW Complete proteome.
SQ
SEQUENCE 497 AA; 57026 MW; B977EF6C53465289 CRC64;

Query Match 52.4%; Score 55.5; DB 2; Length 497;
Best Local Similarity 52.2%; Pred. No. 3.5;
Matches 12; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

QY 2 AIEG-----PTLRQWLHGNGRD 19
DB 104 AMEGSRVIFTLAAMLHANGQVT 126

RESULT 2
ID 076H55; PRELIMINARY; PRT; 71 AA.
AC 076H55;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cto.
GN Name=cro;
OS Salmoneilla typhimurium bacteriophage ST104.
OC Viruses.
OX NCBI_TaxID=221029;
OX [1]
RP SEQUENCE FROM N.A.
RX PubMed=15071057;
RA Tanaka K., Nishimori T., Kanno T.,
RA Ishihara R., Sameshima T., Akiba M., Nakazawa M., Yokomizo Y.,
RA Uchida I.;
RT "Molecular characterization of a prophage of Salmoneilla enterica
RT serotype Typhimurium DT104."
RL J. Clin. Microbiol. 42:1807-1812 (2004).
DR EMBL; AB102868; BAD15187.1; -.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002197; HTH_Fis.
DR InterPro; IPR009061; Putativ_DNA_bind.
DR PRINTS; PR01590; HTHFS.
SQ
SEQUENCE 71 AA; 7484 MW; 577499E7BFP9EAD0 CRC64;

Query Match 48.1%; Score 51; DB 2; Length 71;
Best Local Similarity 50.0%; Pred. No. 2.3;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 IEGPTLRQWLHGNGRD 18
DB 25 VKOPTWRLHGGGID 40

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RESULT 3
ID 089RH2; PRELIMINARY; PRT; 580 AA.
AC 089RH2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE B112800 protein.
GN OrderedlocusNames=b112800;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USD110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Ideawa K., Iiguchi M., Kawashima K.,
RA Kohara M., Matsunoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USD110."
RL DNA Res. 9:189-197 (2002).
DR EMBL; AP005945; BAC48065.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0004648; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_Like.
DR InterPro; IPR001932; PP2C_Like.
DR InterPro; IPR000719; PP2C_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00481; PP2C; 1.
DR ProDom; PD000001; Proc_kinase; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
KW Complete proteome.
SQ
SEQUENCE 580 AA; 64916 MW; 6AD3A06E6FAE143B CRC64;

Query Match 48.1%; Score 51; DB 2; Length 580;
Best Local Similarity 46.7%; Pred. No. 21;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 IEGPTLRQWLHGNGR 17
DB 355 IEGQTLRQWLMDNPR 369

RESULT 4
ID 08CSV9; PRELIMINARY; PRT; 667 AA.
AC 08CSV9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Protein kinase.
GN OrderedlocusNames=SE0895;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950922;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-H.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593 (2003).

```

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AE016746; AAO04492.1; -.
 DR HSSP: P71584; 1067.
 DR GO: GO:0005524; P:ATP binding; IEA.
 DR GO: GO:0008658; P:penicillin binding; IEA.
 DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0016740; P:transferase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011009; Kinase_like.
 DR InterPro: IPR005543; PASTA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR008271; Ser_thr_pkin_AS.
 DR Pfam: PF03793; PASTA_2.
 DR Pfam: PF00069; PKinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00740; PASTA; 3.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR KMW: ATP-binding; Complete proteome; Kinase;
 KMW: Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 667 AA; 7541 MW; 47987784531CD97 CRC64;

Query Match 48.1%; Score 51; DB 2; Length 667;
 Best Local Similarity 57.1%; Pred. No. 25;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 IEGPTLROWLHGNG 16
 DB 90 IEGPTLAETIHSRG 103

RESULT 5
 O82RY5 PRELIMINARY; PRT; 690 AA.
 AC O82RY5;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative transposase.
 GN OrderedLocustNames=SAV7;
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 NC NCB1_TaxID=33903;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=MA-4680;
 RC MEDLINE=22608306; PubMed=12692562;
 RX Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 microorganism Streptomyces avermitilis.";
 RL Nat. Biotechnol. 21:526-531(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osomoe T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
 RT "Genome sequence of an industrial microorganism Streptomyces
 avermitilis: deducing the ability of producing secondary
 metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 DR EMBL: AP005021; BAC67716.1; -.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0015074; P:DNA integration; IEA.
 DR GO: GO:0006310; P:DNA recombination; IEA.
 DR InterPro: IPR011010; DNA_brx_join_enz.
 DR InterPro: IPR002104; Phage_integrase.

DR Pfam: PF00589; Phage_integrase; 1.
 KMW Complete proteome.
 SQ SEQUENCE 690 AA; 77303 MW; 867C6DB9A390EA91 CRC64;

Query Match 48.1%; Score 51; DB 2; Length 690;
 Best Local Similarity 52.4%; Pred. No. 26;
 Matches 11; Conservative 0; Mismatches 4; Indels 6; Gaps 1;

QY 5 GPTLRQW-----LHGNGRDT 19
 DB 486 GPTLRQWDSITPHLHGSDT 506

RESULT 6
 O69KG8 PRELIMINARY; PRT; 326 AA.
 ID O69KG8;
 AC O69KG8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein OSUNBD0066M12.35.
 GN Name=OSUNBD0066M12.35;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NC NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 9, BAC
 clone:OSUNBD0066M12.";
 RL Submitted (NOV-2002) to the EMBL/Genbank/DDBB databases.
 DR EMBL: AP005916; BAC36572.1; -.
 KMW Hypothetical protein.
 SQ SEQUENCE 326 AA; 36239 MW; A4FAF7E1AB6DD9B CRC64;

Query Match 47.2%; Score 50; DB 2; Length 326;
 Best Local Similarity 80.0%; Pred. No. 17;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 ROWLHGNGRD 18
 DB 33 ROWLHGNGDD 42

RESULT 7
 O8XY56 PRELIMINARY; PRT; 407 AA.
 ID O8XY56;
 AC O8XY56;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE PROBABLE PHAGE PH1-105 ORF25-LIKE PROTEIN.
 GN Name=RS04076; OrderedLocustNames=RS01682;
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 NC NCB1_TaxID=305;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=SM111000;
 RC MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlet M., Billault A., Brotier P., Camus J.C., Cactolico L.,
 RA Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
 RA Caspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Signier P., Thebaud J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
 RL Nature 415:497-502(2002).
 DR EMBL: AL646065; CAD15384.1; -.
 DR Pfam: PF04860; Phage_portal; 1.

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DR  TIGRfams; TIGR01537; portal_HK97; 1.
KW  Complete proteome.
SQ  SEQUENCE 407 AA; 45951 MW; CC2236A78B65A06C CRC64;

Query Match
Best Local Similarity 47.2%; Score 50; DB 2; Length 407;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY  3 IEGPLTROMLHGNGRDT 19
    :|:|:|:|:|:|
Db  20 LTGRNLQEWLHGDAAT 36

RESULT 8
ID  Q877P6 PRELIMINARY; PRT; 486 AA.
AC  Q877P6;
DT  01-JUN-2003 (TRENBLrel. 24, Created)
DT  01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT  25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE  ISpy6, transposase.
GN  OrderedlocusNames=PSPT00968, PSPT01418, PSPT01439, PSPT02204,
    PSPT04792;
OS  Pseudomonas syringae (pv. tomato).
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
    Pseudomonadaceae; Pseudomonas.
OX  NCBI_TaxID=323;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=DC3000;
RX  MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
    Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
    Gwin M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
    Madupu R.C., Davidse S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
    Nelson W.C., Davidse S.C., Zafar N., Zhou L., Liu J., Yuan Q.,
    Khouiri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
    Uteerback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
    Deng W.-L., Ramos A.R., Alfano J.R., Cartinour S., Chatterjee A.K.,
    Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
    Bender C.L., White O., Fraser C.M., Collier A.;
    "The complete genome sequence of the Arabidopsis and tomato pathogen
    Pseudomonas syringae pv. tomato DC3000."
    Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).
RL  EMBL; AE016859; AA054502.1; -
DR  EMBL; AE016860; AA054939.1; -
DR  EMBL; AE016863; AA054960.1; -
DR  EMBL; AE016873; AA058222.1; -
DR  TIGR; PSPT00968; -
DR  TIGR; PSPT01418; -
DR  TIGR; PSPT01439; -
DR  TIGR; PSPT02204; -
DR  TIGR; PSPT04792; -
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  GO; GO:0004803; F:transposase activity; IEA.
DR  GO; GO:006513; P:DNA transposition; IEA.
DR  InterPro; IPR002559; Transposase_11.
DR  Pfam; PF01609; Transposase_11; 1.
KW  Complete proteome.
SQ  SEQUENCE 486 AA; 55709 MW; 9690BE7816A32165 CRC64;

Query Match
Best Local Similarity 58.8%; Pred. No. 26;
Matches 10; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY  3 IEGP--TLROWLHGNGR 17
    :|:|:|:|:|
Db  431 VEHFPGNLKQWLFNGNR 447

RESULT 9
ID  Q877Q7 PRELIMINARY; PRT; 486 AA.

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AC  Q877Q7;
DT  01-JUN-2003 (TRENBLrel. 24, Created)
DT  01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT  25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE  ISpy6, transposase.
GN  OrderedlocusNames=PSPT00358, PSPT03734;
OS  Pseudomonas syringae (pv. tomato).
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
    Pseudomonadaceae; Pseudomonas.
OX  NCBI_TaxID=323;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=DC3000;
RX  MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
    Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
    Gwin M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
    Madupu R., Davidse S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
    Nelson W.C., Davidse S.C., Zafar N., Zhou L., Liu J., Yuan Q.,
    Khouiri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
    Uteerback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
    Deng W.-L., Ramos A.R., Alfano J.R., Cartinour S., Chatterjee A.K.,
    Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
    Bender C.L., White O., Fraser C.M., Collier A.;
    "The complete genome sequence of the Arabidopsis and tomato pathogen
    Pseudomonas syringae pv. tomato DC3000."
    Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).
RL  EMBL; AE016857; AA053902.1; -
DR  EMBL; AE016869; AA057203.1; -
DR  TIGR; PSPT00358; -
DR  TIGR; PSPT03734; -
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  GO; GO:0004803; F:transposase activity; IEA.
DR  GO; GO:006513; P:DNA transposition; IEA.
DR  InterPro; IPR002559; Transposase_11.
DR  Pfam; PF01609; Transposase_11; 1.
KW  Complete proteome.
SQ  SEQUENCE 486 AA; 55746 MW; 76343F2F8EBF7B2 CRC64;

Query Match
Best Local Similarity 47.2%; Score 50; DB 2; Length 486;
Matches 10; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY  3 IEGP--TLROWLHGNGR 17
    :|:|:|:|:|
Db  431 VEHFPGNLKQWLFNGNR 447

RESULT 10
ID  Q877V4 PRELIMINARY; PRT; 486 AA.
AC  Q877V4;
DT  01-JUN-2003 (TRENBLrel. 24, Created)
DT  01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT  25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE  ISpy6, transposase.
GN  OrderedlocusNames=PSPT01477, PSPT01567, PSPT01929, PSPT03808,
    PSPT04060, PSPT04485;
OS  Pseudomonas syringae (pv. tomato).
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
    Pseudomonadaceae; Pseudomonas.
OX  NCBI_TaxID=323;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=DC3000;
RX  MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
    Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
    Gwin M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
    Madupu R., Davidse S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
    Nelson W.C., Davidse S.C., Zafar N., Zhou L., Liu J., Yuan Q.,
    Khouiri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
    Uteerback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
    Deng W.-L., Ramos A.R., Alfano J.R., Cartinour S., Chatterjee A.K.,
    Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,

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RA Bander C.L., White O., Fraser C.M., Collmer A.;
 RT "The complete genome sequence of the Arabidopsis and tomato pathogen
 RT Pseudomonas syringae pv. tomato DC3000."
 RT Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).
 DR EMBL: AE016861; AAO54998.1; -
 DR EMBL: AE016861; AAO55087.1; -
 DR EMBL: AE016862; AAO55447.1; -
 DR EMBL: AE016869; AAO57277.1; -
 DR EMBL: AE016870; AAO57517.1; -
 DR EMBL: AE016872; AAO57934.1; -
 DR TIGR: PSP01477; -
 DR TIGR: PSP01567; -
 DR TIGR: PSP01929; -
 DR TIGR: PSP03808; -
 DR TIGR: PSP04060; -
 DR TIGR: PSP04485; -
 DR GO: GO:0003677; P:DNA binding; IEA.
 DR GO: GO:0004803; P:transposase activity; IEA.
 DR GO: GO:0006313; P:DNA transposition; IEA.
 DR InterPro: IPR002559; Transposase_11.
 DR Pfam: PF01609; Transposase_11; 1.
 KW Complete proteome.
 SQ SEQUENCE 486 AA; 55718 MW; 0F90A6895854AD2 CRC64;
 Query Match 47.2%; Score 50; DB 2; Length 486;
 Best Local Similarity 58.8%; Pred. No. 26;
 Matches 10; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
 QY 3 IEGP--TLRQWLHGNGR 17
 Db 431 VEHFGNKLKQWLFNGNR 447
 RESULT 11
 EE42 HUMAN STANDARD; PRT; 690 AA.
 ID EP42 HUMAN STANDARD; PRT; 690 AA.
 AC P16452;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Erythrocyte membrane protein band 4.2 (Erythrocyte protein 4.2)
 DE (P4.2)
 GN Name=EP42; Synonyms=E42p;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RC TISSUE=Reticulocytes;
 RX MEDLINE=9121288; PubMed=2052563;
 RA Korsgren C., Cohen C.M.;
 RT "Organisation of the gene for human erythrocyte membrane protein 4.2:
 RT structural similarities with the gene for the a subunit of factor
 RT XIII.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:4840-4844 (1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM SHORT).
 RC TISSUE=Reticulocytes;
 RX MEDLINE=90138879; PubMed=2300550;
 RA Korsgren C., Lawler J., Lambert S., Speicher D., Cohen C.M.;
 RT "Complete amino acid sequence and homologues of human erythrocyte
 RT membrane protein band 4.2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:613-617 (1990).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RC TISSUE=Reticulocytes;
 RX MEDLINE=90138995; PubMed=1689063;
 RA Sung L.A., Chien S., Chang L.-S., Lambert K., Bliss S.A.,
 RA Boubassira E.E., Nagel R.L., Schwartz R.S., Rybicki A.C.;
 RT "Molecular cloning of human protein 4.2: a major component of the
 RT erythrocyte membrane.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:955-959 (1990).

RN [4]
 RP MYRISTOYLATION.
 RX MEDLINE=92184834; PubMed=1544941;
 RA Ristinger M.A., Dolinas B.M., Cohen C.M.;
 RT "Human erythrocyte protein 4.2, a high copy number membrane protein,
 RT is N-myristylated.";
 RL J. Biol. Chem. 267:5680-5685 (1992).
 RN [5]
 RP PHOSPHORYLATION SITE SER-247.
 RX MEDLINE=93271204; PubMed=8499466; DOI=10.1016/0005-2736(93)90156-T;
 RA Dolinas B., Speicher D.W., Gupta B., Cohen C.M.;
 RT "Structural domain mapping and phosphorylation of human erythrocyte
 RT pallidin (band 4.2).";
 RL Biochim. Biophys. Acta 1148:19-29 (1993).
 RN [6]
 RP VARIANT HS THR-111.
 RX MEDLINE=92216098; PubMed=1558976;
 RA Boubassira E.E., Schwartz R.S., Yawata Y., Ata K., Kanzaki A.,
 RA Oiu J.J.-H., Nagel R.L., Rybicki A.C.;
 RT "An alanine-to-threonine substitution in protein 4.2 cDNA is
 RT associated with a Japanese form of hereditary hemolytic anemia
 RT (protein 4.2 Nippon).";
 RL Blood 79:1846-1854 (1992).
 RN [7]
 RP VARIANT HS THR-111.
 RX MEDLINE=95118828; PubMed=7819064;
 RA Takaoka Y., Ideguchi H., Matsuda M., Sakamoto N., Takeuchi T.,
 RA Fukumaki Y.;
 RT "A novel mutation in the erythrocyte protein 4.2 gene of Japanese
 RT patients with hereditary spherocytosis (protein 4.2 Fukuoka).";
 RL Br. J. Haematol. 88:527-533 (1994).
 RN [8]
 RP VARIANT HS GLN-279.
 RX MEDLINE=95290393; PubMed=7772513;
 RA Hayette S., Morle L., Bozon M., Ghanem A., Ristinger M., Korsgren C.,
 RA Tanner M.J.A., Fatoum S., Cohen C.M., Delannay J.;
 RT "A point mutation in the protein 4.2 gene (allele 4.2 Tozeur)
 RT associated with hereditary haemolytic anemia.";
 RL Br. J. Haematol. 89:762-770 (1995).
 CC -1- FUNCTION: Probably plays an important role in the regulation of
 CC erythrocyte shape and mechanical properties.
 CC -1- SUBUNIT: Oligomer. Interacts with the cytoplasmic domain of
 CC SLC4A1/band 3 anion transport protein.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated (cytoplasmic surface of
 CC erythrocyte membranes) and cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Short;
 CC IsoId=P16452-1; Sequence=Displayed;
 CC Note=Major isoform.
 CC Name=Long;
 CC IsoId=P16452-2; Sequence=VSP_006416;
 CC -1- PTM: Both CAMP-dependent kinase (CAK) and another kinase present
 CC in the red-blood cells seem to be able to phosphorylate EPB42.
 CC -1- DISEASE: Defects in EPB42 are a cause of hereditary spherocytosis
 CC (HS) [MIM:177070], a hematologic disorder leading to chronic
 CC hemolytic anemia and characterized by numerous abnormally shaped
 CC erythrocytes which are generally spheroidal. Absence of band 4.2
 CC associated with spur or target erythrocytes has also been
 CC reported.
 CC -1- MISCELLANEOUS: The substitution of an Ala for a Cys in the active
 CC site may be responsible for the lack of transglutaminase activity
 CC of band 4.2.
 CC -1- SIMILARITY: Belongs to the transglutaminase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----

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DR EMBL: M60298; AAA74589.1; -.
DR EMBL: L06519; AAA52385.1; -.
DR EMBL: L06447; AAA52385.1; JOINED.
DR EMBL: L06448; AAA52385.1; JOINED.
DR EMBL: L06449; AAA52385.1; JOINED.
DR EMBL: L06450; AAA52385.1; JOINED.
DR EMBL: L06511; AAA52385.1; JOINED.
DR EMBL: L06512; AAA52385.1; JOINED.
DR EMBL: L06513; AAA52385.1; JOINED.
DR EMBL: L06515; AAA52385.1; JOINED.
DR EMBL: L06516; AAA52385.1; JOINED.
DR EMBL: L06517; AAA52385.1; JOINED.
DR EMBL: M29339; AAA35798.1; -.
DR EMBL: M30646; AAA36402.1; -.
DR EMBL: M30647; AAA36401.1; -.
DR PIR: A39707; A39707.
DR HSSP: P52181; 1G0D.
DR Gene: HGNC:3381; EPB42.
DR MIM: 177070; -.
DR GO: GO:0005856; C:cytoskeleton; TAS.
DR GO: GO:0005886; C:plasma membrane; TAS.
DR GO: GO:0005524; F:ATP binding; TAS.
DR GO: GO:0005200; F:structural constituent of cytoskeleton; TAS.
DR InterPro: IPR001102; Gluttransfg.
DR InterPro: IPR008958; Transglut_C.
DR InterPro: IPR002931; Transglutase_like.
DR Pfam: PF00927; Transglut_C_2.
DR Pfam: PF01841; Transglut_core; 1.
DR Pfam: PF00868; Transglut_N; 1.
DR PROSITE: PS00547; TRANSGLUTAMINASES; 1.
KW Alternative splicing; Cell shape; Cytoskeleton;
KW Direct protein sequencing; Disease mutation; Erythrocyte maturation;
KW Hereditary hemolytic anemia; Lipoprotein; Myristate; Phosphorylation;
KW Structural protein.
FT INIT MET 0 0
FT SITE 30 38 By similarity. Band 3 binding (By similarity).
FT LIPID 1 1 N-myristoyl glycine.
FT MOD_RES 247 247 Phosphoserine (by PKA) (Probable).
FT VARSPLIC 2 2 Q -> QGSEQRSTGLAGLYAPAAAPVFKSGMD (in isoform long).
FT FT /FTId=VSP_006416.
FT VARIANT 111 111 A -> T (in HS; Nippon/Fukuoka).
FT FT /FTId=VAR_007482.
FT FT R -> Q (in HS; Tozeur).
FT VARIANT 279 279 TRPALP -> KRGLPC (in Ref. 3).
FT CONFLICT 334 339 TRPALP -> KRGLPC (in Ref. 3).
FT CONFLICT 349 349 D -> H (in Ref. 3).
FT CONFLICT 375 375 V -> L (in Ref. 3).
SQ SEQUENCE 690 AA; 76841 MW; C6B605869A0A7A8B CRC64;

Query Match 47.2%; Score 50; DB 1; Length 690;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 PTLROWLHNGR 17
DB 249 PTLROWLHNGR 260

RESULT 12
EP42_MOUSE STANDARD; PRT; 690 AA.
AC P49222;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Erythrocyte membrane protein band 4.2 (Erythrocyte protein 4.2)
DE (P4.2).
GN Name=Ep42; Synonym=Ep4.2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Reticulocytes;
RA MEDLINE=95003352; PubMed=7919657;
RX Rybicki A.C., Schwartz R.S., Qiu J.-H., Gilman J.G.;
RT "Molecular cloning of mouse erythrocyte protein 4.2: a membrane
RT protein with strong homology with the transglutaminase supergene
RT family.";
RL Mamm. Genome 5:438-445(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c, and C57BL/6J; TISSUE=Liver, and Reticulocytes;
RX MEDLINE=95048323; PubMed=7959722;
RA Korgren C., Cohen C.M.;
RT "cDNA sequence, gene sequence, and properties of murine pallidin (band
RT 4.2), the protein implicated in the murine pallid mutation.";
RL Genomics 21:478-485(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Karcay B.B.K., Enzhong X.E.X., Chang L.-S.L.S.;
RT "Murine erythrocyte protein 4.2 gene: similarity and differences in
RT structure and expression from its human counterpart.";
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Probably plays an important role in the regulation of
CC erythrocyte shape and mechanical properties.
CC -! SUBUNIT: Oligomer. Interacts with the cytoplasmic domain of
CC SLC4A1/band 3 anion transport protein.
CC -! SUBCELLULAR LOCATION: Membrane-associated (cytoplasmic surface of
CC erythrocyte membranes) and cytoplasmic.
CC -! MISCELLANEOUS: The substitution of an Ala for a Cys in the active
CC site may be responsible for the lack of transglutaminase activity
CC of band 4.2.
CC -! SIMILARITY: belongs to the transglutaminase family.
CC -! CAUTION: was originally (Ref.2) thought to be pallidin.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U03487; AAA62275.1; -.
DR EMBL: U04055; AAA67916.1; -.
DR EMBL: U04056; AAA67917.1; -.
DR EMBL: L35933; AAA39875.1; -.
DR PIR: A54741; A54741.
DR HSSP: 008188; 1L9M.
DR MGD: MGI:95402; Ep4.2.
DR InterPro: IPR001102; Gluttransfg.
DR InterPro: IPR008958; Transglut_C.
DR InterPro: IPR002931; Transglutase_like.
DR Pfam: PF00927; Transglut_C_2.
DR Pfam: PF00868; Transglut_N; 1.
DR PROSITE: PS00547; TRANSGLUTAMINASES; 1.
KW Cell shape; Cytoskeleton; Erythrocyte maturation; Lipoprotein;
KW Myristate; Phosphorylation; Structural protein.
FT INIT MET 0 0
FT SITE 30 38 By similarity. Band 3 binding (By similarity).
FT LIPID 1 1 N-myristoyl glycine (By similarity).
FT MOD_RES 247 247 Phosphoserine (By similarity).
FT CONFLICT 21 21 Y -> H (in Ref. 2; AAA67917).
FT CONFLICT 223 223 K -> N (in Ref. 2; AAA67917).
FT CONFLICT 397 397 C -> S (in Ref. 2; AAA67917).
FT CONFLICT 449 449 K -> R (in Ref. 2; AAA67917).
FT CONFLICT 527 527 S -> R (in Ref. 2; AAA67917).
FT CONFLICT 620 620 S -> C (in Ref. 2 and 3).
SQ SEQUENCE 690 AA; 76608 MW; 3F6BCFE23DD385A6 CRC64;

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Query Match 47.2%; Score 50; DB 1; Length 690;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 PTLROWLHGNGR 17
 DB 249 PTLROWLHGNGR 260

RESULT 13

O6NXXZ8

ID O6NXXZ8 PRELIMINARY; PRT; 691 AA.

AC O6NXXZ8; 05-JUL-2004 (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)

DE Erythrocyte protein band 4.2.

GN Name=Epb4.2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RC MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Umed T.B., Toshlyuk S., Carninci P., Prange C.,

RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mallahy S.J.,

RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettleson M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalins D.E., Schermer A., Schein J.E.,

RA Jones S.J., Matra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RC Strausberg R.L.

RN Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RC Strausberg R.L.

RN Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

RN EMBL; BC066806; AAH66806.1; -

RN EMBL; BC066194; AAH66194.1; -

RN HSSP; P00488; 1EX0.

RN GO; GO:0018149; P:peptide cross-linking; IEA.

RN InterPro; IPR001102; GlutramifG.

RN InterPro; IPR002114; HPR_Serp_S.

RN InterPro; IPR008958; Transglut_C.

RN InterPro; IPR002931; Transglutase_1like.

RN Pfam; PF00927; Transglut_C; 2.

RN Pfam; PF01841; Transglut_Core; 1.

RN Pfam; PF00868; Transglut_N; 1.

RN SMART; SMO0460; TGC; 1.

RN PROSITE; PS00589; PTS_HPR_SER; UNKNOWN 1.

RN PROSITE; PS00547; TRANSGLUTAMINASES; 1.

RN SEQUENCE 691 AA; 76697 MW; EC3E162348D8E12 CRC64;

Query Match 47.2%; Score 50; DB 2; Length 691;

Best Local Similarity 75.0%; Pred. No. 37;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 PTLROWLHGNGR 17
 DB 250 PTLROWLHGNGR 261

RESULT 14

O8YPC5

ID O8YPC5 PRELIMINARY; PRT; 973 AA.

AC O8YPC5; 01-MAR-2002 (TRENBLrel. 20, Created)

DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE A14273 protein.

GN OrderedlocusNames=a14273;

OS Anabaena sp. (strain PCC 7120).

OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

OX NCBI_TaxID=103690;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=21595285; PubMed=11759840;

RA Kaneko T., Nakamura Y., Wolk C.P., Kurita T., Sasamoto S.,

RA Matanabe A., Iriuchih M., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,

RA Yasuda M., Tabata S.;

RT "Complete genomic sequence of the filamentous nitrogen-fixing

cyanobacterium Anabaena sp. strain PCC 7120.";

RL DNA Res. 8:205-213(2001).

RN EMBL; AP003595; BAB75972.1; -

DR PIR; AB2340; AB2340.

DR GO; GO:0005524; F:ATP binding; IEA.

DR Pfam; PF01590; GAF; 1.

DR Pfam; PF02518; HATPase_C; 1.

DR SMART; SMO0065; GAF; 4.

DR SMART; SMO0387; HATPase_C; 1.

KW Complete Proteome.

SQ SEQUENCE 973 AA; 111533 MW; FD22B2B830C7BB77 CRC64;

Query Match 47.2%; Score 50; DB 2; Length 973;
 Best Local Similarity 72.7%; Pred. No. 53;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 PTLROWLHGNG 16
 DB 649 PTLROWLHGNG 659

RESULT 15

MSAS_PENPA

ID MSAS_PENPA STANDARD; PRT; 1774 AA.

AC P22367; 01-ANG-1991 (Rel. 19, Created)

DT 01-ANG-1991 (Rel. 19, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE 6-methylsalicylic acid synthase (BC 2.3.1.165) (6-MSAS).

OS Penicillium patulum (Penicillium griseofulvum).

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiaceae; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.

OX NCBI_TaxID=5078;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=DSM 62862;

RC MEDLINE=91006137; PubMed=2209605;

RA Beck U., Ripka S., Siegener A., Schiltz E., Schweizer B.;

RT "The multifunctional 6-methylsalicylic acid synthase gene of

Penicillium patulum. Its gene structure relative to that of other

polyketide synthases.";

RT Eur. J. Biochem. 192:487-498(1990).

RN -1- FUNCTION: This multifunctional enzyme is a polyketide synthase. It

catalyzes a total of 11 steps by seven different component

```

CC enzymes, in the biosynthesis of the antibiotic patulin.
CC -1- CARBOLYTIC ACTIVITY: Acetyl-CoA + 3 malonyl-CoA + NADPH = 6-
CC methylsalicylate + 4 COA + 3 CO(2) + NADP(+).
CC -1- PATHWAY: Patulin biosynthesis.
CC -1- SUBUNIT: Homomultimer.
CC -1- INDUCTION: In the late logarithmic growth phase.
CC -1- SIMILARITY: Contains 1 acyl carrier domain.
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CC EMBL; X55776; CAA39295.1; -.
CC PIR; S13178; S13178.
CC InterPro; IPR001227; AC transferase.
CC InterPro; IPR009081; ACP-like.
CC InterPro; IPR00794; Ketoacyl_synth.
CC InterPro; IPR006163; pp_bind.
CC InterPro; IPR006162; Ppantne.S.
CC Pfam; PF00698; Acyl_transf_1; 1.
CC Pfam; PF00109; ketoacyl-synt_1.
CC Pfam; PF02801; ketoacyl-synt_C; 1.
CC Pfam; PF00550; pp-binding; 1.
CC PROSITE; PS00075; ACP DOMAIN; 1.
CC PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
CC PROSITE; PS00012; PHOSPHOPANTHEINE; 1.
CC Antifibiotic biosynthesis: Direct protein sequencing;
CC Multifunctional enzyme; NADP; Phosphopantetheine; Transferase.
CC FT DOMAIN 186 238 Acyltransferase.
CC FT DOMAIN 642 676 Acetyl/malonyl transferases.
CC FT DOMAIN 1403 1450 2-oxoacyl reductase.
CC FT DOMAIN 1700 1769 Acyl carrier (ACP).
CC FT NP_BIND 1419 1424 NADP (Potential).
CC FT ACT_SITE 204 204 Beta-ketoacyl synthase (by similarity).
CC FT ACT_SITE 653 653 Malonyltransferase (by similarity).
CC FT BINDING 1732 1732 Phosphopantetheine (by similarity).
CC SEQUENCE 1774 AA; 190732 MW; 05ED5DD10863F938 CRC64;

Query Match 47.2%; Score 50; DB 1; Length 1774;
Best Local Similarity 44.4%; Pred. No. 1e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LAIEGPTLRQWLHGNGRD 18
| | | | | | | | | |
| : : : : : : : :
Db 488 LALQAKTLDMWTAEKGD 505

RESULT 16
066272 PRELIMINARY; PRT; 245 AA.
AC 066272;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Photosynthetic reaction center L subunit (Fragment).
GN Name=pufl;
OS Erythrobacter litoralis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=39960;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAM14332;
RA MEDLINE=21822632; PubMed=1832943; DOI=10.1038/415630a;
RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
RT Hamada T., Eisen J.A., Fraser C.M., Delong E.F.;
RT "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633(2002).
DR EMBL; AB010981; BAA25791.1; -.

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DR HSSP; P02954; 100V.
DR GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte. . .; IEA.
DR GO; GO:0045156; F:electron transporter transferring electron. . .; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019684; P:photosynthesis, light reaction; IEA.
DR InterPro; IPR005871; Photo_L.
DR InterPro; IPR00484; Photo_RC.
DR Pfam; PF00124; Photo_RC; 1.
DR PRINTS; PR00256; REACTCENTRE.
DR TIGRFAMS; TIGR0157; pufl; 1.
DR PROSITE; PS00244; REACTION_CENTER; 1.
DR NON_TER 1
SQ SEQUENCE 245 AA; 27214 MW; 52B268713E199ABD CRC64;

Query Match 46.2%; Score 49; DB 2; Length 245;
Best Local Similarity 81.8%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AIEGPTLRQWL 12
| | | | | | | |
| : : : : : : :
Db 25 AIEGPTLNPWL 35

RESULT 17
082989 PRELIMINARY; PRT; 249 AA.
AC 082989;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Photosynthetic reaction center L subunit (Fragment).
GN Name=pufl;
OS Erythrobacter sp.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=1042;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MBIC3019;
RA MEDLINE=21822632; PubMed=1832943; DOI=10.1038/415630a;
RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
RA Hamada T., Eisen J.A., Fraser C.M., Delong E.F.;
RT "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633(2002).
DR EMBL; AB015708; BAA32995.1; -.
DR HSSP; P02954; 1YST.
DR GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte. . .; IEA.
DR GO; GO:0045156; F:electron transporter, transferring electron. . .; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019684; P:photosynthesis, light reaction; IEA.
DR InterPro; IPR005871; Photo_L.
DR InterPro; IPR00484; Photo_RC.
DR Pfam; PF00124; Photo_RC; 1.
DR PRINTS; PR00256; REACTCENTRE.
DR TIGRFAMS; TIGR0157; pufl; 1.
DR PROSITE; PS00244; REACTION_CENTER; 1.
DR NON_TER 1
SQ SEQUENCE 249 AA; 27702 MW; 4D68EBC82B7166AD CRC64;

Query Match 46.2%; Score 49; DB 2; Length 249;
Best Local Similarity 81.8%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AIEGPTLRQWL 12
| | | | | | | |
| : : : : : : :
Db 25 AIEGPTLNPWL 35

RESULT 18
09XDVO PRELIMINARY; PRT; 278 AA.
AC 09XDVO;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)

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DT 01-NOV-1999 (TrEMBLrel. 12, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Photosynthetic reaction center L subunit.
GN Name=pslI;
OS Erythrobacter sp. MBIC3960.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=94771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MBIC3960;
RX MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
RA Hamada T., Eisen J.A., Frazer C.M., Delong E.P.;
RT "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633 (2002).
DR EMBL; AB027515; BAA78672.1; -.
DR HSSP; P02954; 1YST.
DR GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte. . .; IEA.
DR GO; GO:0045156; P:electron transporter, transferring electron. . .; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019684; P:photosynthesis, light reaction; IEA.
DR InterPro; IPR005871; Photo_L.
DR Pfam; PF00124; Photo_RC; 1.
DR PRINTS; PR00256; REACTCENTRE.
DR TIGRPFAM; TIGR01157; pufL; 1.
DR PROSITE; PS00244; REACTION_CENTER; 1.
SQ SEQUENCE 278 AA; 30735 MW; 0BE618844B3C54FB CRC64;

Query Match 46.2%; Score 49; DB 2; Length 278;
Best Local Similarity 81.8%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AIEGPTLRQWL 12
DB 54 AIEGPTLRPWL 64

RESULT 19
ID 088D08 PRELIMINARY; PRT; 412 AA.
AC 088D08;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Hypothetical protein.
GN OrderedCusNames=PP4765;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Bindac L.M., Beaman M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapfle E.K., Scanlan D., Tran K.,
RA Moazzaz A., Utecherback T.R., Rizzo W., Lee K., Kosack D., Noesl D.,
RA Medler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Helm S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuenmler B.,
RA Frazer C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AB016791; AAN70335.1; -.
DR TIGR; PP4765; -.
DR GO; GO:0015036; P:disulfide oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000759; Adnrx_redox.
DR InterPro; IPR001327; FAD_DYR_redox.

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DR InterPro; IPR004792; HI0933 like.
DR InterPro; IPR000205; NAD_BS-
DR InterPro; IPR001100; Pyr_redox.
DR Pfam; PF03486; HI0933_like; 1.
DR PRINTS; PR00419; ADKRDASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; FNDRDASRI.
DR ProDom; PD018041; HI0933 like; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 412 AA; 43682 MW; 1FAF5CE361F6D2C0 CRC64;

Query Match 46.2%; Score 49; DB 2; Length 412;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 EGPTRLQWLGNGRDT 19
DB 86 DADALRQWTHGIGRET 101

RESULT 20
ID EREB_ECOLI STANDARD; PRT; 419 AA.
AC P05789;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, last sequence update)
DT 05-JUL-2004 (Rel. 44, last annotation update)
DE Erythromycin esterase type II (EC 3.1.1.-).
GN Name=ereB;
OS Escherichia coli.
OC Plasmid pIP1527.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86259072; PubMed=3523438;
RA Arthur M., Autissier D., Courvalin P.;
RT "Analysis of the nucleotide sequence of the ereB gene encoding the
RT erythromycin esterase type II.";
RL Nucleic Acids Res. 14:4987-4993 (1986).
CC -!- FUNCTION: This enzyme confers resistance to erythromycin through
CC inactivation by hydrolyzing the lactone ring of the antibiotic.
CC -!- MISCELLANEOUS: Erythromycin esterase type I and type II share no
CC significant homology except for the region from 279 to 309.
CC -----
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CC -----
DR EMBL; X03988; CAA7626.1; -.
DR PIR; A24381; EREBGM.
DR InterPro; IPR007815; Erythro_esteras.
DR Pfam; PF05339; Erythro_esteras; 1.
KW Antibiotic resistance; Hydrolase; Plasmid; Serine esterase.
SQ SEQUENCE 419 AA; 48173 MW; BCB07A565DBC8BA4 CRC64;

Query Match 46.2%; Score 49; DB 1; Length 419;
Best Local Similarity 46.7%; Pred. No. 34;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 EGPTRLQWLGNGRDT 18
DB 79 EGGIIMNHGQCTD 93

RESULT 21
ID Q7SF09 PRELIMINARY; PRT; 547 AA.

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AC 07SF09;
AC 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU09091.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OK NCBT_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitchugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Seltrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamel M., Kamywaselis M., Muccelli E., Bielke C., Rudd S., Frisman D.,
RA Kryotova S., Raamsen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Plaman M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Nativg D.O., Alex L.A., Mannheim G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RC -1- CAUTION: The sequence shown here is derived from an
RC NATURE 0:0-0(2003).
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX01000017; EAA35672.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0046873; F:metal ion transporter activity; IEA.
DR GO; GO:0030001; P:metal ion transport; IEA.
DR InterPro; IPR001395; Aldol/ket red.
DR InterPro; IPR002523; Mg2+_transportCoRa.
DR Pfam; PF01544; CoRa; 1.
DR PROSITE; PS00063; ALDOXETO_REDUCTASE_3; UNKNOWN_1.
DR Hypothetical protein.
SQ SEQUENCE 547 AA; 61554 MW; 41F0138ECFCF3E45 CRC64;

Query Match 46.2%; Score 49; DB 2; Length 547;
Best Local Similarity 72.7%; Pred. No. 42;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 PPTLRQWLHNGNG 16
DB 128 PTLREWLFGNG 138

RESULT 22
Q6YS15 PRELIMINARY; PRT; 88 AA.
ID Q6YS15;
AC Q6YS15;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein B1446H1.10.
GN Name=B1446H1.10;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OK NCBT_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; A006532; BAC39962.1; -
KW Hypothetical protein.
SQ SEQUENCE 88 AA; 8887 MW; F163E46DB01AEF57 CRC64;

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Query Match 45.8%; Score 48.5; DB 2; Length 88;
Best Local Similarity 76.9%; Pred. No. 7.3;
Matches 10; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 5 GPTLRQWLHNGGR 17
DB 16 GPTLRQWLHNGGR 27

RESULT 23
Q82S29 PRELIMINARY; PRT; 154 AA.
ID Q82S29;
AC Q82S29;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Glycoside hydrolase family 24 (EC 3.2.1.17).
GN OrderedLocustNames=NE2534;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OK NCBT_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RC MEDLINE=22586410; PubMed=12700255;
RX DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chaur P., Lamerdin J.E., Larimer F.W., Regala W., Iao V., Iand M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Archiero D.M., Hommes N.G., Whitaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea."
RL J. Bacteriol. 185:2759-2773 (2003).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
CC acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
CC heteropolymers of the prokaryotes cell walls.
CC -1- SIMILARITY: Belongs to the glycosyl hydrolase 24 family.
DR EMBL; BX321865; CAD86446.1; -
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0003796; F:lysozyme activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0016998; P:cell wall catabolism; IEA.
DR GO; GO:0019835; P:cytolysis; IEA.
DR GO; GO:0042742; P:defense response to bacteria; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002196; Glyco_hydro_24.
DR Pfam; PF00959; Phage_lysozyme; 1.
KW Bacteriolytic enzyme; Complete proteome; Glycosidase; Hydrolase.
SQ SEQUENCE 154 AA; 17326 MW; BB51D426CA4BC89 CRC64;

Query Match 45.3%; Score 48; DB 2; Length 154;
Best Local Similarity 53.8%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 GPTLRQWLHNGGR 17
DB 123 GQELRWVHGCGK 135

RESULT 24
Q9VA92 PRELIMINARY; PRT; 168 AA.
ID Q9VA92;
AC Q9VA92;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE CG11077-PA (RE55125p).
GN ORFNames=CG11077;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.

```

OK NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amaratunga P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Morten J.R., Richards M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abrell J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Bencs P.V., Berman B.P., Bhandari D., Bolhakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cui S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glaeser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Houtin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheier F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.W., Weissbach J.,
 RA Williams S.M., Woodagat, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.W., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.N., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Munz D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodegren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scher S.E., Myers B.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Croebey M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker U.S., Millburn G.H., Prochownik K.S.,
 RA Smith C.D., Tully J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Beutencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;

RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Croebey M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker U.S., Millburn G.H., Prochownik K.S.,
 RA Smith C.D., Tully J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Beutencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;

Query Match 45.3%; Score 48; DB 2; Length 168;
 Best Local Similarity 61.5%; Pred. No. 17;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 LAIBPTLRQWHL 13
 DB 50 LVFVPTLRWYH 62
 RESULT 25
 Q688F0 PRELIMINARY; PRT; 392 AA.
 AC Q688F0;
 DT 25-OCT-2004 (TRIMBLrel. 28, Created)
 DT 25-OCT-2004 (TRIMBLrel. 28, Last sequence update)
 DE Hypothetical protein OSJNBA0035101.11.
 GN Name=OSJNBA0035101.11;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriophytaceae; Oryzaceae; Oryza.
 OX NCBI_TaxId=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Croebey M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker U.S., Millburn G.H., Prochownik K.S.,
 RA Smith C.D., Tully J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Beutencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;

Db 121 EGATRDSCQWLHGDD 137

RESULT 26

AC 067UT0 PRELIMINARY; PRT; 396 AA.

DT 25-OCT-2004 (TEMBLrel. 28, Created)

DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)

DE Putative serine/threonine protein kinase.

GN Name=P0046G12.38;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

OC NCBI_TaxID=39947;

OX [1]

RP SEQUENCE FROM N.A.

RA Sasaki T., Matsumoto T., Katayose Y.,

RT "Oryza sativa nippondare (GA3) genomic DNA, chromosome 9, PAC clone: P0046G12.";

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF005419; BAD38089.1; -

DR GO; GO:0016301; F.kinase activity; IEA.

DR CO; GO:0004674; F.protein serine/threonine kinase activity; IEA.

DR InterPro; IPR011009; Kinase_like.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00219; Tyrc; 1.

DR SMART; SM00219; Tyrc; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Kinase; Serine/threonine-protein kinase.

SC SEQUENCE 396 AA; 43831 MW; B2C9FE83CF34445E CRC64;

Query Match 45.3%; Score 48; DB 2; Length 396;

Best local Similarity 66.7%; Pred. No. 43;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 IEGPLRLQWLHG 14

Db 193 LTGATLQWLHG 204

RESULT 27

AC 06LP74 PRELIMINARY; PRT; 631 AA.

DT 05-JUN-2004 (TEMBLrel. 27, Created)

DT 05-JUN-2004 (TEMBLrel. 27, Last sequence update)

DT 05-JUN-2004 (TEMBLrel. 27, Last annotation update)

DE Hypothetical protein BL2800.

GN Name=BL2800; OrderedLocustNames=PBPA2520;

OS Photobacterium profundum (Photobacterium sp. (strain SS9)).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium.

OC NCBI_TaxID=74109;

OX [1]

RP SEQUENCE FROM N.A.

RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F., Cestaro A., Malacrida G., Simonati B., Cannata N., Bartlett D., Valle G.,

RT "Genome analysis of Photobacterium profundum reveals the complexity of high pressure adaptations.";

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; CR378671; CAG20902.1; -

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0003824; F:catalytic activity; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR011009; Kinase_like.

DR InterPro; IPR001932; PP2C-like.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00069; Pkinase; 1.

DR Pfam; PF00481; PP2C; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00332; PP2CC; 1.

DR SMART; SM00331; PP2C_SIG; 1.

DR SMART; SM00220; S_TKC; 1.

DR SMART; SM00219; Tyrc; 1.

DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.

KW Complete proteome; Hypothetical protein.

SC SEQUENCE 631 AA; 71260 MW; 4AC862AC45B58C06 CRC64;

Query Match 45.3%; Score 48; DB 2; Length 631;

Best local Similarity 53.8%; Pred. No. 70;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 IEGPLRLQWLHGN 15

Db 404 VEGSLRQWLMDN 416

RESULT 28

EP42 BOVIN STANDARD; PRT; 686 AA.

ID EP42 BOVIN

AC 046510

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Erythrocyte membrane protein band 4.2 (Erythrocyte protein 4.2) (P4.2)

GN Name=EPB42; Synonyms=BBP42;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

OC NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Japanese black;

RX MEDLINE=98244826; PubMed=9576866;

RA Matsumoto M., Inaba M., Ono K.-I.;

RT "Molecular basis of bovine red-cell protein 4.2 polymorphism in Japanese black cattle.";

RL Biochem. J. 332:183-187(1998).

CC -1- FUNCTION: Band 4.2 probably plays an important role in the regulation of erythrocyte shape and mechanical properties. The major membrane binding for band 4.2 is the cytoplasmic domain of the erythrocyte anion transporter, band 3 (By similarity).

CC -1- SUBUNIT: Oligomer (By similarity).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic surface of erythrocyte membranes (By similarity).

CC -1- MISCELLANEOUS: The substitution of an Ala for a Cys in the active site may be responsible for the lack of transglutaminase activity of band 4.2.

CC -1- SIMILARITY: Belongs to the transglutaminase family.

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CC

 DR EMBL; AF030030; AAC4855.1; -.
 DR HSSP; Q08188; 1L9M.
 DR InterPro; IPR001102; GlutransfG.
 DR InterPro; IPR008958; TransglutC.
 DR InterPro; IPR002931; Transglutase_like.
 DR Pfam; PF00927; Transglut_C; 2.
 DR Pfam; PF01841; Transglut_core; 1.
 DR Pfam; PF00868; Transglut_N; 1.
 DR SMART; SM00460; TGC; 1.
 DR PROSITE; PS00547; TRANSGLUTAMINASES; FALSE NEG.
 DR Cell shape; Cytokeleton; Erythrocyte maturation; Lipoprotein;
 KW Myristate; Phosphorylation; Structural protein.
 FT INIT_MET 0
 FT SITE 30 38 By similarity.
 FT LIPID 1 1 N-myristoyl glycine (By similarity).
 FT MOD_RES 246 246 Phosphoserine (By similarity).
 FT SEQUENCE 686 AA; 76485 MW; 71CDB6CC82FE7D CRC64;
 SQ

Query Match 45.3%; Score 48; DB 1; Length 686;
 Best Local Similarity 66.7%; Pred. No. 76;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 PTLRQWLHGNGR 17
 DB 248 PTLRQWVTGNGR 259

RESULT 29
 ID 046509 PRELIMINARY; PRT; 687 AA.
 AC 046509;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Erythrocyte protein 4.2.
 GN Name=BBP42;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98244826; PubMed=9576866;
 RA Matsumoto M., Inaba M., Ono K.;
 RT "Molecular basis of bovine red-cell protein 4.2 polymorphism in
 RT Japanese black cattle";
 RL Biochem. J. 332:183-187(1998).
 DR EMBL; AF030029; AAC4854.1; -.
 DR HSSP; Q08188; 1L9M.
 DR GO; GO:0018149; P:peptide cross-linking; IEA.
 DR InterPro; IPR001102; GlutransfG.
 DR InterPro; IPR002114; HPr_Serp_S.
 DR InterPro; IPR008958; Transglut_C.
 DR InterPro; IPR002931; Transglutase_like.
 DR Pfam; PF00927; Transglut_C; 2.
 DR Pfam; PF01841; Transglut_core; 1.
 DR Pfam; PF00868; Transglut_N; 1.
 DR SMART; SM00460; TGC; 1.
 DR PROSITE; PS00589; PTS_HPR_SER; UNKNOWN 1.
 DR SEQUENCE 687 AA; 76616 MW; 5997086868B355D2D CRC64;
 SQ

Query Match 45.3%; Score 48; DB 2; Length 687;
 Best Local Similarity 66.7%; Pred. No. 76;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 PTLRQWLHGNGR 17
 DB 249 PTLRQWVTGNGR 260

RESULT 30

Q84FF9
 ID 084FF9 PRELIMINARY; PRT; 1916 AA.
 AC 084FF9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative hemagglutinin.
 GN Name=agmC;
 OS Myxococcus xanthus.
 OC Bacteria; Proteobacteria; Delta proteobacteria; Myxococcales;
 OC Cyctobacterineae; Myxococcaceae; Myxococcus.
 NCBI_TaxID=34;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hartzell P.L., Youderian P.A.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY204461; AA022852.1; -.
 DR InterPro; IPR003961; FN_III.
 DR SMART; SM0060; FN3; 2.
 SQ SEQUENCE 1916 AA; 199157 MW; 7BEA8D44BD8A94E CRC64;
 SQ

Query Match 45.3%; Score 48; DB 2; Length 1916;
 Best Local Similarity 55.6%; Pred. No. 2,2e+02;
 Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 LAIEGPTLRQWLHGNGRD 18
 DB 1483 LAEGHTLRVWARGGRE 1500

RESULT 31
 ID 075174 PRELIMINARY; PRT; 182 AA.
 AC 075174;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein OSUJBA0083F15.8.
 GN Name=OSUJBA0083F15.8;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Buell C.R., Yuan Q., Qiyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.U., Jin S.S.,
 RA Padresh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Uterback T.T., Feldlyum T.V.,
 RA Yang Q.Q., Haas B.U., Sun B.B., Peterson J.U., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Buell R.; (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RL Submitted (ACI33398; AAR0177.1; -.
 DR EMBL; ACI33398; AAR0177.1; -.
 DR Hypothetical protein.
 SQ SEQUENCE 182 AA; 19525 MW; 12E4793265F0759B CRC64;
 SQ

Query Match 44.3%; Score 47; DB 2; Length 182;
 Best Local Similarity 61.5%; Pred. No. 27;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 TLRQWLHGNGRDT 19
 DB 70 TLRQWLHGNGRDT 82

RESULT 32
 ID 055838 PRELIMINARY; PRT; 344 AA.
 ID 055838

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AC 055838;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NS5 protein (Fragment).
GN Name=NS5;
OS Yokose virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=64294;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-Oita 36;
RA MEDLINE=98080391; PubMed=9420202;
RA Kuno G., Chang G.J., Tsuchiya K.R., Karabatsos N., Cropp C.B.;
RA "Phylogeny of the genus Flavivirus.";
RL J. Virol. 72:73-83 (1998).
DR EMBL; AF013414; AAC58802.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR00208; Flavi_NS5.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR Pfam; PF00972; Flavi_NS5_1.
FT NON_TER 1 1
SQ SEQUENCE 344 AA; 39610 MW; 3E791624EBCDC6D CRC64;
FT NON_TER 344 344

Query Match 44.3%; Score 47; DB 2; Length 344;
Best Local Similarity 64.3%; Pred. No. 53;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 GPTLRQWLHGNGRD 18
DB 182 GNTLMQWLNGNGED 195

RESULT 33
MOA CAUCR STANDARD; PRT; 349 AA.
ID MOA CAUCR
AC 09AC48;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Molybdenum cofactor biosynthesis protein A.
GN Name=moaA; OrderedLocustNames=CC0018;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=158992;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 19089 / CB15;
RX MEDLINE=2113698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Niernan W.C., Feldberg T.V., Iaub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA DeBoy R.T., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Kolonay J.F., Smit J., Craven M.B., Knouri H.M., Shetty J.,
RA Berry K.J., Uitterbeck T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).
CC -1- FUNCTION: Together with moaC, is involved in the conversion of a
CC guanosine derivative (GMP) into molybdopterin precursor Z (By
CC similarity).
CC -1- COFACTOR: Binds 1 3Fe-4S cluster (By similarity).
CC -1- PATHWAY: Molybdenum cofactor biosynthesis; first step.
CC -1- SIMILARITY: Belongs to the radical SAM superfamily. MoaA family.
CC -----
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CC -----
DR EMBL; AB005676; AAK22006.1; -;
DR PIR; B87251; B87251.
DR TIGR; CC0018; -;
DR HAMAP; MF_01225; -; 1.
DR InterPro; IPR006638; ELP3/MiAB/NiFB.
DR InterPro; IPR000385; MoaA_NiFB_PqGE.
DR InterPro; IPR010505; Mob_Synth_C.
DR InterPro; IPR007197; Radical_SAM.
DR Pfam; PF06463; Mob_Synth_C_1.
DR Pfam; PF04055; Radical_SAM; 1.
DR SMART; SM00729; ELP3; 1.
DR PROSITE; PS01305; MOA_NiFB_PQGE; 1.
DR 3Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding;
KW Molybdenum cofactor biosynthesis.
FT METAL 42 42 Iron-sulfur (3Fe-4S) (Potential).
FT METAL 49 49 Iron-sulfur (3Fe-4S) (Potential).
FT METAL 275 275 Iron-sulfur (3Fe-4S) (Potential).
FT METAL 292 292 Iron-sulfur (3Fe-4S) (Potential).
SQ SEQUENCE 349 AA; 37577 MW; 2D2E7C5273F7A170 CRC64;

Query Match 44.3%; Score 47; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 EGPTLRQWLHGNGRD 18
DB 191 ETPALIQMAHGRGCD 205

RESULT 34
O9HX67 PRELIMINARY; PRT; 391 AA.
ID O9HX67
AC 09HX67;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=PA3949;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PA01;
RX MEDLINE=2043737; PubMed=10984043; DOI=10.1038/35023079;
RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Rolger K.R., Kes A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
DR EMBL; AF004813; AAG07336.1; -;
DR PIR; E83151; E83151.
DR InterPro; IPR004792; H10933_1like.
DR Pfam; PF03486; H10933_1like.
DR ProDom; PD018041; H10933_1like; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 391 AA; 42423 MW; 46F4B0X76BAEC200 CRC64;

Query Match 44.3%; Score 47; DB 2; Length 391;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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Qy      4 EGFTRQWHLGNGRDT 19
Db      64 DADALRAWIHGIDT 79

RESULT 35
Q8S6J0      PRELIMINARY;      PRT;      483 AA.
ID          08S6J0;
AC          08S6J0;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE Hypothetical protein OSJNB0023M11.3.
GN Name=OSJNB0023M11.3;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nipponbare;
RA McCombie W.R., de la Bastide M., Spiegel L., Preston R., Kirchoff K.,
RA Kuit K., Nacimento L., Baker J., Santos L., Zutavern T., Miller B.,
RA Cummins D.M., Katzenberger F., Muller S., Bell M., Balija V., Shah R.,
RA King L., Yang C., Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092749; AM08549.1; -.
DR Gramene; Q8S6J0; -.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR005162; Retrotrans_gag.
DR InterPro; IPR008916; Retrov_capsid_C.
DR Pfam; PF03732; Retrotrans_gag; 1.
KM Hypothetical protein.
SQ SEQUENCE 483 AA; 54631 MW; 1EAC123961BF76F6 CRC64;

Query Match      44.3%; Score 47; DB 2; Length 483;
Best Local Similarity 61.5%; Pred. No. 76;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      7 TLKRWLHNGRDT 19
Db      12 SVRSWLHGLPRDT 24

RESULT 36
Q7G676      PRELIMINARY;      PRT;      483 AA.
ID          Q7G676;
AC          Q7G676;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein OSJNB0078C13.19 (putative gag-pol).
GN Name=OSJNB0078C13.19; ORFNames=OSJNB0023M11.3;
OS Oryza sativa (Japanese cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA McCombie W.R., de la Bastide M., Spiegel L., Preston R., Ferraro K.,
RA Kuit K., Nacimento L., Zutavern T., Balija V., Bell M., Baker J.,
RA Miller B., Katzenberger F., Muller S., King L., Sullivan P., Yang C.,
RA Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR [2]
RP SEQUENCE FROM N.A.
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569 (2003).

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RN      [3]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC123594; AAM74436.1; -.
DR EMBL; AE017081; AAP53204.1; -.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR005162; Retrotrans_gag.
DR InterPro; IPR008916; Retrov_capsid_C.
DR Pfam; PF03732; Retrotrans_gag; 1.
KM Hypothetical protein.
SQ SEQUENCE 483 AA; 54631 MW; 1EAC123961BF76F6 CRC64;

Query Match      44.3%; Score 47; DB 2; Length 483;
Best Local Similarity 61.5%; Pred. No. 76;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      7 TLKRWLHNGRDT 19
Db      12 SVRSWLHGLPRDT 24

RESULT 37
Q7T918      PRELIMINARY;      PRT;      3425 AA.
ID          Q7T918;
AC          Q7T918;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Polypeptide.
OS Yokose virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=64294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Oita 36;
RA Tajima S., Takasaki T., Yabe S., Matsuno S., Nomura H., Kurane I.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB114858; BAC79364.1; -.
DR HSSP; Q9Q4T1; IBER.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003724; F:RNA helicase activity; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001122; Flavi_capsid_C.
DR InterPro; IPR011492; Flavi_DEAD.
DR InterPro; IPR000366; Flavi_glycoprote.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR000157; Flavi_NS1.
DR InterPro; IPR000752; Flavi_NS2A.
DR InterPro; IPR000487; Flavi_NS2B.
DR InterPro; IPR000404; Flavi_NS4A.
DR InterPro; IPR001528; Flavi_NS4B.
DR InterPro; IPR000208; Flavi_NS5.
DR InterPro; IPR002535; Flavi_prop.
DR InterPro; IPR001850; Peptidase_S7.
DR InterPro; IPR007095; RNA_pol_DS_PS.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR InterPro; IPR002877; Rtmfctd_mtfase.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF07652; Flavi_DEAD; 1.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.

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DR Pfam: PF01004; Flavi_M; 1.
DR Pfam: PF00948; Flavi_NSI; 1.
DR Pfam: PF01005; Flavi_NSI2; 1.
DR Pfam: PF01002; Flavi_NSI2B; 1.
DR Pfam: PF01350; Flavi_NSI4A; 1.
DR Pfam: PF01349; Flavi_NSI4B; 1.
DR Pfam: PF00972; Flavi_NSI5; 1.
DR Pfam: PF01570; Flavi_NSI5p; 1.
DR Pfam: PF01728; Flavi_NSI5p; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR Pfam: PF00949; Helicase_S7; 1.
DR Pfam: PD001556; Flavi_Glycoprote; 1.
DR Pfam: PD001496; Flavi_NSI1; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC_C; 1.
DR ATP-binding; Helicase; Hydrolase; Polypeptide.
KW SEQUENCE 3425 AA; 384202 MW; 467B9A5CEA1C1EE CRC64;
SQ

Query Match 44.3%; Score 47; DB 2; Length 3425;
Best Local Similarity 64.3%; Pred. No. 6e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 GPTLRQWLHGNGRD 18
Db 3163 GNTLMQWLHNGRD 3176

RESULT 38
Q7MP20 PRELIMINARY; PRT; 495 AA.
AC Q7MP20;
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein VV0544.
GN OrderedLocustNames=VV0544;
OS Vibrio vulnificus (strain VJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OC NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
DR EMBL: AP005332; BAC93308.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 495 AA; 57275 MW; 2C121F9AC6051DB4 CRC64;

Query Match 43.9%; Score 46.5; DB 2; Length 495;
Best Local Similarity 52.6%; Pred. No. 94;
Matches 10; Conservative 1; Mismatches 3; Indels 5; Gaps 1;

QY 2 AIEG-----PTLRQWLHNG 15
Db 99 AMEGSSRVLEPTLAAMLIHAN 117

RESULT 39
Q931U2 PRELIMINARY; PRT; 600 AA.
AC Q931U2;
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BidKB; putative ABC transport system lipoprotein.
GN ORFNames=SCBAC31E11.09;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

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OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2) / M145;
RC MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Lathe J., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- SIMILARITY: Belongs to the bacterial extracellular solute-binding
CC protein family 5.
DR EMBL: AL939122; CAC44320.1; -.
DR GO: GO:0005215; P:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000914; SBP_bac_5.
DR Pfam: PF00496; SBP_bac_5; 1.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 600 AA; 65533 MW; 9CAD7DF4B5D95E95 CRC64;

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Query Match 43.9%; Score 46.5; DB 2; Length 600;
Best Local Similarity 64.3%; Pred. No. 1.1e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 4 EGPT-LRQWLHGNG 16
Db 174 DGPTYLQWLHSGDG 187

RESULT 40
P72407 PRELIMINARY; PRT; 602 AA.
AC P72407;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE BidKB.
GN Name=bidKB;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=M145;
RA Nowell J. R., McGovern K., Josick R.;
RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the bacterial extracellular solute-binding
CC protein family 5.
DR EMBL: U68036; AAB09555.1; -.
DR PIR: T45278; T45278.
DR GO: GO:0005215; P:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000914; SBP_bac_5.
DR Pfam: PF00496; SBP_bac_5; 1.
KW Complete proteome.
SQ SEQUENCE 602 AA; 65851 MW; 5CTF74FC4C9C0FBA CRC64;

Query Match 43.9%; Score 46.5; DB 2; Length 602;
Best Local Similarity 64.3%; Pred. No. 1.2e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 4 EGPT-LRQWLHGNG 16
Db 174 DGPTYLQWLHSGDG 187

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RESULT 41
Q8RSL6 PRELIMINARY; PRT; 85 AA.
ID Q8RSL6
AC Q8RSL6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical protein.
OS uncultured bacterium.
OG Plasmid PB4.
OC Bacteria; environmental samples.
NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22477408; PubMed=12589432;
RA Tsuch A., Schluter A., Bischoff N., Goesmann A., Meyer F., Puhler A.;
RT "The 79,370-bp conjugative plasmid PB4 consists of an IncP- $\beta$ 
RT backbone loaded with a chromate resistance transposon, the strA-strB
RT streptomycin resistance gene pair, the oxacillinase gene blaNDP-1, and
RT a tripartite antibiotic efflux system of the resistance-nodulation-
RT division family."
RL Mol. Genet. Genomics 268:570-584(2003).
DR EMBL: AJ231260; CADD4344.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 85 AA; 9445 MW; DC06B2B0121D5EB4 CRC64;

Query Match 43.4%; Score 46; DB 2; Length 85;
Best Local Similarity 47.4%; Pred. No. 18;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 LAIEPTLRQWLHNGRDT 19
DB 50 MEIEASCLFAMLRGHFRDT 68

RESULT 42
Q9NB63 PRELIMINARY; PRT; 256 AA.
ID Q9NB63
AC Q9NB63;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Galactose-binding protein.
OS Tachypleus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypleus.
NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21167756; PubMed=11133989; DOI=10.1074/jbc.M008414200;
RA Chen S.-C., Yeh C.-H., Yeh M.-S., Huang C.-J., Liu T.-Y.;
RT "Biochemical Properties and cDNA Cloning of Two New Lectins from the
RT Plasma of Tachypleus tridentatus. Tachypleus plasma lectin 1 and 2."
RL J. Biol. Chem. 276:9631-9639(2001).
DR EMBL: AF264067; AAF74773.1; -.
DR InterPro: IPR006624; TCCPR.
DR SMART: SM00706; TCCPR; 6.
SQ SEQUENCE 256 AA; 28517 MW; SEC0272B88F44FF8 CRC64;

Query Match 43.4%; Score 46; DB 2; Length 256;
Best Local Similarity 46.7%; Pred. No. 56;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 IEGLPTLRQWLHNGR 17
DB 18 VVSPTLRQWLHNGR 32

RESULT 43
Q6HSY4 PRELIMINARY; PRT; 279 AA.
ID Q6HSY4
AC Q6HSY4;

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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative receptor-like kinase.
GN Name=P0620H05.17;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
NCBI_TaxID=3947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AP005194; BAD25865.1; -.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006468; F:protein amino acid phosphorylation; IEA.
DR InterPro: IPR011009; Kinase_like.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_kinase_AS.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PSS0108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 279 AA; 31269 MW; F201A2700EF5F2EF CRC64;

Query Match 43.4%; Score 46; DB 2; Length 279;
Best Local Similarity 61.5%; Pred. No. 61;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 GPTLRQWLHNGR 17
DB 85 GCCLHNGR 97

RESULT 44
MOA RHIME STANDARD; PRT; 349 AA.
ID MOA RHIME
AC Q92PB4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Molybdenum cofactor biosynthesis protein A.
GN Name=moaA; OrderedLocNames=R01864; ORFName=SMC00144;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021.
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kles E., Lelaire V., Masny D.,
RA Pohl T., Portetelle D., Puhler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weiner S., Gallibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -1- FUNCTION: Together with moaC, is involved in the conversion of a
CC guanosine derivative (GMP) into molybdopterin precursor Z (By

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CC similarity).
CC -1- COFACTOR: Binds 1 3Fe-4S cluster (By similarity).
CC -1- PATHWAY: Molybdenum cofactor biosynthesis, first step.
CC -1- SIMILARITY: Belongs to the radical SAM superfamily. MoaA family.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AL591788; CAC64643.1; -.
DR HAMAP: MF_01225; -.
DR InterPro: IPR006638; EIP3/MiaB/NiFB.
DR InterPro: IPR000385; MoaA_NiFB_PqGE.
DR InterPro: IPR010505; Mob synth C.
DR InterPro: IPR007197; Radical SAM.
DR Pfam: PF06463; Mob synth C; T.
DR Pfam: PF04055; Radical SAM; I.
DR SMART: SM00729; EIP3; I.
DR PROSITE: PS01305; MOA_NiFB_PQGE; 1.
DR 3Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding;
DR Molybdenum cofactor biosynthesis.
KW METAL 40 40 Iron-sulfur (3Fe-4S) (Potential).
FT METAL 47 47 Iron-sulfur (3Fe-4S) (Potential).
FT METAL 273 273 Iron-sulfur (3Fe-4S) (Potential).
FT METAL 290 290 Iron-sulfur (3Fe-4S) (Potential).
SQ SEQUENCE 349 AA; 38915 MW; 768B3A86EFD1C0A6 CRC64;

Query Match 43.4%; Score 46; DB 1; Length 349;
Best Local Similarity 53.3%; Pred. NO. 78;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 EGGPTLRQWLHNGRD 18
DB 189 EIPELRMWAHGRGMD 203

RESULT 45
074061 PRELIMINARY; PRT; 434 AA.
ID 074061;
AC 074061;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glutamate-1-semialdehyde aminotransferase.
GN Name=gslat;
OS Cenarchaeum symbiosum.
OC Archaea; Crenarchaeota; Thermoprotei; Cenarchaeales; Cenarchaeaceae;
OC Cenarchaeum.
OX NCBI_TaxID=46770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B.
RX MEDLINE=98422450; PubMed=9748430;
RA Schlieper C., DeLong E.F., Preston C.M., Feldman R.A., Wu K.Y.,
RA Swanson R.V.;
RT "Genomic analysis reveals chromosomal variation in natural populations
RT of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";
RL J. Bacteriol. 180:5003-5009(1998).
CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
CC aminotransferase family.
CC EMBL: AF083072; AAC62704.1; -.
DR PIR: T31313; T31313.
DR HSSP: P24630; 4GSA.
DR GO: GO:0030170; F:pyridoxal phosphate binding; IEA.
DR GO: GO:0008483; F:transaminase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR InterPro: IPR005814; Aminotrans_3.
DR Pfam: PF00202; Aminotran 3; 1.
DR PROSITE: PS00600; AA_TRANSFER_CLASS_3; UNKNOWN_1.

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KW Aminotransferase; Pyridoxal phosphate; Transferase.
SQ SEQUENCE 434 AA; 46931 MW; 171C80F06B3C6F25 CRC64;

Query Match 43.4%; Score 46; DB 2; Length 434;
Best Local Similarity 41.2%; Pred. NO. 98;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 AIEGPTLRQWLHNGRD 18
DB 81 AVEGQLRGRWHTGTANE 97

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Search completed: September 1, 2005, 16:21:14
Job time : 74.6691 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:02 ; Search time 64.3597 Seconds

(without alignments)
84.131 Million cell updates/sec

Title: US-10-083-768-12

Perfect score: 85
Sequence: 1 CADGPTLRWISFC 14Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database: A_Geneseq_16Dec04:*

```
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	14	2	AAW09466 Thrombopo
2	85	100.0	14	2	AAW09462 Thrombopo
3	85	100.0	14	2	AAW09465 Thrombopo
4	85	100.0	14	2	AAW09482 Thrombopo
5	85	100.0	14	2	AAW33031 Thrombopo
6	85	100.0	14	2	AAW36633 Thrombopo
7	85	100.0	14	2	AAW33029 Thrombopo
8	85	100.0	14	2	AAW35401 Thrombopo
9	85	100.0	14	2	AAW36647 Thrombopo
10	85	100.0	14	2	AAW35400 Thrombopo
11	85	100.0	14	2	AAW33032 Thrombopo
12	85	100.0	14	3	AAW17014 TPO-mimet
13	85	100.0	14	4	AAU25826 Human thr
14	85	100.0	14	4	AAU25822 Human thr
15	85	100.0	14	4	AAU25866 Human thr
16	85	100.0	14	5	ABW72900 TPO mimet
17	85	100.0	14	7	ADJ73051 TPO mimet
18	85	100.0	14	7	ADJ52686 CHI delet
19	85	100.0	14	8	ADJ51647 CHI delet
20	85	100.0	18	2	AAW09456 Thrombopo
21	85	100.0	18	2	AAW33023 Thrombopo
22	85	100.0	18	3	AAW17020 TPO-mimet
23	85	100.0	18	4	AAU25820 Human thr
24	85	100.0	18	5	ABW72906 TPO mimet
25	85	100.0	18	7	ADJ73058 TPO mimet

26	85	100.0	18	8	ADJ52693 CHI delet
27	85	100.0	18	8	ADJ51654 CHI delet
28	85	100.0	19	2	AAW09458 Thrombopo
29	85	100.0	19	2	AAW33025 Thrombopo
30	85	100.0	19	2	AAW33028 Human thr
31	76	89.4	13	2	AAW09467 Thrombopo
32	76	89.4	13	2	AAW35399 Thrombopo
33	76	89.4	13	2	AAW35417 Thrombopo
34	76	89.4	13	2	AAW33033 Thrombopo
35	76	89.4	13	2	AAW35413 Thrombopo
36	76	89.4	13	2	AAW35406 Thrombopo
37	76	89.4	13	2	AAW35422 Thrombopo
38	76	89.4	13	2	AAW35397 Thrombopo
39	76	89.4	13	4	AAU25997 Human thr
40	76	89.4	14	2	AAW35398 Human thr
41	76	89.4	14	2	AAW35386 Thrombopo
42	76	89.4	14	2	AAW35366 Thrombopo
43	76	89.4	14	2	AAW35402 Thrombopo
44	76	89.4	14	4	AAU25987 Human thr
45	76	89.4	14	4	AAU25983 Human thr
46	76	89.4	14	4	AAU25985 Human thr
47	72	84.7	12	4	AAW35423 Thrombopo
48	72	84.7	12	4	AAU26000 Human thr
49	67	78.8	13	2	AAW35404 Thrombopo
50	67	78.8	13	2	AAW35405 Thrombopo
51	67	78.8	13	4	AAU25994 Human thr
52	67	78.8	13	4	AAU25991 Human thr
53	67	78.8	13	4	AAU25990 Human thr
54	67	78.8	14	2	AAW35412 Thrombopo
55	67	78.8	14	2	AAW35407 Thrombopo
56	67	78.8	14	2	AAW35408 Thrombopo
57	67	78.8	14	2	AAW35403 Thrombopo
58	67	78.8	14	4	AAU25993 Human thr
59	67	78.8	14	4	AAU25989 Human thr
60	67	78.8	14	4	AAU25995 Human thr
61	67	78.8	14	4	AAU25992 Human thr
62	67	78.8	14	4	AAU25986 Human thr
63	67	78.8	14	4	AAU25988 Human thr
64	67	78.8	25	4	AAU26042 Human thr
65	67	78.8	25	8	ADW72531 TPO mimet
66	66	77.6	11	2	AAW35425 Thrombopo
67	66	77.6	11	4	AAU26001 Human thr
68	65	75.3	13	4	AAU26041 Human thr
69	64	75.3	14	3	AAW17017 TPO-mimet
70	64	75.3	14	5	ABW72903 CHI delet
71	64	75.3	14	8	ADJ51650 CHI delet
72	64	75.3	14	8	ADJ51650 CHI delet
73	60	70.6	10	2	AAW35427 Thrombopo
74	60	70.6	10	4	AAU26002 Human thr
75	57	67.1	12	8	AAU26039 TPO mimet
76	57	67.1	13	4	AAU26039 Human thr
77	57	67.1	13	4	ADW72529 TPO mimet
78	57	67.1	13	8	ADW72528 TPO mimet
79	57	67.1	14	2	AAW66732 Peptide C
80	57	67.1	14	4	AAU26040 Human thr
81	56	65.9	13	3	AAW17015 TPO-mimet
82	56	65.9	13	5	ABW72901 TPO mimet
83	56	65.9	13	7	ADJ73054 TPO mimet
84	56	65.9	13	7	ADJ73052 TPO mimet
85	56	65.9	13	7	ADJ73056 TPO mimet
86	56	65.9	13	7	ADJ73053 TPO mimet
87	56	65.9	13	7	ADJ73055 TPO mimet
88	56	65.9	13	7	ADJ73055 CHI delet
89	56	65.9	13	8	ADJ52687 CHI delet
90	55	64.7	15	3	AAW17018 TPO-mimet
91	55	64.7	15	5	ABW72904 TPO mimet
92	55	64.7	15	8	ADJ52691 CHI delet
93	55	64.7	15	8	ADJ52690 CHI delet
94	55	64.7	15	8	ADJ51652 CHI delet
95	55	64.7	15	8	ADJ51651 CHI delet
96	55	64.7	18	7	ADN59672 Thrombopo
97	55	64.7	22	7	ADN59839 TWP pepti
98	55	64.7	25	7	ADN59744 Thrombopo

99 54 63.5 14 2 AAW09479 Thrombopo
100 54 63.5 14 2 AAW36630 Thrombopo

ALIGNMENTS

```

RESULT 1
ID AAW09466 standard; protein; 14 AA.
XX
XX AAW09466;
AC
XX 10-SEP-1997 (first entry)
DT
XX Thrombopoietin receptor binding compound cyclic peptide.
DE
XX Haematology; thrombocytopenia; TPO; TR; proliferation; cyclic;
KM bone marrow transfusion; chemotherapy; radiation therapy.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Disulfide-bond 1..14
FT Modified-site /note="in acetyl form"
FT Modified-site 14
FT Modified-site /note="in amide form"
XX
XX MO9640189-A1.
XX
XX 19-DEC-1996.
XX
XX 05-JUN-1996; 96WO-US008998.
XX
XX 07-JUN-1995; 95US-00472371.
PR 07-JUN-1995; 95US-00473604.
PR 07-JUN-1995; 95US-00476168.
PR 07-JUN-1995; 95US-00478128.
PR 07-JUN-1995; 95US-00484090.
PR 07-JUN-1995; 95US-00485301.
XX
XX (GLAXO) GLAXO GROUP LTD.
XX
XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX
XX WPI; 1997-051883/05.
XX
XX Thrombopoietin receptor-binding/activating peptide(s) and peptide
PT mimetic(s) - useful in treatment of haematological disorders, esp.
PT thrombocytopenia resulting from chemotherapy, etc.
XX
XX Claim 30; Page 91; 106pp; English.
XX
XX The present sequence is a compound which binds to thrombopoietin (TPO)
CC receptor (TR). The compound can be used for treating patients suffering
CC from haematological disorders and thrombocytopenia resulting from
CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide
CC may also be used to maintain the proliferation and growth of TPO-
CC dependent cell lines and for use in biological research, for detecting
CC TPO receptors on living cells
XX
XX Sequence 14 AA;
XX
XX Query Match 100.0%; Score 85; DB 2; Length 14;
XX Best Local Similarity 100.0%; Pred. NO. 6.9e-07;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 CADGPTLRWISFC 14
XX 1 CADGPTLRWISFC 14
XX Db

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RESULT 2
ID AAW09462 standard; protein; 14 AA.
XX
XX AAW09462;
AC
XX 10-SEP-1997 (first entry)
DT
XX Thrombopoietin receptor binding compound peptide.
DE
XX Haematology; thrombocytopenia; TPO; TR; proliferation;
KM bone marrow transfusion; chemotherapy; radiation therapy.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 1..14
FT /note="Preferably linkages are selected from: -
FT CH2OC(O)NR-; Phosphonate; -CH2S(O)2NR-; -CH2NR-; -C(O)NR6
FT ; -NRC(O)NH; where R is hydrogen or lower alkyl and R6 is
FT lower alkyl"
FT
FT Modified-site
FT 1
FT /note="Preferably N-terminus is selected from: -NRR1; -
FT NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NHR; succinimide;
FT benzoyloxycarbonyl-NH; benzoyloxycarbonyl-NH with 1-3
FT substitutions on the phenyl ring selected from lower
FT alkyl, lower alkoxy, chloro, bromo; where R and R1 are
FT independently selected from hydrogen and lower alkyl"
FT 14
FT /note="Preferably C-terminus is -C(O)R2 where R2 is
FT selected from hydroxy, lower alkoxy, and -NR3R4, where R3
FT and R4 are independently selected from hydrogen and lower
FT alkyl, and where the nitrogen atom of the -NR3R4 group
FT can optionally be the amine group of the N-terminus of
FT the peptide forming a cyclic peptide"
XX
XX MO9640189-A1.
XX
XX 19-DEC-1996.
XX
XX 05-JUN-1996; 96WO-US008998.
XX
XX 07-JUN-1995; 95US-00472371.
PR 07-JUN-1995; 95US-00473604.
PR 07-JUN-1995; 95US-00476168.
PR 07-JUN-1995; 95US-00478128.
PR 07-JUN-1995; 95US-00484090.
PR 07-JUN-1995; 95US-00485301.
XX
XX (GLAXO) GLAXO GROUP LTD.
XX
XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX
XX WPI; 1997-051883/05.
XX
XX The present sequence is a compound which binds to thrombopoietin (TPO)
CC receptor (TR). It has a molecular weight of < 8000 Da, and a binding
CC affinity to TR as expressed by an IC50 of no more than about 100 nm. The
CC compound (especially if modified, see features table) can be used for
CC treating patients suffering from haematological disorders and
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC marrow transfusions. The peptide may also be used to maintain the
CC proliferation and growth of TPO-dependent cell lines and for use in
CC biological research, for detecting TPO receptors on living cells
XX

```


SQ Sequence 14 AA;

Query Match 100.0%; Score 85; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CADGPTLRWISFC 14
 |||||
 DB 1 CADGPTLRWISFC 14

RESULT 3

AAW09465 standard; protein; 14 AA.

AAW09465;

10-SEP-1997 (first entry)

Thrombopoietin receptor binding compound cyclic peptide.

Haematology; thrombocytopenia; TPO; TR; proliferation; cyclic;
 bone marrow transfusion; chemotherapy; radiation therapy.

Synthetic.

Key Location/Qualifiers

Disulfide-bond 1..14

WO9640189-A1.

19-DEC-1996.

05-JUN-1996; 96WO-US008998.

07-JUN-1995; 95US-00472371.

07-JUN-1995; 95US-00473604.

07-JUN-1995; 95US-00476168.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00484090.

07-JUN-1995; 95US-00485301.

(GLAX) GLAXO GROUP LTD.

Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

WPI; 1997-051883/05.

Thrombopoietin receptor-binding/activating peptide(s) and peptide

mimetic(s) - useful in treatment of haematological disorders, esp.

thrombocytopenia resulting from chemotherapy, etc.

Claim 30; Page 91; 106pp; English.

Sequence 14 AA;

Query Match 100.0%; Score 85; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 6.9e-07; Mismatches 0; Indels 0; Gaps 0;

QY 1 CADGPTLRWISFC 14
 |||||
 DB 1 CADGPTLRWISFC 14

RESULT 4

AAW09482 standard; protein; 14 AA.

AAW09482;

10-SEP-1997 (first entry)

Thrombopoietin receptor binding peptide.

Haematology; thrombocytopenia; TPO; TR; proliferation;
 bone marrow transfusion; chemotherapy; radiation therapy.

Synthetic.

WO9640189-A1.

19-DEC-1996.

05-JUN-1996; 96WO-US008998.

07-JUN-1995; 95US-00472371.

07-JUN-1995; 95US-00473604.

07-JUN-1995; 95US-00476168.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00484090.

07-JUN-1995; 95US-00485301.

(GLAX) GLAXO GROUP LTD.

Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

WPI; 1997-051883/05.

Thrombopoietin receptor-binding/activating peptide(s) and peptide

mimetic(s) - useful in treatment of haematological disorders, esp.

thrombocytopenia resulting from chemotherapy, etc.

Disclosure; Page 26; 106pp; English.

Sequence 14 AA;

Query Match 100.0%; Score 85; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 6.9e-07; Mismatches 0; Indels 0; Gaps 0;

QY 1 CADGPTLRWISFC 14
 |||||
 DB 1 CADGPTLRWISFC 14

RESULT 5

AAW33031 standard; peptide; 14 AA.

AAW33031;

11-MAR-1998 (first entry)

Thrombopoietin receptor binding peptide.

Thrombopoietin receptor; binding peptide; treatment; agonist;
 haematological disorder; thrombocytopenia; chemotherapy;

PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX Claim 19; Page 89; 106pp; English.

XX

CC The present peptide binds the thrombopoietin receptor (TR), has a

CC molecular weight of less than 8000 Da and a TR binding affinity as

CC expressed by an IC50 of no more than about 100 microm. It can be used to

CC treat disorders which are susceptible to treatment with a thrombopoietin

CC agonist, preferably haematological disorders and thrombocytopenia

CC resulting from chemotherapy, radiation therapy or bone marrow

CC transfusions. It can also be used diagnostically, e.g. to investigate the

CC mechanism of thrombopoietin signal transduction and receptor activation,

CC or to maintain the proliferation and growth of thrombopoietin dependent

CC cell lines

CC

XX

SQ Sequence 14 AA;

Query Match 100.0%; Score 85; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. NO. 6.9e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CADGPTLRWISFC 14

Db 1 CADGPTLRWISFC 14

RESULT 8

AAW35401

ID AAW35401 standard; peptide; 14 AA.

XX

AC AAW35401;

XX

DT 11-MAR-1998 (first entry)

XX

XX Thrombopoietin receptor binding peptide.

DE

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

XX

OS Synthetic.

XX

FX Key Location/Qualifiers

FT Disulfide-bond 1. .14

FT Modified-site 14

FT /note= "NH2-D-Cys"

XX

XX WO9640750-A1.

XX

XX 19-DEC-1996.

XX

PF 07-JUN-1996; 96WO-US009623.

XX

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX

XX (GLAXO) GLAXO GROUP LTD.

XX

PI Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;

PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX

XX WPI; 1997-052226/05.

XX

PT Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX

XX Example 6; Page 63; 106pp; English.

XX

CC The present peptide, which binds the thrombopoietin receptor (TR), can be

CC used to treat disorders which are susceptible to treatment with a

CC thrombopoietin agonist, preferably haematological disorders and

CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone

CC marrow transfusions. It can also be used diagnostically, e.g. to

CC investigate the mechanism of thrombopoietin signal transduction and

CC receptor activation, or to maintain the proliferation and growth of

CC thrombopoietin dependent cell lines

XX

SQ Sequence 14 AA;

Query Match 100.0%; Score 85; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. NO. 6.9e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CADGPTLRWISFC 14

Db 1 CADGPTLRWISFC 14

RESULT 9

AAW36647

ID AAW36647 standard; peptide; 14 AA.

XX

AC AAW36647;

XX

DT 11-MAR-1998 (first entry)

XX

XX Thrombopoietin receptor binding peptide.

DE

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

KW signal transduction; receptor activation; cell culture.

XX

OS Synthetic.

XX

PN WO9640750-A1.

XX

PD 19-DEC-1996.

XX

PF 07-JUN-1996; 96WO-US009623.

XX

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX

XX (GLAXO) GLAXO GROUP LTD.

XX

PI Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;

PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX

XX WPI; 1997-052226/05.

XX

PT Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological

PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX

XX Disclosure; Page 26; 106pp; English.

XX

CC The present peptide, which binds the thrombopoietin receptor (TR), can be

CC used to treat disorders which are susceptible to treatment with a

CC thrombopoietin agonist, preferably haematological disorders and

CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone

CC marrow transfusions. It can also be used diagnostically, e.g. to

CC investigate the mechanism of thrombopoietin signal transduction and

CC receptor activation, or to maintain the proliferation and growth of

CC thrombopoietin dependent cell lines

XX

SQ Sequence 14 AA;

Query Match 100.0%; Score 85; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. NO. 6.9e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CADGPTLRWISFC 14

Db 1 CADGPTLRWISFC 14

RESULT 10
AAW35400 standard; peptide; 14 AA.

XX
XX AAW35400;
XX
XX
XX 11-MAR-1998 (first entry)
XX
XX Thrombopoietin receptor binding peptide.
DE Thrombopoietin receptor; binding peptide; treatment; agonist;
XX haematological disorder; thrombocytopaenia; chemotherapy;
XX radiation therapy; bone marrow transfusion; diagnosis;
XX signal transduction; receptor activation; cell culture.
KM
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 1.14
FT Misc-difference 1 /note= "D-form residue"
FT Modified-site 14 /note= "NH2-D-Cys"
FT
XX
XX MO9640750-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US009623.
XX
XX 07-JUN-1995; 95US-00478128.
PR 07-JUN-1995; 95US-00485301.
XX
XX (GLAXO) GLAXO GROUP LTD.
XX
XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX
XX WPI; 1997-052226/05.
XX
XX Peptides and peptide mimetics which bind to and activate the
PT thrombopoietin receptor - useful in treatment of haematological
PT disorders, esp. thrombocytopaenia resulting from chemotherapy, etc.
XX
XX PS Example 6; Page 63; 106pp; English.
XX
XX CC The present peptide, which binds the thrombopoietin receptor (TR), can be
CC used to treat disorders which are susceptible to treatment with a
CC thrombopoietin agonist, preferably haematological disorders and
CC thrombocytopaenia resulting from chemotherapy, radiation therapy or bone
CC marrow transfusions. It can also be used diagnostically, e.g. to
CC investigate the mechanism of thrombopoietin signal transduction and
CC receptor activation, or to maintain the proliferation and growth of
CC thrombopoietin dependent cell lines
XX
XX Sequence 14 AA;
SQ

Query Match 100.0%; Score 85; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CADGPTLRWISFC 14
DB 1 CADGPTLRWISFC 14

RESULT 11
AAW33032 standard; peptide; 14 AA.

AC AAW33032;
XX
XX 11-MAR-1998 (first entry)
XX
XX Thrombopoietin receptor binding peptide.
DE Thrombopoietin receptor; binding peptide; treatment; agonist;
XX haematological disorder; thrombocytopaenia; chemotherapy;
XX radiation therapy; bone marrow transfusion; diagnosis;
XX signal transduction; receptor activation; cell culture.
KM
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 1.14
FT Modified-site 1 /note= "acylated"
FT Modified-site 14 /note= "amidated"
FT
XX
XX MO9640750-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US009623.
XX
XX 07-JUN-1995; 95US-00478128.
PR 07-JUN-1995; 95US-00485301.
XX
XX (GLAXO) GLAXO GROUP LTD.
XX
XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX
XX WPI; 1997-052226/05.
XX
XX Peptides and peptide mimetics which bind to and activate the
PT thrombopoietin receptor - useful in treatment of haematological
PT disorders, esp. thrombocytopaenia resulting from chemotherapy, etc.
XX
XX PS Claim 30; Page 91; 106pp; English.
XX
XX CC The present peptide binds the thrombopoietin receptor (TR), has a
CC molecular weight of less than 8000 Da and a TR binding affinity as
CC expressed by an IC50 of no more than about 100 microm. It can be used to
CC treat disorders which are susceptible to treatment with a thrombopoietin
CC agonist, preferably haematological disorders and thrombocytopaenia
CC resulting from chemotherapy, radiation therapy or bone marrow
CC transfusions. It can also be used diagnostically, e.g. to investigate the
CC mechanism of thrombopoietin signal transduction and receptor activation,
CC or to maintain the proliferation and growth of thrombopoietin dependent
CC cell lines
XX
XX Sequence 14 AA;
SQ

Query Match 100.0%; Score 85; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CADGPTLRWISFC 14
DB 1 CADGPTLRWISFC 14

RESULT 12
AAB17014 standard; peptide; 14 AA.

XX
XX AAB17014;
XX
XX 31-OCT-2000 (first entry)
XX
XX TPO-mimetic peptide sequence SEQ ID NO: 70.
DE

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KM autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KM immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KM inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KM cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KM vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KM thrombosis; pharmaceutical.
 OS Synthetic.
 XX WO200024782-A2.
 XX
 XX 04-MAY-2000.
 XX
 XX 25-OCT-1999; 99WO-US025044.
 XX
 XX 23-OCT-1998; 98US-0105371P.
 XX 22-OCT-1999; 99US-00428082.
 XX
 XX (AMGEN-) AMGEN INC.
 XX
 XX Feige U, Liu C, Cheetham J, Boone TC;
 XX WPI; 2000-350702/30.
 XX
 XX Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 XX
 XX Claim 19; Page 218; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)-a-F1-(X2)-b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from: -(L1)-C-P1, -(L1)-C-P1-(L2)-d-P2, -(L1)-C-P1-
 CC (L2)-d-P2-(L3)-e-P3, or -(L1)-C-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AA69443 to AA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 CC
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 100.0%; Score 85; DB 3; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CADGPTLRWISFC 14
 Db 1 CADGPTLRWISFC 14
 XX
 RESULT 13
 AAU25826 standard; peptide; 14 AA.
 XX
 AC AAU25826;
 XX
 XX 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #12.
 XX
 KM Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KM hemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;

KM bone marrow transplantation; haematological disorder; platelet disorder;
 KM enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KM tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KM in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 OS Homo sapiens.
 XX US6251864-B1.
 XX
 XX 26-JUN-2001.
 XX
 XX 01-MAR-2000; 2000US-00516704.
 XX
 XX 07-JUN-1995; 95US-00478128.
 XX 07-JUN-1995; 95US-00485301.
 XX 07-JUN-1996; 96WO-US009623.
 XX 15-AUG-1996; 96US-00699027.
 XX
 XX (GLAXO) GLAXO GROUP LTD.
 XX
 XX Dower WJ, Barrett RW, Cwila SE, Gates CM, Scharz PJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Depirince RB, Poddaturi S;
 PI Yn Q;
 XX
 XX WPI; 2001-564142/63.
 XX
 XX Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 XX Disclosure; Col 67-68; 128pp; English.
 XX
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 CC
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 100.0%; Score 85; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CADGPTLRWISFC 14
 Db 1 CADGPTLRWISFC 14
 XX
 RESULT 14
 AAU25852 standard; peptide; 14 AA.
 XX
 AC AAU25852;
 XX
 XX 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #38.
 XX
 KM Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ,
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;
 PI Yin Q;
 XX
 DR WPI; 2001-564142/63.
 XX
 PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 PS Disclosure; Col 20; 128pp; English.
 XX
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 CC
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 85; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CADGPTLRWISFC 14
 DB 1 CADGPTLRWISFC 14
 RESULT 15
 AAU25866
 ID AAU25866 standard; peptide; 14 AA.
 XX
 AC AAU25866;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human thrombopoietin receptor (TPO-R) activator peptide #52.
 XX

KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX
 OS Homo sapiens.
 XX
 PN US6251864-B1.
 XX
 PD 26-JUN-2001.
 XX
 PF 01-MAR-2000; 2000US-00516704.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ,
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;
 PI Yin Q;
 XX
 DR WPI; 2001-564142/63.
 XX
 PT Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 PS Disclosure; Col 20; 128pp; English.
 XX
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 CC
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 85; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CADGPTLRWISFC 14
 DB 1 CADGPTLRWISFC 14
 RESULT 16
 ABB72900
 ID ABB72900 standard; peptide; 14 AA.
 XX
 AC ABB72900;
 XX
 DT 05-APR-2002 (first entry)
 XX
 DE TPO mimetic peptide SEQ ID NO:70.
 XX

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
 KM erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KM TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
 KM TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KM MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KM cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KM antihaemic; anorectic; antifertility; haemostatic; dermatological;
 KM neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KM cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KM sleep disorder; neurological degenerative disease; anaemia;
 KM thrombocytopenia; metastatic tumour; systemic lupus erythematosus;
 KM Fanconi's syndrome.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200183525-A2.
 PN WO200183525-A2.
 XX 08-NOV-2001.
 PD 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US014310.
 PF 02-MAY-2001; 2001WO-US014310.
 XX 03-MAY-2000; 2000US-00563286.
 PR 03-MAY-2000; 2000US-00563286.
 XX (AMGE-) AMGEN INC.
 PA (AMGE-) AMGEN INC.
 PI Feige U, Liu C, Cheatham JC, Boone TC, Gudas JM;
 XX WPI; 2002-130313/17.
 DR WPI; 2002-130313/17.
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 XX
 PS Claim 39; Page 44; 176pp; English.
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antihaemic, anorectic, antifertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention
 CC
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 85; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CADGPTLRWISFC 14
 |||||
 Db 1 CADGPTLRWISFC 14

ID ADJ73051 standard; peptide; 14 AA.
 XX
 AC ADJ73051;
 XX
 XX 06-MAY-2004 (first entry)
 DT 06-MAY-2004 (first entry)
 XX
 DE TPO mimetic peptide sequence SeqID 505.
 XX
 KM mimetic; CDR mimetbody; gene therapy; transgenic; immune;
 KM cardiovascular; infectious; malignant; neurologic disease; anaemia;
 KM immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
 KM TPO.
 XX
 OS Synthetic.
 XX
 XX WO2003084477-A2.
 PN WO2003084477-A2.
 XX 16-OCT-2003.
 PD 16-OCT-2003.
 XX 24-MAR-2003; 2003WO-US009139.
 PF 24-MAR-2003; 2003WO-US009139.
 XX 29-MAR-2002; 2002US-0368791P.
 PR 29-MAR-2002; 2002US-0368791P.
 XX (CENZ) CENTOCOR INC.
 PA (CENZ) CENTOCOR INC.
 XX
 PI Heavner GA, Knight DM, Scallion BJ, Ghayeb J;
 XX WPI; 2003-804237/75.
 DR WPI; 2003-804237/75.
 XX
 PT New CDR mimetbody comprising a portion of a heavy or light chain
 PT variable region comprising human framework or ligand binding region,
 PT useful for preparing a composition for treating e.g., immune,
 PT cardiovascular or neurologic disease.
 PT
 XX
 PS Disclosure; SEQ ID NO 505; 97pp; English.
 CC This invention relates to novel mammalian CDR mimetbodies, specific
 CC portions or variants thereof. Specifically, it refers to an antibody
 CC fragment where a protein has been inserted into, or replaces a portion
 CC of, one or more CDR regions, such that each CDR mimetbody comprises at
 CC least one portion of a heavy chain or light chain variable region, which
 CC itself comprises at least one human framework region and at least one
 CC ligand binding region (LBR). The present invention describes human
 CC mimetbodies, including modified immunoglobulins and cleavage products
 CC that can be useful in gene therapy and the generation of transgenic
 CC plants and animals. Furthermore, the CDR mimetbody is useful for
 CC preparing compositions for modulating, treating or reducing the symptoms
 CC of immune, cardiovascular, infectious, malignant and/ or neurologic
 CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
 CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
 CC peptide sequence is a TPO mimetic peptide sequence used to make a
 CC mimetbody of the invention.
 CC
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 85; DB 7; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 CADGPTLRWISFC 14
 |||||
 Db 1 CADGPTLRWISFC 14

RESULT 17
 ADJ73051

RESULT 18
 ADJ52686
 ID ADJ52686 standard; peptide; 14 AA.
 XX
 AC ADJ52686;
 XX
 XX 06-MAY-2004 (first entry)
 DT 06-MAY-2004 (first entry)
 XX
 DE CH1 deleted mimetbody-related peptide SeqID505.

XX CHI deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
 KW hypotensive; neuroprotective; nootropic; antibacterial; virucide;
 KW fungicide; gene therapy; immune disorder; cardiovascular disease;
 KW arrhythmia; hypertension; heart failure; neurodegenerative;
 KW multiple sclerosis; dementia; Alzheimer's disease; anaemia;
 KW cancerous condition; infectious disease; bacterial infection;
 KW viral infection; fungal infection.
 XX Unidentified.
 OS Synthetic.
 PN WO2004002417-A2.
 XX
 PD 08-JAN-2004.
 XX
 PF 27-JUN-2003; 2003WO-US020347.
 XX
 PR 28-JUN-2002; 2002US-0392431P.
 XX
 PA (CENZ) CENTOCOR INC.
 PI Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
 PI Kutolowski KA;
 DR WPI; 2004-082870/08.
 XX
 PT New CHI-deleted mimetibody polypeptides and nucleic acids, useful for
 PT modulating, treating, alleviating, preventing an immune, cardiovascular,
 PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
 PT diseases.
 XX
 PS Claim 2; SEQ ID NO 505; 129pp; English.
 XX
 CC This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an immunosuppressive,
 CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
 CC antibacterial, virucide or fungicide activity. In addition, the disclosed
 CC sequences may prove useful for gene therapy. The CHI-deleted mimetibody
 CC is useful for diagnosing or treating a disease condition in a cell,
 CC tissue, organ or animal, specifically for modulating, treating,
 CC alleviating, preventing the incidence or reducing the symptoms of an
 CC immune, cardiovascular (for example arrhythmia, hypertension or heart
 CC failure), or neurodegenerative (for example multiple sclerosis, dementia
 CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
 CC conditions, or infectious diseases (for example bacterial, viral or
 CC fungal infection). The present sequence is that of a peptide which may be
 CC used during the creation of a mimetibody of the invention.
 CC
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 85; DB 8; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CADGPTLRWISFC 14
 |||||
 Db 1 CADGPTLRWISFC 14

KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KW antiallergic; muscular-Gen; cyrostatic; antiinflammatory; neuroleptic;
 KW ophthalmologic; nephrotropic; respiratory-Gen; tumour necrosis factor;
 KW TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KW dental disorder; oral disorder; dermatological disorder; ear disorder;
 KW nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KW gastrointestinal disorder; gynaecological disorder; hepatic disorder;
 KW obstetric disorder; haematologic disorder; immunological disorder;
 KW allergic disorder; infectious disorder; musculoskeletal disorder;
 KW oncological disorder; neurological disorder; nutritional disorder;
 KW ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KW renal disorder; pulmonary disorder.
 XX Unidentified.
 OS Synthetic.
 PN WO2004002424-A2.
 XX
 PD 08-JAN-2004.
 XX
 PF 30-JUN-2003; 2003WO-US020495.
 XX
 PR 28-JUN-2002; 2002US-0392431P.
 PR 19-SEP-2002; 2002US-0412144P.
 XX
 PA (CENZ) CENTOCOR INC.
 PI Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
 PI Kutolowski KA;
 DR WPI; 2004-082872/08.
 XX
 PT New CHI deleted mimetibody polypeptide and nucleic acid, useful for
 PT diagnosing, preventing or treating cardiovascular, dermatologic, and
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
 PT nutritional disorders.
 XX
 PS Claim 15; SEQ ID NO 505; 123pp; English.
 XX
 CC This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an osteopathic,
 CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
 CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
 CC immunomodulator, antiallergic, muscular-Gen, cyrostatic,
 CC antiinflammatory, neuroleptic, ophthalmologic, nephrotropic or
 CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
 CC modulator or cytokine-agonist. The methods and compositions of the
 CC present invention are useful for the diagnosis, prevention and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the CHI deleted mimetibody, such as a bone or joint,
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
 CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
 CC obstetric, haematologic, immunological, allergic, infectious,
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
 CC pediatric, psychiatric, renal or pulmonary disorders. The present
 CC sequence is that of a peptide which may be used during the creation of a
 CC mimetibody of the invention.
 CC
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 85; DB 8; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.9e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CADGPTLRWISFC 14
 |||||
 Db 1 CADGPTLRWISFC 14

RESULT 20
 AAM09456
 ID AAM09456 standard; protein; 18 AA.

XX	AA09456;		
AC	10-SEP-1997	(first entry)	
XX	Thrombopoietin receptor binding compound peptide.		
DT	Thrombopoietin receptor binding compound peptide.		
XX	Haematology; thrombocytopenia; TPO; TR; proliferation;		
DE	bone marrow transfusion; chemotherapy; radiation therapy.		
XX	Synthetic.		
OS			
XX	Key	Location/Qualifiers	
XX	Misc-difference 1, 18	/note= "preferably linkages are selected from: -	
FT		CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -C(O)NR6	
FT		; -NHC(O)NH; where R is hydrogen or lower alkyl and R6 is	
FT		lower alkyl"	
FT	Modified-site	1	
FT		/note= "preferably N-terminus is selected from: -NRR1;	
FT		NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NHR; succinimide;	
FT		benzylloxycarbonyl-NH; benzylloxycarbonyl-NH with 1-3	
FT		substitutions on the phenyl ring selected from lower	
FT		alkyl, lower alkoxy, chloro, bromo; where R and R1 are	
FT		independently selected from hydrogen and lower alkyl"	
FT	Modified-site	18	
FT		/note= "preferably C-terminus is -C(O)R2 where R2 is	
FT		selected from hydroxy, lower alkoxy, and -NR3R4, where R3	
FT		and R4 are independently selected from hydrogen and lower	
FT		alkyl, and where the nitrogen atom of the -NR3R4 group	
FT		can optionally be the amine group of the N-terminus of	
FT		the peptide forming a cyclic peptide"	
XX	WO9640189-A1.		
PN	19-DEC-1996.		
PD			
XX	05-JUN-1996;	96WO-US008998.	
PF			
XX	07-JUN-1995;	95US-00472371.	
PR		95US-00473604.	
PR	07-JUN-1995;	95US-00476168.	
PR	07-JUN-1995;	95US-00478128.	
PR	07-JUN-1995;	95US-00484090.	
PR	07-JUN-1995;	95US-00485301.	
XX	(GLAXO GROUP LTD.		
PA			
XX	Dower WJ, Barrett RW, Cwirila SE, Duffin DJ, Gates CM, Johnson SS;		
PI	Mattheakis LC, Schatz PJ, Wagstrom CR, Wighton NC;		
PI			
DR	WPI, 1997-051883/05.		
XX	Thrombopoietin receptor-binding/activating peptide(s) and peptide		
PT	mimetic(s) - useful in treatment of haematological disorders, esp.		
PT	thrombocytopenia resulting from chemotherapy, etc.		
XX	Claim 18; Page 89; 106pp; English.		
XX	The present sequence is a compound which binds to thrombopoietin (TPO)		
CC	receptor (TR). It has a molecular weight of < 8000 Da, and a binding		
CC	affinity to TR as expressed by an IC50 of no more than about 100 nM. The		
CC	compound (especially if modified, see features table) can be used for		
CC	treating patients suffering from haematological disorders and		
CC	thrombocytopenia resulting from chemotherapy, radiation therapy or bone		
CC	marrow transfusions. The peptide may also be used to maintain the		
CC	proliferation and growth of TPO-dependent cell lines and for use in		
CC	biological research, for detecting TPO receptors on living cells		
XX	Sequence 18 AA;		
XX	Query Match	100.0%;	Score 85; DB 2; Length 18;
XX	Best Local Similarity	100.0%;	Pred. No. 9e-07;

Matches	14;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
QY	1	CADGPTLRWISFC 14							
Db	3	CADGPTLRWISFC 16							
RESULT 21									
ID	AAW33023	AAW33023 standard; peptide; 18 AA.							
XX	AAW33023;								
AC	AAW33023;								
XX									
DT	11-MAR-1998	(first entry)							
XX									
DE	Thrombopoietin receptor binding peptide.								
XX									
KW	Thrombopoietin receptor; binding peptide; treatment; agonist;								
KW	haematological disorder; thrombocytopaenia; chemotherapy;								
KW	radiation therapy; bone marrow transfusion; diagnosis;								
KW	signal transduction; receptor activation; cell culture.								
XX									
OS	Synthetic.								
XX									
PN	WO9640750-A1.								
XX									
PD	19-DEC-1996.								
XX									
PF	07-JUN-1996;	96WO-US009623.							
XX									
PR	07-JUN-1995;	95US-00478128.							
PR	07-JUN-1995;	95US-00485301.							
XX									
PA	(GLAX) GLAXO GROUP LTD.								
PI	Dower WJ, Barrett RM, Cwiirja SE, Duffin DJ, Gates CM, Johnson SS;								
PI	Mattheakis LC, Schatz PJ, Wagerstrom CR, Wrighton NC;								
XX									
DR	WPI; 1997-052226/05.								
XX									
PT	Peptides and peptide mimetics which bind to and activate the								
PT	thrombopoietin receptor - useful in treatment of haematological								
PT	disorders, esp. thrombocytopenia resulting from chemotherapy, etc.								
XX									
PS	Claim 19; Page 89; 106pp; English.								
XX									
CC	The present peptide binds the thrombopoietin receptor (TR), has a								
CC	molecular weight of less than 8000 Da and a TR binding affinity as								
CC	expressed by an IC50 of no more than about 100 microm, it can be used to								
CC	treat disorders which are susceptible to treatment with a thrombopoietin								
CC	agonist, preferably haematological disorders and thrombocytopaenia								
CC	resulting from chemotherapy, radiation therapy or bone marrow								
CC	transfusions. It can also be used diagnostically, e.g. to investigate the								
CC	mechanism of thrombopoietin signal transduction and receptor activation,								
CC	or to maintain the proliferation and growth of thrombopoietin dependent								
CC	cell lines								
XX									
SQ	Sequence 18 AA;								
Query Match	100.0%;	Score 85;	DB 2;	Length 18;					
Best Local Similarity	100.0%;	Pred. NO. 9e-07;							
Matches 14;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;	
QY	1	CADGPTLRWISFC 14							
Db	3	CADGPTLRWISFC 16							
RESULT 22									
ID	AAAB17020	AAAB17020 standard; peptide; 18 AA.							
XX									
AC	AAAB17020;								

XX 31-OCT-2000 (first entry)
 DT TPO-mimetic peptide sequence SEQ ID NO:76.
 XX
 DE Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTUA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.
 XX Synthetic.
 OS
 XX WO200024782-A2.
 PN
 XX 04-MAY-2000.
 PD
 XX 25-OCT-1999; 99WO-US025044.
 PF
 XX 23-OCT-1998; 98US-0105371P.
 PR 22-OCT-1999; 99US-00428082.
 XX
 PA (AMGEN-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 PI WPI; 2000-350702/30.
 DR
 XX
 XX Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides; useful for treating cancer and autoimmune diseases.
 XX
 XX Claim 19; Page 220; 608pp; English.
 PS
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)-a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)-c-P1, -(L1)-c-P1-(L2)d-P2, -(L1)-c-P1-
 CC (L2)-d-P2-(L3)-e-P3, or -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3-(L4)f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAm69443 to AAm69526 and AAm6955 to
 CC AAm18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 CC
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 85; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CADGPTLRWISFC 14
 DB 3 CADGPTLRWISFC 16
 ID AAm25820 standard; peptide; 18 AA.
 XX AAm25820;
 AC
 XX 17-DEC-2001 (first entry)
 DT
 XX

DE Human thrombopoietin receptor (TPO-R) activator peptide #6.
 XX
 KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX
 OS Homo sapiens.
 XX
 XX US6251864-B1.
 PN
 XX 26-JUN-2001.
 PD
 XX 01-MAR-2000; 2000US-00516704.
 PF
 XX 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96WO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RW, Cwirila SE, Gates CM, Schatz PJ,
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprience RB, Podduturi S;
 PI Yin Q;
 PI WPI; 2001-564142/63.
 DR
 XX
 XX Activating thrombopoietin receptors in cells, used to treat
 PT thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 XX
 XX Disclosure; Col 65-66; 128pp; English.
 PS
 XX Sequences AAm25815-AAm26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 CC
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 85; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CADGPTLRWISFC 14
 DB 3 CADGPTLRWISFC 16
 ID ABB72906 standard; peptide; 18 AA.
 XX ABB72906;
 AC
 XX 05-APR-2002 (first entry)
 DT
 XX

XX TPO mimetic peptide SEQ ID NO:76.
 DE
 XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
 KM erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KM TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
 KM TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KM MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KM cyclostatic; antirheumatic; antidiabetic; haemostatic; dermatological;
 KM antianemic; anorectic; antifertility; haemostatic; dermatological;
 KM neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KM cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KM sleep disorder; neurological degenerative disease; anaemia;
 KM thrombocytopenia; metastatic tumour; systemic lupus erythematosus;
 KM Fanconi's syndrome.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX WO200183525-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX 02-MAY-2001; 2001WO-US014310.
 PF
 XX 03-MAY-2000; 2000US-00563286.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX
 XX Peige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
 PI WPI; 2002-130313/17.
 DR
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 XX
 PS Claim 39; Page 44; 176pp; English.
 XX
 XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cyrostatic, antirheumatic, antidiabetic, antidiabetic, ophthalmological,
 CC antianemic, anorectic, antifertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (II), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL5695 to ABL5777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention
 CC
 XX Sequence 18 AA;
 SQ
 Query Match 100.0%; Score 85; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. NO. 9e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 25
 ADJ73058
 ID ADJ73058 standard; peptide; 18 AA.
 XX
 XX ADJ73058;
 AC
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE TPO mimetic peptide sequence SeqID 512.
 XX
 XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;
 XX cardiovascular; infectious; malignant; neurologic disease; anaemia;
 KM immunomodulator; cardiant; antimicrobial; cyclostatic; neuroprotective;
 KM TPO.
 KM
 XX
 XX Synthetic.
 OS
 XX
 XX WO2003084477-A2.
 PN
 XX 16-OCT-2003.
 PD
 XX 24-MAR-2003; 2003WO-US009139.
 PF
 XX 29-MAR-2002; 2002US-0368791P.
 PR
 XX (CBNZ) CENTOCOR INC.
 PA
 XX
 XX Heavner GA, Knight DM, Scallion BJ, Chrayeb J;
 PI WPI; 2003-804237/75.
 DR
 XX
 XX New CDR mimetibody comprising a portion of a heavy or light chain
 PT variable region comprising human framework or ligand binding region,
 PT useful for preparing a composition for treating e.g., immune,
 PT cardiovascular or neurologic disease.
 XX
 PS Disclosure; SEQ ID NO 512; 97pp; English.
 XX
 XX This invention relates to novel mammalian CDR mimetibodies, specific
 CC portions or variants thereof. Specifically, it refers to an antibody
 CC fragment where a protein has been inserted into, or replaces a portion
 CC of, one or more CDR regions, such that each CDR mimetibody comprises at
 CC least one portion of a heavy chain or light chain variable region, which
 CC itself comprises at least one human framework region and at least one
 CC ligand binding region (LBR). The present invention describes human
 CC mimetibodies, including modified immunoglobulins and cleavage products
 CC that can be useful in gene therapy and the generation of transgenic
 CC plants and animals. Furthermore, the CDR mimetibody is useful for
 CC preparing compositions for modulating, treating or reducing the symptoms
 CC of immune, cardiovascular, infectious, malignant and/or neurologic
 CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
 CC cardiant, antimicrobial, cyclostatic and neuroprotective activities. This
 CC peptide sequence is a TPO mimetic peptide sequence used to make a
 CC mimetibody of the invention.
 CC
 XX Sequence 18 AA;
 SQ
 Query Match 100.0%; Score 85; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. NO. 9e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CADGPTLRWISFC 14
 |||||
 DB 3 CADGPTLRWISFC 16

RESULT 26
 ADJ52693
 ID ADJ52693 standard; peptide; 18 AA.
 XX
 XX ADJ52693;
 AC
 XX
 DT 06-MAY-2004 (first entry)

[illegible]

XX CH1 deleted mimetibody; osteopathic; cardiovascular-Gen;
KM dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
KW antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
KM ophthalmologic; nephrotropic; respiratory-Gen; tumour necrosis factor;
KM TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
KM dental disorder; oral disorder; dermatological disorder; ear disorder;
KM nose disorder; throat disorder; endocrine disorder; metabolic disorder;
KM gastrointestinal disorder; gynaecological disorder; hepatic disorder;
KM gastroenteral disorder; haematologic disorder; immunologic disorder;
KM allergic disorder; infectious disorder; musculoskeletal disorder;
KM oncological disorder; neurological disorder; nutritional disorder;
KM ophthalmologic disorder; pediatric disorder; psychiatric disorder;
KM renal disorder; pulmonary disorder.

OS Unidentified.
XS Synthetic.

PN WO2004002424-A2.

PD 08-JAN-2004.

PP 30-JUN-2003; 2003WO-US020495.

PR 28-JUN-2002; 2002US-0392431P.
PR 19-SEP-2002; 2002US-0412144P.

PA (CENZ) CENTOCOR INC.

PI Hearner GA, Knight DM, Ghayeb J, Scallion BJ, Neespor TC;
PL Kutolosh KA;
XX WPI; 2004-082872/08.

PT New CH1 deleted mimetibody polypeptide and nucleic acid, useful for
PT diagnosing, preventing or treating cardiovascular, dermatologic,
PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
PT nutritional disorders.

PS Claim 15; SEQ ID NO 512; 123pp; English.

XX This invention relates to CH1 deleted mimetibodies (and the DNA sequences
CC which encode them), compositions, methods and uses. The invention may be
CC useful for the development of compounds with an osteopathic,
CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
CC gastroenteral-Gen, gynaecological-Gen, hepatotropic, haemostatic,
CC immunomodulatory, antiallergic, muscular-Gen, cytostatic,
CC antiinflammatory, neuroleptic, ophthalmologic, nephrotropic or
CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
CC modulator or cytokine-agonist. The methods and compositions of the
CC present invention are useful for the diagnosis, prevention and/or
CC treatment of diseases or conditions associated with aberrant expression
CC or activity of the CH1 deleted mimetibody, such as a bone or joint,
CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
CC obstructive, hematologic, immunological, allergic, infectious,
CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
CC pediatric, psychiatric, renal or pulmonary disorders. The present
CC sequence is that of a peptide which may be used during the creation of a
CC mimetibody of the invention.

XX Sequence 18 AA;

QY Query Match 100.0%; Score 85; DB 8; Length 18;
Db Best Local Similarity 100.0%; Pred. No. 9e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CADGPTLEWISFC 14
|||||
3 CADGPTLEWISFC 16

RESULT 28

AAW09458	AAW09458 standard; protein; 19 AA.
ID	AAW09458 standard; protein; 19 AA.
XX	
AC	AAW09458;
XX	
DT	10-SEP-1997 (first entry)
XX	
DE	Thrombopoietin receptor binding compound peptide.
XX	
KW	Haematology; thrombocytopenia; TPO; TR; proliferation; bone marrow transfusion; chemotherapy; radiation therapy.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Misc-difference
FT	1. .19
FT	/note= "preferably linkages are selected from: -
FT	CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-; -C(O)NR6
FT	; -NRC(O)NH; where R is hydrogen or lower alkyl and R6 is
FT	lower alkyl"
FT	1
FT	/note= "preferably N-terminus is selected from: -NRR1; -
FT	NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NHR; succinimide;
FT	benzoyloxycarbonyl-NH; benzoyloxycarbonyl-NH with 1-3
FT	substitutions on the phenyl ring selected from lower
FT	alkyl, lower alkoxy, chloro, bromo; where R and R1 are
FT	independently selected from hydrogen and lower alkyl"
FT	19
FT	/note= "preferably C-terminus is -C(O)R2 where R2 is
FT	selected from hydroxy, lower alkoxy, and -NR3R4, where R3
FT	and R4 are independently selected from hydrogen and lower
FT	alkyl, and where the nitrogen atom of the -NR3R4 group
FT	can optionally be the amine group of the N-terminus of
FT	the peptide forming a cyclic peptide"
XX	
PN	WO9640189-A1.
XX	
PD	19-DEC-1996.
XX	
PF	05-JUN-1996; 96WO-US008998.
XX	
PR	07-JUN-1995; 95US-00472371.
PR	07-JUN-1995; 95US-00473604.
PR	07-JUN-1995; 95US-00476168.
PR	07-JUN-1995; 95US-00478128.
PR	07-JUN-1995; 95US-00484090.
PR	07-JUN-1995; 95US-00485301.
XX	
PA	(GLAXO) GLAXO GROUP LTD.
XX	
P1	Dower WJ, Barrecl RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
P1	Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX	
DR	WPI; 1997-051883/05.
XX	
PT	Thrombopoietin receptor-binding/activating peptide(s) and peptide
PT	mimetic(s) - useful in treatment of hematological disorders, esp.
PT	thrombocytopenia resulting from chemotherapy, etc.
XX	
PS	Claim 18; Page 89; 106pp; English.
XX	
CC	The present sequence is a compound which binds to thrombopoietin (TPO)
CC	receptor (TR). It has a molecular weight of < 8000 Da, and a binding
CC	affinity to TR as expressed by an IC50 of no more than about 100 nM. The
CC	compound (especially if modified, see features table) can be used for
CC	treating patients suffering from hematological disorders and
CC	thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC	marrow transfusions. The peptide may also be used to maintain the
CC	proliferation and growth of TPO-dependent cell lines and for use in
CC	biological research, for detecting TPO receptors on living cells
XX	
SEQ	Sequence 19 AA;

Query Match	100.0%	Score 85;	PB 2;	Length 19;
Best Local Similarity	100.0%;	Pred. No.	9.6e-07;	
Matches	14;	Conservative	0;	Mismatches 0; Gaps 0.
QY	1	CADGPTLRNWSFC	14	
b	3	CADGPTLRNWSFC	16	

RESULT 29

ID AAW33025 standard; peptide; 19 AA.

AC PAAW33025;

DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

KW Thrombopoietin receptor; binding peptide; treatment; agonist;

KW radiation therapy; bone marrow transfusion; diagnosis;

XX

XX

XX

XX

XX

PR 07-JUN-1995; 95US-00485301.

PA (GLAX) GLAXO GROUP LTD.

PI Dower WJ, Barret RW, Cwirila SE, Duffin DJ, Gates CM, Johnson SS;

XX

XX

PT thrombopoietin receptor - useful in treatment of haematological

XX

XX

CC molecular weight of less than 8000 Da and a TR binding affinity as

CC treat disorders which are susceptible to treatment with a thrombopoietin

CC resulting from chemotherapy, radiation therapy or bone marrow

CC mechanism of thrombopoietin signal transduction and receptor activation

cc cell lines

SQ Sequence 19 AA;

Query Match	Score	DB 2;	Length
100.0%	85;	DB 2;	Length 19;

Matches	14;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0.
---------	-----	--------------	----	------------	----	--------	----	------	----

QY 1 CADGPTLREWISFC 14

Db 3 CADGPTLREWISFC 16

RESULT 30

AAU25822 standard; peptide; 19 AA

ID	AAU25822	standard; peptide; 19 AA
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
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82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

```

XX AC AAU25822;
XX DT 17-DEC-2001 (first entry)
XX DE Human thrombopoietin receptor (TPO-R) activator peptide #8.
XX KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
XX KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
XX KW bone marrow transplantation; haematological disorder; platelet disorder;
XX KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
XX KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
XX KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.
XX OS Homo sapiens.
XX PN US6251864-B1.
XX PD 26-JUN-2001.
XX PF 01-MAR-2000; 2000US-00516704.
XX PR 07-JUN-1995; 95US-00478128.
XX PR 07-JUN-1995; 95US-00485301.
XX PR 07-JUN-1996; 96WO-US009623.
XX PR 15-AUG-1996; 96US-00699627.
XX PA (GLAXO ) GLAXO GROUP LTD.
XX PI Dower WJ, Barrett RM, Cwiria SE, Gates CM, Schatz PJ,
XX PI Balasubramanian P, Magstrom CR, Hendren RM, Deprince RB, Podduturi S,
XX PI Yin Q,
XX DR WPI; 2001-564142/63.
XX PT Activating thrombopoietin receptors in cells, used to treat
XX PT thrombocytopenia and hematological disorders, comprises contacting cells
XX PT with peptides and peptide mimetics attached to hydrophilic polymers.
XX PS Disclosure; Col 67-68; 128pp; English.
XX XX
XX XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
XX CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
XX CC of activating thrombopoietin receptors in cells comprise contacting the
XX CC cells with effective amounts of peptides and peptide mimetics attached to
XX CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
XX CC as that due to chemotherapy, radiation therapy or bone-marrow
XX CC transplantation and to prevent thrombocytopenia in patients at risk. The
XX CC sequences are used to treat and prevent haematological disorders
XX CC including thrombocytopenia and platelet disorders. They are used in vitro
XX CC as unique tools for understanding the biological role of thrombopoietin
XX CC (TPO) and to develop other compounds that bind to and activate the TPO
XX CC receptor. The peptides can be used to detect TPO receptors on living
XX CC cells and fixed cells, in biological fluids, in tissue homogenates, and
XX CC in purified or natural biological materials. They may also be used for in
XX CC situ staining, fluorescence-activated cell sorting, Western blotting and
XX CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
XX CC be used for in vitro expansion of megakaryocytes and their committed
XX CC progenitors alone or in conjunction with additional cytokines
XX SQ Sequence 19 AA;
XX
XX Query Match 100.0%; Score 85; DB 4; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 9.6e-07;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

ID AAU09467 standard; protein; 13 AA.
XX AC AAU09467;
XX DT 10-SEP-1997 (first entry)
XX DE Thrombopoietin receptor binding compound cyclic peptide.
XX KW Haematology; thrombocytopenia; TPO; TR; proliferation; cyclic;
XX KW bone marrow transfusion; chemotherapy; radiation therapy.
XX OS Synthetic.
XX FH Key
XX FT Modified-site 1 Location/Qualifiers
XX FT /note= "The Ala is linked with the modified Cys at
XX FT position 13"
XX FT Modified-site 14
XX FT /label= OTHER
XX FT /note= "S-carboxymethyl-cysteine alpha-carboxamide; the
XX FT forming a linkage onto the Ala at position one with the
XX FT delta C of this residue"
XX PN WO9640189-A1.
XX PD 19-DEC-1996.
XX PR 05-JUN-1996; 96WO-US008998.
XX PR 07-JUN-1995; 95US-00472371.
XX PR 07-JUN-1995; 95US-00473604.
XX PR 07-JUN-1995; 95US-00476168.
XX PR 07-JUN-1995; 95US-00478128.
XX PR 07-JUN-1995; 95US-00484090.
XX PR 07-JUN-1995; 95US-00485301.
XX PA (GLAXO ) GLAXO GROUP LTD.
XX PI Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
XX PI Mattheakis LC, Schatz PJ, Magstrom CR, Wighton NC;
XX DR WPI; 1997-051883/05.
XX PT Thrombopoietin receptor-binding/activating peptide(s) and peptide
XX PT mimetic(s) - useful in treatment of haematological disorders, esp.
XX PT thrombocytopenia resulting from chemotherapy, etc.
XX PS Claim 30, Page 91; 106pp; English.
XX XX
XX XX The present sequence is a compound which binds to thrombopoietin (TPO)
XX CC receptor (TR). The compound can be used for treating patients suffering
XX CC from haematological disorders and thrombocytopenia resulting from
XX CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide
XX CC may also be used to maintain the proliferation and growth of TPO-
XX CC dependent cell lines and for use in biological research, for detecting
XX CC TPO receptors on living cells
XX XX
XX SQ Sequence 13 AA;
XX
XX Query Match 89.4%; Score 76; DB 2; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-05;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 31
AAW09467

1 CADGPTLRWISFC 14
3 CADGPTLRWISFC 16

RESULT 32
AAW35399
ID AAW35399 standard; peptide; 13 AA.
XX AC AAW35399;

```

XX 11-MAR-1998 (first entry)
DT Thrombopoietin receptor binding peptide.
XX
XX Thrombopoietin receptor; binding peptide; treatment; agonist;
DE haematological disorder; thrombocytopenia; chemotherapy;
KW radiation therapy; bone marrow transplantation; diagnosis;
KW signal transduction; receptor activation; cell culture.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "COCH2-alanine linked via CH2 group to Cys13"
FT Modified-site 13
FT /note= "NH2-cytosine linked via sulfoxidised thiol group
FT to Ala1"
XX
XX WO9640750-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96MO-US009623.
XX
XX 07-JUN-1995; 95US-00478128.
XX
XX 07-JUN-1995; 95US-00485301.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX
XX WPI; 1997-052226/05.
XX
XX Peptides and peptide mimetics which bind to and activate the
PT thrombopoietin receptor - useful in treatment of haematological
PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX
XX Example 6; Page 63; 106pp; English.
XX
XX The present peptide, which binds the thrombopoietin receptor (TR), can be
CC used to treat disorders which are susceptible to treatment with a
CC thrombopoietin agonist, preferably haematological disorders and
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC marrow transfusions. It can also be used diagnostically, e.g. to
CC investigate the mechanism of thrombopoietin signal transduction and
CC receptor activation, or to maintain the proliferation and growth of
CC thrombopoietin dependent cell lines
XX
XX
SQ Sequence 13 AA;
Query Match 89.4%; Score 76; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ADGPTLRWISFC 14
DB 1 ADGPTLRWISFC 13

```

```

KW radiation therapy; bone marrow transfusion; diagnosis;
KW signal transduction; receptor activation; cell culture.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Cross-links 1
FT /note= "linked via disulfide bond to Cys1 of identical
FT peptide"
FT Modified-site 13
FT /note= "NH2-Phe"
XX
XX WO9640750-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96MO-US009623.
XX
XX 07-JUN-1995; 95US-00478128.
XX
XX 07-JUN-1995; 95US-00485301.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX
XX WPI; 1997-052226/05.
XX
XX Peptides and peptide mimetics which bind to and activate the
PT thrombopoietin receptor - useful in treatment of haematological
PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX
XX Example 9; Page 73; 106pp; English.
XX
XX The present peptide, which binds the thrombopoietin receptor (TR), can be
CC used to treat disorders which are susceptible to treatment with a
CC thrombopoietin agonist, preferably haematological disorders and
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC marrow transfusions. It can also be used diagnostically, e.g. to
CC investigate the mechanism of thrombopoietin signal transduction and
CC receptor activation, or to maintain the proliferation and growth of
CC thrombopoietin dependent cell lines
XX
XX
SQ Sequence 13 AA;
Query Match 89.4%; Score 76; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CADGPTLRWISF 13
DB 1 CADGPTLRWISF 13

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```

RESULT 33
AAW35417
ID AAW35417 standard; peptide; 13 AA.
XX
XX AAW35417;
AC
XX
DT 11-MAR-1998 (first entry)
XX
XX Thrombopoietin receptor binding peptide.
DE
XX Thrombopoietin receptor; binding peptide; treatment; agonist;
KW haematological disorder; thrombocytopenia; chemotherapy;

```

```

RESULT 34
AAW33033
ID AAW33033 standard; peptide; 13 AA.
XX
XX AAW33033;
AC
XX
DT 11-MAR-1998 (first entry)
XX
XX Thrombopoietin receptor binding peptide.
DE
XX Thrombopoietin receptor; binding peptide; treatment; agonist;
KW haematological disorder; thrombocytopenia; chemotherapy;
KW radiation therapy; bone marrow transfusion; diagnosis;
KW signal transduction; receptor activation; cell culture.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1

```

```

FT      /note= "COCH2-alanine linked via CH2 group to Cys13"
FT Modified-site 13
FT      /note= "NH2-cytosine linked via thiol group to Ala1"
XX
XX
XX      MO9640750-Al.
XX
XX      19-DEC-1996.
XX
XX      07-JUN-1996; 96WO-US009623.
XX
XX      07-JUN-1995; 95US-00478128.
XX      07-JUN-1995; 95US-00485301.
XX
XX      (GLAXO ) GLAXO GROUP LTD.
XX
XX      Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
XX      Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX      WPI; 1997-052226/05.
XX
XX      Peptides and peptide mimetics which bind to and activate the
XX      thrombopoietin receptor - useful in treatment of haematological
XX      disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX
XX      Claim 30; Page 91; 106pp; English.
XX
XX      The present peptide binds the thrombopoietin receptor (TR), has a
XX      molecular weight of less than 8000 Da and a TR binding affinity as
XX      expressed by an IC50 of no more than about 100 microm. It can be used to
XX      treat disorders which are susceptible to treatment with a thrombopoietin
XX      agonist, preferably haematological disorders and thrombocytopenia
XX      resulting from chemotherapy, radiation therapy or bone marrow
XX      transfusions. It can also be used diagnostically, e.g. to investigate the
XX      mechanism of thrombopoietin signal transduction and receptor activation,
XX      or to maintain the proliferation and growth of thrombopoietin dependent
XX      cell lines
XX
XX      Sequence 13 AA;
XX
XX      Query Match      89.4%; Score 76; DB 2; Length 13;
XX      Best Local Similarity 100.0%; Pred. No. 1.9e-05;
XX      Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      2 ADGPTLRWISFC 14
XX      |||||
XX      1 ADGPTLRWISFC 13
XX
XX      Db
XX
XX      RESULT 35
XX      AAW35413
XX      ID      AAW35413 standard; peptide; 13 AA.
XX
XX      AC      AAW35413;
XX
XX      DT      11-MAR-1998 (first entry)
XX
XX      DE      Thrombopoietin receptor binding peptide.
XX
XX      KW      Thrombopoietin receptor; binding peptide; treatment; agonist;
XX      haematological disorder; thrombocytopenia; chemotherapy;
XX      radiation therapy; bone marrow transfusion; diagnosis;
XX      signal transduction; receptor activation; cell culture.
XX
XX      OS      Synthetic.
XX
XX      FH      Key      Location/Qualifiers
XX      FT      Modified-site 1 /note= "Br-Ala"
XX      FT      Modified-site 13 /note= "NH2-Cys"
XX      FT      Modified-site 13 /note= "NH2-Cys"
XX
XX      PN      MO9640750-Al.
XX

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PD      19-DEC-1996.
XX
XX      07-JUN-1996; 96WO-US009623.
XX
XX      07-JUN-1995; 95US-00478128.
XX      07-JUN-1995; 95US-00485301.
XX
XX      (GLAXO ) GLAXO GROUP LTD.
XX
XX      Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
XX      Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX      WPI; 1997-052226/05.
XX
XX      Peptides and peptide mimetics which bind to and activate the
XX      thrombopoietin receptor - useful in treatment of haematological
XX      disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
XX
XX      Example 9; Page 73; 106pp; English.
XX
XX      The present peptide, which binds the thrombopoietin receptor (TR), can be
XX      used to treat disorders which are susceptible to treatment with a
XX      thrombopoietin agonist, preferably haematological disorders and
XX      thrombocytopenia resulting from chemotherapy, radiation therapy or bone
XX      marrow transfusions. It can also be used diagnostically, e.g. to
XX      investigate the mechanism of thrombopoietin signal transduction and
XX      receptor activation, or to maintain the proliferation and growth of
XX      thrombopoietin dependent cell lines
XX
XX      Sequence 13 AA;
XX
XX      Query Match      89.4%; Score 76; DB 2; Length 13;
XX      Best Local Similarity 100.0%; Pred. No. 1.9e-05;
XX      Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      2 ADGPTLRWISFC 14
XX      |||||
XX      1 ADGPTLRWISFC 13
XX
XX      Db
XX
XX      RESULT 36
XX      AAW35406
XX      ID      AAW35406 standard; peptide; 13 AA.
XX
XX      AC      AAW35406;
XX
XX      DT      11-MAR-1998 (first entry)
XX
XX      DE      Thrombopoietin receptor binding peptide.
XX
XX      KW      Thrombopoietin receptor; binding peptide; treatment; agonist;
XX      haematological disorder; thrombocytopenia; chemotherapy;
XX      radiation therapy; bone marrow transfusion; diagnosis;
XX      signal transduction; receptor activation; cell culture.
XX
XX      OS      Synthetic.
XX
XX      FH      Key      Location/Qualifiers
XX      FT      Modified-site 1 /note= "CO-CH(Ph)-alanine linked via CH group to Cys13"
XX      FT      Modified-site 13 /note= "NH2-cytosine linked via thiol group to Ala1"
XX      FT      Modified-site 13 /note= "NH2-cytosine linked via thiol group to Ala1"
XX
XX      PN      MO9640750-Al.
XX
XX      PD      19-DEC-1996.
XX
XX      07-JUN-1996; 96WO-US009623.
XX
XX      07-JUN-1995; 95US-00478128.
XX      07-JUN-1995; 95US-00485301.
XX
XX      (GLAXO ) GLAXO GROUP LTD.
XX

```


XX Dower WJ, Barret RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX WPI; 1997-052226/05.
 DR
 XX Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Example 6; Page 64; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 CC
 XX
 SQ Sequence 13 AA;
 Query Match 89.4%; Score 76; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ADGPTLRWISFC 14
 Db 1 ADGPTLRWISFC 13
 RESULT 37
 ID AAM35422 standard; peptide; 13 AA.
 XX
 AC AAM35422;
 XX
 DT 11-MAR-1998 (first entry)
 XX
 DE Thrombopoietin receptor binding peptide.
 XX
 KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "optionally acylated"
 FT Cross-links 13 /note= "linked via disulfide bond to Cys13 of identical
 FT peptide"
 XX
 FT W09640750-A1.
 XX
 PN 19-DEC-1996.
 PD
 XX 07-JUN-1996; 96WO-US009623.
 PF
 XX 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barret RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX WPI; 1997-052226/05.
 DR
 XX Peptides and peptide mimetics which bind to and activate the

PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 XX Example 9; Page 74; 106pp; English.
 PS
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 CC
 XX
 SQ Sequence 13 AA;
 Query Match 89.4%; Score 76; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ADGPTLRWISFC 14
 Db 1 ADGPTLRWISFC 13
 RESULT 38
 ID AAM35397 standard; peptide; 13 AA.
 XX
 AC AAM35397;
 XX
 DT 11-MAR-1998 (first entry)
 XX
 DE Thrombopoietin receptor binding peptide.
 XX
 KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "COCCH2-alanine linked via CH2 group to Cys13"
 FT Modified-site 13 /note= "NH2-cytosine linked via thiol group to Ala1"
 FT
 XX
 PN W09640750-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009623.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barret RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX WPI; 1997-052226/05.
 DR
 XX Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Example 6; Page 63; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and

CC thrombocytopaenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transplants. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

XX Sequence 13 AA;

Query Match 89.4%; Score 76; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADGPTLRWISFC 14

Db 1 ADGPTLRWISFC 13

RESULT 39

AAU25997

ID AAU25997 standard; peptide; 13 AA.

AC AAU25997;

DT 17-DEC-2001 (first entry)

DE Human thrombopoietin receptor (TPO-R) activator peptide #183.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

KW haemostatic; thrombocytopaenia; chemotherapy; radiation therapy; ELISA;

KW bone marrow transplantation; haematological disorder; platelet disorder;

KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;

KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;

KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.

XX Homo sapiens.

OS US6251864-B1.

PN 26-JUN-2001.

PD 01-MAR-2000; 2000US-00516704.

PF 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PR 07-JUN-1996; 96WO-US009623.

PR 15-AUG-1996; 96US-00699027.

XX (GLAXO) GLAXO GROUP LTD.

PA Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;

PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Poddaturi S;

PI yin Q;

XX WPI; 2001-564142/63.

DR Activating thrombopoietin receptors in cells, used to treat

XX thrombocytopaenia and hematological disorders, comprises contacting cells

PT with peptides and peptide mimetics attached to hydrophilic polymers.

XX Disclosure; Col 143-144; 128pp; English.

CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines

XX Sequence 13 AA;

Query Match 89.4%; Score 76; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CADGPTLRWISF 13

Db 1 CADGPTLRWISF 13

RESULT 40

AAU25984

ID AAU25984 standard; peptide; 13 AA.

AC AAU25984;

DT 17-DEC-2001 (first entry)

DE Human thrombopoietin receptor (TPO-R) activator peptide #170.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

KW haemostatic; thrombocytopaenia; chemotherapy; radiation therapy; ELISA;

KW bone marrow transplantation; haematological disorder; platelet disorder;

KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;

KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;

KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.

XX Homo sapiens.

OS US6251864-B1.

PN 26-JUN-2001.

PD 01-MAR-2000; 2000US-00516704.

PF 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PR 07-JUN-1996; 96WO-US009623.

PR 15-AUG-1996; 96US-00699027.

XX (GLAXO) GLAXO GROUP LTD.

PA Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;

PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Poddaturi S;

PI yin Q;

XX WPI; 2001-564142/63.

DR Activating thrombopoietin receptors in cells, used to treat

XX thrombocytopaenia and hematological disorders, comprises contacting cells

PT with peptides and peptide mimetics attached to hydrophilic polymers.

XX Disclosure; Col 137; 128pp; English.

CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines

XX
 SQ Sequence 13 AA;

Query Match 89.4%; Score 76; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.9e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADGPTLRWISFC 14
 |||||
 1 ADGPTLRWISFC 13

RESULT 41
 AAW35398
 ID AAW35398 standard; peptide; 14 AA.

XX
 AC AAW35398;
 XX
 DT 11-MAR-1998 (first entry)

XX Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;
 KM haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KM signal transduction; receptor activation; cell culture.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1.14

FT Modified-site 1
 /note= "Homocysteine"

FT Modified-site 14
 /note= "NH2-Cys"

PN MO9640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96MO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barret RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

DR WPI; 1997-052226/05.

PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

PS Example 6; Page 63; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

XX
 SQ Sequence 14 AA;

Query Match 89.4%; Score 76; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADGPTLRWISFC 14
 |||||
 2 ADGPTLRWISFC 14

RESULT 42
 AAW35396
 ID AAW35396 standard; peptide; 14 AA.

XX
 AC AAW35396;
 XX
 DT 11-MAR-1998 (first entry)

XX Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;
 KM haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KM signal transduction; receptor activation; cell culture.

XX Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1.14

FT Modified-site 1
 /note= "penicillamine"

FT Modified-site 14
 /note= "NH2-Cys"

PN MO9640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96MO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barret RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

DR WPI; 1997-052226/05.

PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

PS Example 6; Page 63; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

XX
 SQ Sequence 14 AA;

Query Match 89.4%; Score 76; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ADGPTLRWISFC 14
 DB 2 ADGPTLRWISFC 14

RESULT 43

AAW35402 standard; peptide; 14 AA.

AAW35402;

11-MAR-1998 (first entry)

Thrombopoietin receptor binding peptide.

Thrombopoietin receptor; binding peptide; treatment; agonist;

haematological disorder; thrombocytopenia; chemotherapy;

radiation therapy; bone marrow transfusion; diagnosis;

signal transduction; receptor activation; cell culture.

Synthetic.

Key

Disulfide-bond 1.14

Modified-site /note= "D-form residue, Penicillamine"

Modified-site 14

/note= "NH2-D-Cys"

WO9640750-A1.

19-DEC-1996.

07-JUN-1996; 96WO-US009623.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00485301.

(GLAXO) GLAXO GROUP LTD.

Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

Mattheaetis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

WPI; 1997-052226/05.

peptides and peptide mimetics which bind to and activate the

thrombopoietin receptor - useful in treatment of haematological

disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

Example 6; Page 64; 106pp; English.

The present peptide, which binds the thrombopoietin receptor (TR), can be

used to treat disorders which are susceptible to treatment with a

thrombopoietin agonist, preferably haematological disorders and

thrombocytopenia resulting from chemotherapy, radiation therapy or bone

marrow transfusions. It can also be used diagnostically, e.g. to

investigate the mechanism of thrombopoietin signal transduction and

receptor activation, or to maintain the proliferation and growth of

thrombopoietin dependent cell lines

Sequence 14 AA;

Query Match 89.4%; Score 76; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. NO. 2e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ADGPTLRWISFC 14

DB 2 ADGPTLRWISFC 14

RESULT 44

AAU25987

ID AAU25987 standard; peptide; 14 AA.

AAU25987;

18-DEC-2001 (first entry)

Human thrombopoietin receptor (TPO-R) activator peptide #173.

Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

haematological disorder; chemotherapy; radiation therapy; ELISA;

bone marrow transplantation; haematological disorder; platelet disorder;

enzyme-linked immunosorbent assay; in situ staining; biological fluid;

tissue homogenate; fluorescence-activated cell sorting; Western blotting;

in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacti gene.

Homo sapiens.

US6251864-B1.

26-JUN-2001.

01-MAR-2000; 2000US-00516704.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00485301.

07-JUN-1995; 96WO-US009623.

15-AUG-1996; 96US-00699027.

(GLAXO) GLAXO GROUP LTD.

Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;

Balasubramanian P, Wagstrom CR, Hendren RW, Depince RB, Podduturi S;

vin Q;

WPI; 2001-564142/63.

Activating thrombopoietin receptors in cells, used to treat

thrombocytopenia and hematological disorders, comprises contacting cells

with peptides and peptide mimetics attached to hydrophilic polymers.

Disclosure; Col 139; 128pp; English.

Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that

bind to and activate the human thrombopoietin receptor (TPO-R). Methods

of activating thrombopoietin receptors in cells comprise contacting the

cells with effective amounts of peptides and peptide mimetics attached to

hydrophilic polymers. The methods are used to treat thrombocytopenia such

as that due to chemotherapy, radiation therapy or bone-marrow

transplantation and to prevent thrombocytopenia in patients at risk. The

sequences are used to treat and prevent haematological disorders

including thrombocytopenia and platelet disorders. They are used in vitro

as unique tools for understanding the biological role of thrombopoietin

(TPO) and to develop other compounds that bind to and activate the TPO

receptor. The peptides can be used to detect TPO receptors on living

cells and fixed cells, in biological fluids, in tissue homogenates, and

in purified or natural biological materials. They may also be used for in

situ staining, fluorescence-activated cell sorting, Western blotting and

enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can

be used for in vitro expansion of megakaryocytes and their committed

progenitors alone or in conjunction with additional cytokines

Sequence 14 AA;

Query Match 89.4%; Score 76; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. NO. 2e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CADGPTLRWISF 13

DB 1 CADGPTLRWISF 13

RESULT 45

AAU25983
ID AAU25983 standard; peptide; 14 AA.
XX
AC AAU25983;
XX

DT 18-DEC-2001 (first entry)
XX

DE Human thrombopoietin receptor (TPO-R) activator peptide #169.
XX

KM peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
KM haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
KM bone marrow transplantation; haematological disorder; platelet disorder;
KM enzyme-linked immunosorbent assay; in situ staining; biological fluid;
KM tissue homogenate; fluorescence-activated cell sorting; Western blotting;
KM in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.
XX

OS Homo sapiens.
XX

PN US6251864-B1.
XX

PD 26-JUN-2001.
XX

PF 01-MAR-2000; 2000US-00516704.
XX

PR 07-JUN-1995; 95US-00478128.
XX

PR 07-JUN-1995; 95US-00485301.
XX

PR 07-JUN-1996; 96WO-US009623.
XX

PR 15-AUG-1996; 96US-00699027.
XX

PA (GLAXO) GLAXO GROUP LTD.
XX

PI Dower WJ, Barrett RW, Cwirja SE, Gates CM, Schatz PJ,
PI Balaabramanian P, Wagsstrom CR, Hendren RW, Deprience RB, Podduturi S;
PI Yin Q;
XX

DR WPI; 2001-564142/63.
XX

PT Activating thrombopoietin receptors in cells, used to treat
PT thrombocytopenia and hematological disorders, comprises contacting cells
PT with peptides and peptide mimetics attached to hydrophilic polymers.
XX

PS Disclosure; Col 135-137; 128pp; English.
XX

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
CC of activating thrombopoietin receptors in cells comprise contacting the
CC cells with effective amounts of peptides and peptide mimetics attached to
CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
CC as that due to chemotherapy, radiation therapy or bone-marrow
CC transplantation and to prevent thrombocytopenia in patients at risk. The
CC sequences are used to treat and prevent haematological disorders
CC including thrombocytopenia and platelet disorders. They are used in vitro
CC as unique tools for understanding the biological role of thrombopoietin
CC (TPO) and to develop other compounds that bind to and activate the TPO
CC receptor. The peptides can be used to detect TPO receptors on living
CC cells and fixed cells, in biological fluids, in tissue homogenates, and
CC in purified or natural biological materials. They may also be used for in
CC situ staining, fluorescence-activated cell sorting, Western blotting and
CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
CC be used for in vitro expansion of megakaryocytes and their committed
CC progenitors alone or in conjunction with additional cytokines
XX

XX Sequence 14 AA;
SQ

Query Match 89.4%; Score 76; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ADGPTLRWISFC 14
| | | | | | | | | | | | | | | |
Db 2 ADGPTLRWISFC 14

Search completed: September 1, 2005, 16:12:14
Job time : 65.3597 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:57:33 ; Search time 10.6763 Seconds
(without alignments)
126.171 Million cell updates/sec

Title: US-10-083-768-12

Perfect score: 85
Sequence: 1 CADGPTLRWISFC 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : PIR 79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	45	52.9	108	2 T49731	hypothetical prote
2	44	51.8	974	2 S34189	starch phosphoryla
3	44	51.8	1022	1 S00503	Na+/K+-exchanging
4	44	51.8	1023	2 A24414	Na+/K+-exchanging
5	43	50.6	245	2 T47701	translational initia
6	43	50.6	490	2 T09084	phosphatidylinosit
7	43	50.6	1010	2 B37227	Na+/K+-exchanging
8	43	50.6	1013	1 S00801	Na+/K+-exchanging
9	43	50.6	1013	2 C24639	Na+/K+-exchanging
10	43	50.6	1017	2 A37227	Na+/K+-exchanging
11	43	50.6	1020	2 A34474	Na+/K+-exchanging
12	43	50.6	1020	2 B24639	Na+/K+-exchanging
13	43	50.6	1021	1 PWSHNA	Na+/K+-exchanging
14	43	50.6	1021	1 S04630	Na+/K+-exchanging
15	43	50.6	1021	2 A28199	Na+/K+-exchanging
16	43	50.6	1021	2 B24862	Na+/K+-exchanging
17	43	50.6	1022	2 S49137	Na+/K+-exchanging
18	43	50.6	1023	1 A24639	Na+/K+-exchanging
19	43	50.6	1023	1 S24650	Na+/K+-exchanging
20	43	50.6	1025	2 A60444	Na+/K+-exchanging
21	43	50.6	1027	1 PWCNMA	Na+/K+-exchanging
22	43	50.6	1038	1 S03632	Na+/K+-exchanging
23	42.5	50.0	1004	2 JH0470	Na+/K+-exchanging
24	42	49.4	522	2 F86876	hypothetical prote
25	42	49.4	522	2 D69226	hypothetical prote
26	42	49.4	725	2 S62941	conserved membrane
27	42	49.4	842	2 A11544	starch phosphoryla
28	42	49.4	842	2 T12091	hypothetical prote
29	41	48.2	189	2 S07755	hypothetical prote

30	41	48.2	273	2 H70849	hypothetical prote
31	41	48.2	955	2 E84853	hypothetical prote
32	41	48.2	973	2 T10947	starch phosphoryla
33	41	48.2	966	2 P8P0AG	starch phosphoryla
34	41	48.2	971	2 T09210	starch phosphoryla
35	41	48.2	1000	2 S47243	starch phosphoryla
36	41	48.2	1616	2 T17884	S-layer protein -
37	40	47.1	98	2 A70301	ribosomal protein
38	40	47.1	152	2 S21826	T-cell receptor be
39	40	47.1	169	1 ICMS2	interleukin-2 prec
40	40	47.1	169	2 S37289	hypothetical prote
41	40	47.1	169	2 E95908	pol polyprotein -
42	40	47.1	217	2 S46354	probable hydrolase
43	40	47.1	352	2 B97072	corrinoid/iron-sul
44	40	47.1	389	2 B69096	LIS-1 protein - hu
45	40	47.1	409	2 S36113	platelet-activatin
46	40	47.1	410	2 S48052	UDP-N-acetylglucos
47	40	47.1	457	2 C82720	58.5K hypothetical
48	40	47.1	526	2 A86440	pol polyprotein -
49	40	47.1	656	2 S30484	pol polyprotein -
50	40	47.1	656	2 S30483	starch phosphoryla
51	40	47.1	838	1 A40995	HIV-1 retropepsin
52	40	47.1	1034	1 GNLJCA	HIV-1 retropepsin
53	40	47.1	1035	1 GNLJGG	HIV-1 retropepsin
54	40	47.1	1036	1 GNLJG2	HIV-1 retropepsin
55	40	47.1	1055	1 GNLJST	HIV-1 retropepsin
56	40	47.1	1055	2 S53092	pol polyprotein -
57	40	47.1	1733	1 RNBRY2L	DNA-directed RNA p
58	40	47.1	3083	2 AH2493	hypothetical prote
59	39	45.9	113	2 D72595	hypothetical prote
60	39	45.9	180	2 T44944	hypothetical prote
61	39	45.9	207	2 B75327	hypothetical prote
62	39	45.9	331	2 B48445	glyceralddehyde-3-p
63	39	45.9	361	2 F91207	hypothetical prote
64	39	45.9	361	2 H86053	hypothetical prote
65	39	45.9	361	2 C65171	ubiquinol-cytochro
66	39	45.9	379	2 I48133	ubiquinol-cytochro
67	39	45.9	379	2 I48132	ubiquinol-cytochro
68	39	45.9	379	2 I48134	ubiquinol-cytochro
69	39	45.9	379	2 I48180	ubiquinol-cytochro
70	39	45.9	428	2 JH0634	site-specific DNA-
71	39	45.9	491	2 F83383	probable flavin-bi
72	39	45.9	534	2 S69714	hypothetical prote
73	39	45.9	566	2 B84271	glutamy]-tRNA synt
74	39	45.9	591	2 S54788	calcium-stimulated
75	39	45.9	789	2 S28259	androgen-regulated
76	39	45.9	817	2 A82511	glycogen phosphory
77	39	45.9	942	2 A12530	hypothetical prote
78	39	45.9	1008	2 S38003	translation elonga
79	38.5	45.3	505	2 T19971	hypothetical prote
80	38.5	45.3	506	2 T19973	hypothetical prote
81	38	44.7	56	2 T03658	phosphoenolpyruvat
82	38	44.7	142	2 AF0961	heat shock protein
83	38	44.7	154	2 AC0496	heat shock protein
84	38	44.7	252	2 C84522	22 kDa peroxisomal
85	38	44.7	266	2 E90354	hypothetical prote
86	38	44.7	410	1 DBPSXA	3-methyl-2-oxobuta
87	38	44.7	410	2 C83365	2-oxoisovalerate d
88	38	44.7	477	2 T25798	hypothetical prote
89	38	44.7	480	2 H84747	probable steroid d
90	38	44.7	511	2 D70522	probable PAPAI pro
91	38	44.7	566	2 T09154	glucose-6-phosphat
92	38	44.7	568	2 S57830	glucose-6-phosphat
93	38	44.7	569	2 S23542	glucose-6-phosphat
94	38	44.7	569	2 S41806	glucose-6-phosphat
95	38	44.7	569	2 S57831	conserved hypochet
96	38	44.7	725	1 AB1187	replication licens
97	38	44.7	770	1 T03920	conserved hypochet
98	38	44.7	777	1 G69733	starch phosphoryla
99	38	44.7	841	2 T45633	starch phosphoryla
100	38	44.7	886	1 JCS085	replication licens

ALIGNMENTS

```
RESULT 1
T49731
hypothetical protein B24B19.30 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
C:Accession: T49731
R:Schlute, U.; Aigm, V.; Hohensei, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: Z25022
A:Accession: T49731
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <SCH>
A:Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.30
A:Experimental source: BAC clone B24B19; strain OR74A
C:Genetics:
A:Gene: NCSP:B24B19.30
A:Map position: 6
C:Superfamily: Neurospora crassa hypothetical protein B24B19.30

Query Match          52.9%; Score 45; DB 2; Length 108;
Best Local Similarity 50.0%; Pred. No. 3.6;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 CADPTLRWISFC 14
      |||||
Db      70 CQCQPIRWISMC 83

RESULT 2
S34189
starch phosphorylase (EC 2.4.1.1) L - potato
C:Species: Solanum tuberosum (potato)
C:Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S53489; S34189
R:Sommerwald, U.; Basner, A.; Greve, B.; Steup, M.
Plant Mol. Biol. 27, 567-576, 1995
A:Title: A second L-type isozyme of potato glucan phosphorylase: cloning, antisense inh
A:Reference number: S53489; MUID:95201249; PMID:7694019
A:Accession: S53489
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-974 <SO2>
A:Cross-references: UNIPROT:P53535; EMBL:X73684; NID:G313348; PIDN:CAA52036.1; PID:G3133
C:Superfamily: glucan phosphorylase
C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphate
F:820/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match          51.8%; Score 44; DB 2; Length 974;
Best Local Similarity 58.3%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 DGPTLRWISFC 14
      |||||
Db      619 NGVTPRRWISFC 630

RESULT 3
S00503
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - Pacific electric ray
C:Species: Torpedo californica (Pacific electric ray)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: S00503; S28885; S29880
R:Kawakami, K.; Noguchi, S.; Noda, M.; Takahashi, H.; Ohta, T.; Kawamura, M.; Nojima, H.
Nature 316, 733-736, 1985
A:Title: Primary structure of the alpha-subunit of Torpedo californica Na(+)+K(+)ATPase
A:Reference number: S00503; MUID:85296307; PMID:2993905
A:Accession: S00503
A:Molecule type: mRNA
A:Residues: 1-1022 <KAW1>
```

```
A:Cross-references: UNIPROT:P05025; EMBL:X02810; NID:G64399; PIDN:CAA26578.1; PID:G64400
A:Accession: S28885
A:Molecule type: protein
A:Residues: 228-240;431-438;535-550;671-690;1011-1022 <KAW2>
R:Ohta, T.; Nagano, K.; Yoshida, M.
Proc. Natl. Acad. Sci. U.S.A. 83, 2071-2075, 1986
A:Title: The active site structure of Na(+)/K(+)-transporting ATPase: location of the 5'
A:Reference number: S29880; MUID:86177549; PMID:3008150
A:Accession: S29880
A:Molecule type: protein
A:Residues: 386-402;502-512;671-689;887-906 <OHT>
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: Atp; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F:96-120/Domain: transmembrane #status predicted <TM1>
F:130-149/Domain: transmembrane #status predicted <TM2>
F:150-290/Domain: intracellular #status predicted <INT2>
F:291-318/Domain: transmembrane #status predicted <TM3>
F:320-348/Domain: transmembrane #status predicted <TM4>
F:349-785/Domain: intracellular #status predicted <INT3>
F:586-782/Domain: ATPase nucleotide-binding domain homology <ATN>
F:786-809/Domain: transmembrane #status predicted <TM5>
F:848-873/Domain: transmembrane #status predicted <TM6>
F:874-951/Domain: intracellular #status predicted <INT4>
F:952-977/Domain: transmembrane #status predicted <TM7>
F:978-1022/Domain: extracellular #status predicted <EXT>
F:376/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:507/Binding site: Atp (Lys) #status predicted
F:716,720,725/Active site: Asp, Asp, Lys #status predicted

Query Match          51.8%; Score 44; DB 1; Length 1022;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 PTLRWISFC 14
      |||||
Db      84 PTLRWISFC 93

RESULT 4
A24414
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - human
N:Alternate names: sodium pump; sodium/potassium transporting ATPase alpha-A chain
C:Species: Homo sapiens (man)
C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 09-Jul-2004
C:Accession: A24414; A27795; A39910; 160116; S09171
R:Kawakami, K.; Ohta, T.; Nojima, H.; Nagano, K.
J. Biochem. 100, 389-397, 1986
A:Title: Primary structure of the alpha-subunit of human Na,K-ATPase deduced from cDNA s
A:Reference number: A24414; MUID:87057096; PMID:2430951
A:Accession: A24414
A:Molecule type: mRNA
A:Residues: 1-1023 <KAW>
A:Cross-references: UNIPROT:P05023; EMBL:X04297; NID:G28926; PIDN:CAA27840.1; PID:G28927
R:Shull, M.M.; Lingrel, J.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
A:Title: Multiple genes encode the human Na+,K+-ATPase catalytic subunit.
A:Reference number: A9418; MUID:87231946; PMID:3035563
A:Accession: A27795
A:Molecule type: DNA
A:Residues: 168-189;213-214,'X',216-244 <SHU>
R:Chenab, F.F.; Kan, Y.W.; Law, M.L.; Hartz, J.; Kao, F.T.; Blotstein, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7901-7905, 1987
A:Title: Human placental Na+,K+-ATPase alpha subunit: cDNA cloning, tissue expression, E
A:Reference number: A39910; MUID:88068506; PMID:2891135
A:Accession: A39910
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 199-942 <CHE>
A:Cross-references: GB:J03007
R:Shull, M.M.; Pugh, D.G.; Lingrel, J.B.
Genomics 6, 451-460, 1990
A:Title: The human Na,K-ATPase alpha 1 gene: characterization of the 5'-flanking region
A:Reference number: I60116; MUID:90228961; PMID:1970326
```


A:Accession: I60116
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 C:Species: Arabidopsis thaliana
 A:Molecule type: DNA
 A:Residues: 1-61 <RBS>
 A:Cross-references: GB:M30310; NID:g179206; PIDN:AAAS1801.1; PID:g179208
 C:Genetics:
 A:Gene: GDB:ATP1A1
 A:Cross-references: GDB:119711; OMIM:182310
 A:Map position: 1p13-1p11
 C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;
 F:6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MT>
 F:6-95/Domain: intracellular #status predicted <INT1>
 F:96-120/Domain: transmembrane #status predicted <TM1>
 F:130-149/Domain: transmembrane #status predicted <TM2>
 F:150-290/Domain: intracellular #status predicted <INT2>
 F:291-313/Domain: transmembrane #status predicted <TM3>
 F:320-348/Domain: transmembrane #status predicted <TM4>
 F:349-786/Domain: intracellular #status predicted <INT3>
 F:587-783/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:787-810/Domain: transmembrane #status predicted <TM5>
 F:849-874/Domain: transmembrane #status predicted <TM6>
 F:875-952/Domain: intracellular #status predicted <INT4>
 F:953-978/Domain: transmembrane #status predicted <TM7>
 F:979-1023/Domain: extracellular #status predicted <EXT>
 F:376/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:508/Binding site: ATP (lys) #status predicted
 F:717,721,726/Active site: Asp, Asp, Lys #status predicted

Query Match 51.8%; Score 44; DB 2; Length 1023;
 Best Local Similarity 70.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14
 DB 84 PTPPEWIKFC 93

RESULT 5
 T47701
 translation initiation factor eIF-6-like protein [imported] - Arabidopsis thaliana
 M:Alternate names: protein F116.30
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C:Accession: T47701
 R:Bens, V.; Murnbach, E.; Dronek, H.; Ansgorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: Z24473
 A:Accession: T47701
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-245 <BEN>
 A:Cross-references: UNIPROT:Q9W060; EMBL:AL161667
 A:Experimental source: cultivar Columbia; BAC clone F116
 C:Genetics:
 A:Map position: 3
 A:Introns: 4/1; 36/2; 65/1; 80/1; 123/3; 160/3
 A:Note: F116.30
 C:Superfamily: conserved hypothetical protein YPR016c

Query Match 50.6%; Score 43; DB 2; Length 245;
 Best Local Similarity 53.8%; Pred. No. 17;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 ADGPTLRWISFC 14
 DB 194 AAGTVDWTSFC 206

RESULT 6
 T09084
 phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment)
 C:Species: Chlamydomonas reinhardtii

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: T09084
 R:Molendijk, A.J.; Irvine, R.F.
 Plant Mol. Biol. 37, 53-66, 1998
 A:Title: Inositolide signalling in Chlamydomonas: Characterization of a phosphatidylinositol
 A:Reference number: Z16411; MUID:98281574; PMID:9620264
 A:Accession: T09084
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-430 <MOL>
 A:Cross-references: UNIPROT:O04270; EMBL:U97663; NID:g2109290; PIDN:AAAS0018.1; PID:g210
 A:Experimental source: strain cw-15
 C:Genetics:
 A:Introns: 265/3; 331/3; 370/3; 455/1; 481/3

Query Match 50.6%; Score 43; DB 2; Length 490;
 Best Local Similarity 57.1%; Pred. No. 33;
 Matches 8; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 3 DGPPLR--EWISFC 14
 DB 250 DGPSTARWDEWLTFC 263

RESULT 7
 B37227
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
 C:Accession: B37227; 150395
 R:Takeyasu, K.; Lemas, V.; Fambrough, D.M.
 Am. J. Physiol. 259, C619-C630, 1990
 A:Title: Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms in evolution.
 A:Reference number: A37227; MUID:91023019; PMID:2171348
 A:Accession: B37227
 A:Molecule type: mRNA
 A:Residues: 1-1010 <TA2>
 A:Cross-references: UNIPROT:P24798; GB:M59960; NID:g212407; PIDN:AA48982.1; PID:g212407
 C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C:Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium c
 F:574-770/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:202-470/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:363/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:495/Binding site: ATP (lys) #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1010;
 Best Local Similarity 60.0%; Pred. No. 64;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14
 DB 71 PTPPEWIKFC 80

RESULT 8
 S00801
 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - human
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
 C:Accession: S00801; S04019; A27397; S02275
 R:Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Broude, N.E.; Ushkarev, Y.A.; Melkov, A.M.;
 dyanov, N.N.; Sverdlov, E.D.
 FEBS Lett. 233, 87-94, 1988
 A:Title: Family of human Na,K-ATPase genes. Structure of the gene for the catalytic sub
 A:Reference number: S00801; MUID:8825304; PMID:2838329
 A:Accession: S00801
 A:Molecule type: DNA
 A:Residues: 1-1013 <OV>
 A:Cross-references: UNIPROT:P13637; EMBL:M37456
 R:Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkarev, Y.A.; Melkov, A.M.; Smir
 ov, N.N.; Ovchinnikov, Y.A.
 Dokl. Biochem. 297, 426-431, 1987
 A:Title: Family of human Na(+),K(+)-ATPase genes. Structure of the gene of isoform alph

A:Reference number: S04019
 A:Accession: S04019
 A:Molecule type: DNA
 A:Residues: 1, 'E1H', 3-1013 <SVE1>
 A:Cross-references: EMBL:X12910; NID:Q28963
 A:Note: the authors translated the codon TTC for residue 283 as Ser and TCT for residue A:Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk S R.Sverdlov, E.D.; Monastyrskaya, G.S.; Broide, N.E.; Ushakov, Y.A.; Alilmet, R.L.; M lina, M.B.; Sverdlov, V.B.; Modyanov, N.N.; Ovchinnikov, Y.A.
 FEBS Lett. 217, 275-278, 1987
 A:Title: The family of human Na⁺/K⁺-ATPase genes. No less than five genes and/or pseudog
 A:Reference number: A27397; MUID:87247232; PMID:3036582
 A:Accession: A27397
 A:Molecule type: mRNA
 A:Residues: 243-434 <SVE2>
 A:Cross-references: GB:M27570
 C:Genetics:
 A:Gene: GDB:ATPIA3
 A:Cross-references: GDB:119713; OMIM:182350
 A:Map position: 19q13.2-19q13.2
 A:Intons: 2/3; 31/3; 51/3; 119/3; 157/3; 202/3; 242/1; 331/3; 398/1; 435/2; 479/3; 544/
 C:Superfamily: Na⁺/K⁺-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
 F:86-110/Domain: transmembrane #status predicted <TM1>
 F:120-138/Domain: transmembrane #status predicted <TM2>
 F:140-280/Domain: intracellular #status predicted <TM3>
 F:281-303/Domain: transmembrane #status predicted <TM4>
 F:310-333/Domain: transmembrane #status predicted <TM5>
 F:339-776/Domain: intracellular #status predicted <INT3>
 F:577-773/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:777-800/Domain: transmembrane #status predicted <TM5>
 F:839-864/Domain: transmembrane #status predicted <TM6>
 F:865-942/Domain: intracellular #status predicted <INT4>
 F:943-966/Domain: transmembrane #status predicted <TM7>
 F:969-1013/Domain: extracellular #status predicted <EXT>
 F:366/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:498/Binding site: Asp (Lys) #status predicted
 F:707,711,716/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 1; Length 1013;
 Best Local Similarity 60.0%; Pred. No. 64;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PTLREWISFC 14
 |||:
 Db 74 PTPPEWVKFC 83

RESULT 9
 Na⁺/K⁺-exchanging ATPase (EC 3.6.3.9) alpha-3 chain - rat
 C:Accession: C24639
 N:Alternate names: Na⁺/K⁺-transporting ATPase alpha(III) chain
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1988 #sequence revision 23-Apr-1993 #text_change 09-Jul-2004
 C:Accession: C24639; S00514; B27180; A60470
 R:Shull, G.E.; Greeb, U.; Lingrel, J.B.
 Biochemistry 25, 8125-8132, 1986
 A:Title: Molecular cloning of three distinct forms of the Na⁺/K⁺-ATPase alpha-subunit fr
 A:Reference number: A90512; MUID:87128908; PMID:3028470
 A:Accession: C24639
 A:Molecule type: mRNA
 A:Residues: 1-1013 <SHU>
 A:Cross-references: UNIPROT:P06687; EMBL:M14513; NID:G203030; PIDN:AAA40777.1; PID:G2030
 A:Note: in the authors' translation 405-Ser is shown after residue 409 and, consequently
 J.Harz, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Kojima, T.; Ohta, T.; N
 J Biochem 102, 43-58, 1987
 A:Title: Primary structures of two types of alpha-subunit of rat brain Na(+) ,K(+) -ATPase
 A:Reference number: S00460; MUID:88032933; PMID:2822682
 A:Accession: S00514
 A:Molecule type: mRNA
 A:Residues: 1-907, 'C', 909-1013 <HAR>
 A:Cross-references: EMBL:X05883; NID:G55769; PIDN:CAA29307.1; PID:G55770
 R:Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard, B.

J. Cell Biol. 105, 1855-1865, 1987
 A:Title: Three differentially expressed Na⁺/K⁺-ATPase alpha subunit isoforms: structural a
 A:Reference number: A52749; MUID:88033255; PMID:2822726
 A:Accession: B27180
 A:Molecule type: mRNA
 A:Residues: 1, 'NL', 4-103, 'R', 105-113, 'E', 115-127, 'G', 129-148, 'Q', 150-151, 'T', 153-165, 'D'
 A:Cross-references: EMBL:M26648; NID:G205633; PIDN:AAA1672.1; PID:G205634
 A:Note: the authors translated the codon CAG for residue 149 as Glu, CGC for residue 194
 R.Hsu, Y.M.; Guidotti, G.
 Biochemistry 28, 569-573, 1989
 A:Title: Rat brain has the alpha3 form of the (Na⁺/K⁺)ATPase.
 A:Reference number: A60470; MUID:89229049; PMID:2540801
 A:Accession: A60470
 A:Molecule type: protein
 A:Residues: 117-132;586-595, 'X', 597-601 <HSU>
 C:Comment: The alpha-3 form appears to be highly ouabain-inhibitable, as is alpha-2 but
 C:Genetics:
 A:Gene: NKAA3
 C:Superfamily: Na⁺/K⁺-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
 F:86-110/Domain: transmembrane #status predicted <TM1>
 F:120-138/Domain: transmembrane #status predicted <TM2>
 F:140-280/Domain: intracellular #status predicted <INT2>
 F:281-303/Domain: transmembrane #status predicted <TM3>
 F:310-338/Domain: transmembrane #status predicted <TM4>
 F:339-776/Domain: intracellular #status predicted <INT3>
 F:577-773/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:777-800/Domain: transmembrane #status predicted <TM5>
 F:839-864/Domain: transmembrane #status predicted <TM6>
 F:865-942/Domain: intracellular #status predicted <INT4>
 F:943-966/Domain: transmembrane #status predicted <TM7>
 F:969-1013/Domain: extracellular #status predicted <EXT>
 F:366/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:498/Binding site: Asp (Lys) #status predicted
 F:707,711,716/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1013;
 Best Local Similarity 60.0%; Pred. No. 64;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PTLREWISFC 14
 |||:
 Db 74 PTPPEWVKFC 83

RESULT 10
 Na⁺/K⁺-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 16-Sep-1992 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C:Accession: I50394; A37227
 R:Takeyasu, K.; Lemas, M.; Fambrough, D.M.
 Am. J. Physiol. 259, C619-C630, 1990
 A:Title: Stability of the Na⁺/K⁺-ATPase alpha-subunit isoforms in evolution.
 A:Reference number: A37227; MUID:91023019; PMID:2171348
 A:Accession: A37227
 A:Molecule type: mRNA
 A:Residues: 3-1017 <TA2>
 C:Superfamily: Na⁺/K⁺-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C:Keywords: ATP; glycoprotein; hydrolase; phosphoprotein
 F:1581-777/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:210,478/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:371/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1017;
Best Local Similarity 60.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PTLREWISFC 14
DB 79 PTLPEWVKFC 88

RESULT 11

A34474
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - human
N/Alternate names: Na+/K+-exchanging ATPase alpha chain-4; sodium/potassium transporting
C/Species: Homo sapiens (man)
C/Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C/Accession: A34474; B27795; D27397
R/Shull, M.M.; Pugh, D.G.; Lingrel, J.B.
J. Biol. Chem. 264, 17532-17543, 1989
A/Title: Characterization of the human Na,K-ATPase alpha2 gene and identification of int
A/Reference number: A34474; MUID:90008924; PMID:2477373
A/Accession: A34474
A/Molecule type: DNA
A/Residues: 1-1020 <SHU>
A/Cross-references: UNIPROT:P50993; GB:J05096; NID:g179164; PIDN:AAA51797.1; PID:g179165
R/Shull, M.M.; Lingrel, J.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 4039-4043, 1987
A/Title: Multiple genes encode the human Na+,K+-ATPase catalytic subunit.
A/Reference number: A94158; MUID:87231946; PMID:3035563
A/Accession: B27795
A/Molecule type: DNA
A/Residues: 211-249 <SH2>
A/Cross-references: GB:M16795; NID:g179196; PIDN:AAA51799.1; PID:g553194
R/Sverdlov, E.D.; Monastyrskaya, G.S.; Broude, N.E.; Ushkaryov, Y.A.; Allikmets, R.L.; W
PNS, M.B.; Sverdlov, V.E.; Modyanov, N.N.; Ovchinnikov, Y.A.
FEBS Lett. 217, 275-278, 1987
A/Title: The family of human Na+,K+-ATPase genes. No less than five genes and/or pseudog
A/Reference number: A27397; MUID:87247232; PMID:3036582
A/Accession: D27397
A/Molecule type: DNA
A/Residues: 251-442 <SVE>
A/Cross-references: GB:M27571
C/Genetics: GDB:ATP1A2
A/Gene: GDB:ATP1A2
A/Cross-references: GDB:119712; OMIM:182340
A/Map position: 1q21-1q23
C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C/Keyword: ATP, heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F/6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MAT>
F/6-93/Domain: intracellular #status predicted <INT1>
F/94-118/Domain: transmembrane #status predicted <TM1>
F/128-147/Domain: transmembrane #status predicted <TM2>
F/148-288/Domain: intracellular #status predicted <INT2>
F/189-311/Domain: transmembrane #status predicted <TM3>
F/318-346/Domain: transmembrane #status predicted <INT3>
F/347-783/Domain: intracellular #status predicted <INT4>
F/584-780/Domain: ATPase nucleotide-binding domain homology <ATN>
F/784-807/Domain: transmembrane #status predicted <TM5>
F/846-871/Domain: transmembrane #status predicted <TM6>
F/872-949/Domain: intracellular #status predicted <INT4>
F/950-975/Domain: transmembrane #status predicted <TM7>
F/976-1020/Domain: extracellular #status predicted <EXT>
F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
F/505/Binding site: ATP (lys) #status predicted
F/714,718,723/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1020;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PTLREWISFC 14
DB 82 PTLPEWVKFC 91

RESULT 12

B24639

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-2 chain - rat

N/Alternate names: Na+/K+-transporting ATPase alpha-plus chain

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004

C/Accession: B24639

R/Shull, G.E.; Greed, J.; Lingrel, J.B.

Biochemistry 25, 8125-8132, 1986

A/Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit f

A/Reference number: A90512; MUID:87128908; PMID:3028470

A/Accession: B24639

A/Molecule type: mRNA

A/Residues: 1-1020 <SHU>

A/Cross-references: UNIPROT:P06686; EMBL:M14512; NID:g203028; PIDN:AAA40776.1; PID:g203

C/Genetics: NKA2

C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain

C/Keyword: ATP, heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans

F/6-1020/Product: Na+/K+-transporting ATPase alpha-2 chain #status predicted <MAT>

F/6-93/Domain: intracellular #status predicted <INT1>

F/94-119/Domain: transmembrane #status predicted <TM1>

F/128-147/Domain: transmembrane #status predicted <INT2>

F/148-288/Domain: intracellular #status predicted <INT3>

F/189-311/Domain: transmembrane #status predicted <TM3>

F/318-346/Domain: transmembrane #status predicted <INT4>

F/347-783/Domain: intracellular #status predicted <INT5>

F/584-780/Domain: ATPase nucleotide-binding domain homology <ATN>

F/784-807/Domain: transmembrane #status predicted <TM5>

F/846-871/Domain: transmembrane #status predicted <TM6>

F/872-949/Domain: intracellular #status predicted <INT4>

F/950-975/Domain: transmembrane #status predicted <TM7>

F/976-1020/Domain: extracellular #status predicted <EXT>

F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted

F/505/Binding site: ATP (lys) #status predicted

F/714,718,723/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1020;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PTLREWISFC 14
DB 82 PTLPEWVKFC 91

RESULT 13

PMSHNA

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - sheep

N/Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha cha

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004

C/Accession: A01074; A35426

R/Shull, G.E.; Schwartz, A.; Lingrel, J.B.

Nature 316, 691-695, 1985

A/Title: Amino-acid sequence of the catalytic subunit of the (Na(+)+K(+)) ATPase deduce

A/Reference number: A01074; MUID:85296299; PMID:2993903

A/Accession: A01074

A/Molecule type: mRNA

A/Residues: 1-1021 <SHU>

A/Cross-references: UNIPROT:P04074; GB:X02813; NID:g1205; PIDN:CAA6581.1; PID:g1206

R/Hinz, H.R.; Kiley, T.L.

J. Biol. Chem. 265, 10260-10265, 1990

A/Title: Lysine 480 is an essential residue in the putative ATP site of lamb kidney (Na

A/Reference number: A35426; MUID:90285144; PMID:2162343

A/Accession: A35426

A/Molecule type: preliminary

A/Status: preliminary

A/Residues: 475-492 <HIN>

C/Comment: This is the catalytic component of the active enzyme, which catalyzes the hy

n function.

C/Comment: This enzyme is specifically inhibited by cardiac glycosides such as digoxin
 C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C/Keywords: ATP; hydrolase; phosphoprotein; potassium transport; sodium transport; trans
 F/6-1021/Product: Na+/K+-transporting ATPase alpha chain #status predicted <MAT>
 F/128-114/Domain: transmembrane #status predicted <TM1>
 F/128-115/Domain: transmembrane #status predicted <TM2>
 F/289-311/Domain: transmembrane #status predicted <TM3>
 F/318-346/Domain: transmembrane #status predicted <TM4>
 F/585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
 F/785-808/Domain: transmembrane #status predicted <TM5>
 F/847-872/Domain: transmembrane #status predicted <TM6>
 F/951-976/Domain: transmembrane #status predicted <TM7>
 F/315/Binding site: cardiac glycoside (TTP) #status predicted
 F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F/506/Binding site: ATP (Lys) #status predicted

Query Match 50.6%; Score 43; DB 1; Length 1021;
 Best Local Similarity 60.0%; Pred. No. 65;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWSFC 14
 |||:
 Db 82 PTPPEWVKFC 91

RESULT 14

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - horse
 S04630
 C/Species: Equus caballus (domestic horse)
 C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004

C/Accession: S04630
 R/Kano, I.; Nagai, F.; Satoh, K.; Ushiyama, K.; Nakao, T.; Kano, K.
 FEBS Lett. 250, 91-98, 1989
 A/Title: Structure of the alpha(1) subunit of horse Na,K-ATPase gene.
 A/Reference number: S04630; MUID:89290042; PMID:2544461

A/Accession: S04630
 A/Molecule type: DNA

A/Residues: 1-1021 <KAN>
 A/Reference number: UNIPROT:P18907; EMBL:X16773; NID:g1010; PIDN:CAA34716.1; PID:8871026

C/Genetics:
 A/Introns: 4/3; 39/3; 127/3; 165/3; 210/3; 339/3; 406/1; 442/3; 487/3; 552/
 C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp

F/6-1021/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>
 F/6-93/Domain: intracellular #status predicted <INT1>
 F/94-118/Domain: transmembrane #status predicted <TM1>
 F/128-147/Domain: transmembrane #status predicted <TM2>
 F/148-288/Domain: intracellular #status predicted <INT2>
 F/289-311/Domain: transmembrane #status predicted <TM3>
 F/318-346/Domain: transmembrane #status predicted <TM4>
 F/347-784/Domain: intracellular #status predicted <INT3>
 F/585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
 F/785-808/Domain: transmembrane #status predicted <TM5>
 F/847-872/Domain: transmembrane #status predicted <TM6>
 F/873-950/Domain: intracellular #status predicted <INT4>
 F/951-976/Domain: transmembrane #status predicted <TM7>
 F/977-1021/Domain: extracellular #status predicted <EXT1>
 F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F/506/Binding site: ATP (Lys) #status predicted

F/715-719,724/Active site: Asp, Asp, Lys #status predicted
 Query Match 50.6%; Score 43; DB 1; Length 1021;
 Best Local Similarity 60.0%; Pred. No. 65;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWSFC 14
 |||:
 Db 82 PTPPEWVKFC 91

Qy 5 PTLREWSFC 14
 |||:
 Db 82 PTPPEWVKFC 91

RESULT 15

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - chicken
 A28199

C/Species: Gallus gallus (chicken)
 C/Date: 21-Sep-1988 #sequence_revision 21-Sep-1988 #text_change 09-Jul-2004
 C/Accession: A28199
 R/Takeyasu, K.; Tamkun, M.M.; Renaud, K.U.; Fambrough, D.M.
 J. Biol. Chem. 263, 4347-4354, 1988

A/Title: Ouabain-sensitive (Na(+)+K(+))-ATPase activity expressed in mouse L cells by
 A/Reference number: A28199; MUID:88153759; PMID:2831227

A/Accession: A28199
 A/Status: preliminary; not compared with conceptual translation

A/Residues: 1-1021 <TAK>
 A/Molecule type: mRNA

A/Accession: UNIPROT:P09572; GB:J03230; NID:g211219; PIDN:AAA48607.1; PID:g211220
 C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C/Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; transmembrane protein
 F/585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
 F/213,481/Binding site: carboxylate (Asn) (covalent) #status predicted
 F/374/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F/506/Binding site: ATP (Lys) #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1021;
 Best Local Similarity 60.0%; Pred. No. 65;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWSFC 14
 |||:
 Db 82 PTPPEWVKFC 91

RESULT 16

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - pig
 B24862
 N/Alternate names: sodium pump alpha chain; sodium/potassium-dependent ATPase alpha cha

C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C/Accession: B24862; 146572; A35504; S00011; S00502; S02569; S29762

R/Ovchinnikov, Y.A.; Modyanov, N.N.; Browde, N.E.; Petrunkin, K.E.; Grishin, A.V.; Arzam
 FEBS Lett. 201, 237-245, 1986
 A/Title: Pig kidney Na+,K+-ATPase. Primary structure and spatial organization.
 A/Reference number: A31361; MUID:86220813; PMID:2423371

A/Accession: B24862
 A/Molecule type: mRNA

A/Residues: 1-1021 <OVCA>
 A/Cross-References: UNIPROT:P05024; EMBL:X03938; NID:g1897; PIDN:CAA27576.1; PID:g1898

A/Note: the authors translated the codon TGC for residue 391 as Phe, TGC for residue 723
 A/Note: part of this sequence, including the amino and carboxyl end of the mature protei

R/Ovchinnikov, Y.A.; Monastyrskaya, G.S.; Arsenyan, S.G.; Browde, N.E.; Petrunkin, K.E.;
 Dokl. Biochem. 283, 270-272, 1985
 A/Title: Amino acid sequence of the 17-kilodalton fragment of the cytoplasmic region of

A/Reference number: 146572
 A/Accession: 146572

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA

A/Residues: 469-617 <OVCA>
 A/Cross-References: GB:M2512; NID:g164385; PIDN:AAA31004.1; PID:g164386

R/Karlish, S.J.D.; Goldsleger, R.; Stein, W.D.
 Proc. Natl. Acad. Sci. U.S.A. 87, 4566-4570, 1990
 A/Title: A 19-kDa C-terminal tryptic fragment of the alpha chain of Na/K-ATPase is essen

A/Reference number: A35504; MUID:90280416; PMID:2162048
 A/Accession: A35504

A/Molecule type: protein
 A/Residues: 836-845, 'R', 847-851 <KAR>

R/Ovchinnikov, Y.A.; Arzamazova, N.M.; Arystarkhova, E.A.; Gevondyan, N.M.; Aldanova, N.
 FEBS Lett. 217, 269-274, 1987
 A/Title: Detailed structural analysis of exposed domains of membrane-bound Na+,K+-ATPase
 A/Reference number: S00011; MUID:87247231; PMID:3036581

A/Contents: annotation; membrane topology
 R/Ovchinnikov, Y.A.; Luneva, N.M.; Arystarkhova, E.A.; Gevondyan, N.M.; Arzamazova, N.M.
 FEBS Lett. 227, 230-234, 1988
 A/Title: Topology of Na, K-ATPase: identification of the extra- and intracellular hydroxy

A/Reference number: S02569; MUID:88112252; PMID:2448169
 A/Contents: annotation; membrane topology
 C/Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C/Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp

F:6-1021/Product: Na+/K+-transporting ATPase alpha chain #status experimental <MAT>
 F:6-93/Domain: intracellular #status predicted <INT1>
 F:194-118/Domain: transmembrane #status predicted <TM1>
 F:128-147/Domain: transmembrane #status predicted <TM2>
 F:148-288/Domain: intracellular #status predicted <INT2>
 F:289-311/Domain: transmembrane #status predicted <TM3>
 F:318-346/Domain: transmembrane #status predicted <TM4>
 F:347-784/Domain: intracellular #status predicted <INT3>
 F:585-781/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:785-808/Domain: transmembrane #status predicted <TM5>
 F:847-872/Domain: transmembrane #status predicted <TM6>
 F:873-950/Domain: intracellular #status predicted <INT4>
 F:951-976/Domain: transmembrane #status predicted <TM7>
 F:977-1021/Domain: extracellular #status predicted <EXT>
 F:374/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:506/Binding site: ATP (lys) #status predicted
 F:715,719,724/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1021;
 Best Local Similarity 60.0%; Pred. No. 65;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14
 DB 82 PTPPEWVKFC 91

RESULT 17

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - European eel
 S49127
 C:Species: Anguilla anguilla (European eel)
 C:Date: 01-Feb-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
 C:Accession: S49127

R:Cutler, C.; Sanders, I.L.; Cramb, G.

Submitted to the EMBL Data Library, November 1993

A:Reference number: S45093

A:Accession: S49127

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1022 <CUT>

C:Cross-references: UNIPROT:Q92030; EMBL:X76108; NID:G509405; PIDN:CAA53714.1; PID:G5094
 C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C:Keywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; transmem-
 F:586-782/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:214,482/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:375/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:507/Binding site: ATP (lys) #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1022;
 Best Local Similarity 60.0%; Pred. No. 65;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14
 DB 83 PTPPEWVKFC 92

RESULT 18

Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain [validated] - rat
 A24639
 N:Alternate names: Na+/K+-transporting ATPase alpha chain, kidney-type
 N:Containing: Na+/K+-transporting ATPase alpha-S chain
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
 C:Accession: A24639; S00460; A27180; S11020; A25171; S29877; S10758
 R:Shull, G.E.; Greeb, J.; Lingrel, J.B.

Biochemistry 25, 8125-8132, 1986

A:Title: Molecular cloning of three distinct forms of the Na+,K+-ATPase alpha-subunit fr

A:Accession: A24639

A:Molecule type: mRNA

A:Residues: 1-1023 <SHU>

A:Cross-references: UNIPROT:P06685; EMBL:M14511; NID:G203026; PIDN:AAA40775.1; PID:G2030

R:Hara, Y.; Urayama, O.; Kawakami, K.; Nojima, H.; Nagamune, H.; Kojima, T.; Ohta, T.; I
 U. Biochem. 102, 43-58, 1987

A:Title: Primary structures of two types of alpha-subunit of rat brain Na(+),K(+)-ATPase

A:Reference number: S00460; MUID:88032933; PMID:2822682

A:Accession: S00460

A:Molecule type: mRNA

A:Residues: 1-1023 <HAR>

A:Cross-references: EMBL:X05882; NID:G55771; PIDN:CAA29306.1; PID:G55772

R:Herrera, V.L.M.; Emanuel, J.R.; Ruiz-Opazo, N.; Levenson, R.; Nadal-Ginard, B.

J. Cell Biol. 105, 1855-1865, 1987

A:Title: Three differentially expressed Na,K-ATPase alpha subunit isoforms: structural

A:Reference number: A92749; MUID:88033255; PMID:2822726

A:Accession: A27180

A:Molecule type: mRNA

A:Residues: 1-67, 'PV', 70-174, 'E', 176-187, 'V', 189-334, 'V', 336-1023 <HER>

A:Cross-references: EMBL:X28647; NID:G205631; PIDN:AAA41671.1; PID:G205632

R:Yagawa, Y.; Kawakami, K.; Nagano, K.

Biochim. Biophys. Acta 1049, 286-292, 1990

A:Title: Cloning and analysis of the 5'-flanking region of rat Na(+)/K(+)-ATPase alpha-1

A:Reference number: S11020; MUID:90344872; PMID:2166579

A:Accession: S11020

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-41 <YAG>

A:Cross-references: EMBL:X53233

R:Schneider, J.W.; Mercer, R.W.; Caolan, M.; Emanuel, J.R.; Sweadner, K.J.; Benz Jr., B

Proc. Natl. Acad. Sci. U.S.A. 82, 6357-6361, 1985

A:Title: Molecular cloning of rat brain Na,K-ATPase alpha-subunit cDNA.

A:Reference number: A25171; MUID:85298352; PMID:2994074

A:Accession: A25171

A:Molecule type: mRNA

A:Residues: 489-533 <SCH>

R:Lytton, J.

Biochem. Biophys. Res. Commun. 132, 764-769, 1985

A:Title: The catalytic subunits of the (Na(+),K(+))-ATPase alpha and alpha(+) isozymes

A:Reference number: S29877; MUID:86050667; PMID:2998384

A:Accession: S29877

A:Status: preliminary

A:Molecule type: protein

A:Residues: 6-19 <LYT>

R:Kurimura, K.; Hosoi, K.; Kodama, A.; Ueha, T.

Biochim. Biophys. Acta 1039, 234-240, 1990

A:Title: A new electrophoretic variant of alpha subunit of Na(+)/K(+)-ATPase from the B

A:Reference number: S10758; MUID:90304196; PMID:2163680

A:Accession: S10758

A:Molecule type: protein

A:Residues: 6, 'X', 8-10, 'X', 12-16 <KUR>

A:Experimental source: submandibular gland

A>Note: designated alpha-S form; thought to arise from alpha-1 chain by post-translation

C:Genetics:

A:Gene: NKXAI

A:Introns: 4/3

A>Note: the list of introns may be incomplete

C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain

C:Keywords: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium trans

F:6-95/Domain: intracellular #status predicted <INT1>
 F:6-95/Domain: intracellular #status predicted <INT2>
 F:130-149/Domain: transmembrane #status predicted <TM1>
 F:150-290/Domain: intracellular #status predicted <INT2>
 F:291-313/Domain: transmembrane #status predicted <TM2>
 F:320-348/Domain: transmembrane #status predicted <TM3>
 F:349-786/Domain: intracellular #status predicted <INT3>
 F:587-783/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:787-810/Domain: transmembrane #status predicted <TM5>
 F:849-874/Domain: transmembrane #status predicted <TM6>
 F:875-952/Domain: intracellular #status predicted <INT4>
 F:953-978/Domain: transmembrane #status predicted <TM7>
 F:979-1023/Domain: extracellular #status predicted <EXT>
 F:376/Active site: Asp (aspartylphosphate intermediate) #status predicted
 F:508/Binding site: ATP (lys) #status predicted
 F:717,721,726/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 1; Length 1023;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PTLREWISFC 14
|||:|
Db 84 PTPPEWVKFC 93

RESULT 19
S24650
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha-1 chain - giant toad
C/Species: Bufo marinus (giant toad)
C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C/Accession: A43451; S24650
R./Jalil, F.; Canessa, C.M.; Horisberger, J.D.; Rossier, B.C.
J. Biol. Chem. 267, 16895-16903, 1992
A./Title: Primary sequence and functional expression of a novel ouabain-resistant Na,K-ATPase
A./Reference number: A43451; MUID:92380991; PMID:1380956
A./Accession: A43451
A./Status: preliminary
A./Molecule type: mRNA
A./Residues: 1-1023 <JAI>
A./Cross-references: UNIPROT:P30714; EMBL:Z11798; NID:G62491; PIDN:CAA77842.1; PID:G62492
A./Note: submitted to the EMBL Data Library, March 1992
A./Note: sequence extracted from NCBI backbone (NCBIP:111876)
C./Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C./Keywords: ATP, heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F.6-1023/Product: Na+/K+-transporting ATPase alpha-1 chain #status predicted <MAT>
F.6-99/Domain: intracellular #status predicted <INT1>
F.96-120/Domain: transmembrane #status predicted <TM2>
F.130-149/Domain: transmembrane #status predicted <INT2>
F.150-290/Domain: intracellular #status predicted <INT2>
F.291-313/Domain: transmembrane #status predicted <TM3>
F.320-348/Domain: transmembrane #status predicted <INT3>
F.349-786/Domain: intracellular #status predicted <INT3>
F.587-783/Domain: ATPase nucleotide-binding domain homology <ATN>
F.787-810/Domain: transmembrane #status predicted <TM5>
F.849-874/Domain: transmembrane #status predicted <TM5>
F.875-956/Domain: intracellular #status predicted <INT4>
F.953-978/Domain: transmembrane #status predicted <TM7>
F.979-1023/Domain: extracellular #status predicted <EXT>
F.376/Active site: Asp (aspartylphosphate intermediate) #status predicted
F.508/Binding site: Asp (Lys) #status predicted
F.717,721,726/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 1; Length 1023;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PTLREWISFC 14
|||:|
Db 84 PTPPEWVKFC 93

RESULT 20
A60444
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain precursor - African clawed frog
N./Alternate names: sodium pump alpha chain
C/Species: Xenopus laevis (African clawed frog)
C/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C/Accession: A60444
R./Verrey, F.; Kailou, P.; Schaefer, E.; Fuentes, P.; Geering, K.; Rossier, B.C.; Kraehe
Am. J. Physiol. 256, F1034-F1043, 1989
A./Title: Primary sequence of Xenopus laevis Na(+)-K(+)-ATPase and its localization in A6
A./Reference number: A60444; MUID:89285429; PMID:2544104
A./Accession: A60444
A./Status: not compared with conceptual translation
A./Molecule type: mRNA
A./Residues: 1-1025 <VER>
A./Cross-references: UNIPROT:Q92123; GB:U10108; NID:G499225; PIDN:AAA19022.1; PID:G499226
C./Note: The alpha chain is the catalytic chain.

C./Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C./Keywords: ATP, glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium tr
F.583-785/Domain: ATPase nucleotide-binding domain homology <ATN>
F.217,485/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.378/Active site: Asp (aspartylphosphate intermediate) #status predicted
F.510/Binding site: ATP (Lys) #status predicted

Query Match 50.6%; Score 43; DB 2; Length 1025;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PTLREWISFC 14
|||:|
Db 86 PTPPEWVKFC 95

RESULT 21
PMCCMN
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - white sucker
C/Species: Catostomus commersoni (white sucker)
C/Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C/Accession: S14740
R./Schoenrock, C.; Morley, S.D.; Okawara, Y.; Lederis, K.; Richter, D.
Biol. Chem. Hoppe-Seyler 372, 279-286, 1991
A./Title: Sodium and potassium ATPase of the teleost fish Catostomus commersoni. Sequence
A./Reference number: S14740; MUID:91282983; PMID:1711856
A./Accession: S14740
A./Molecule type: mRNA
A./Residues: 1-1027 <SCH>
A./Cross-references: UNIPROT:P25489; EMBL:X58629; NID:G62641; PIDN:CAA41483.1; PID:G62642
C./Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C./Keywords: ATP, hydrolase, ion transport, phosphoprotein; potassium transport; sodium t
F.99-124/Domain: transmembrane #status predicted <TM1>
F.133-152/Domain: transmembrane #status predicted <INT2>
F.153-293/Domain: intracellular #status predicted <INT2>
F.294-316/Domain: transmembrane #status predicted <TM3>
F.323-351/Domain: transmembrane #status predicted <INT3>
F.352-790/Domain: intracellular #status predicted <INT3>
F.591-787/Domain: ATPase nucleotide-binding domain homology <ATN>
F.791-814/Domain: transmembrane #status predicted <TM5>
F.853-878/Domain: transmembrane #status predicted <TM6>
F.879-956/Domain: intracellular #status predicted <INT4>
F.957-987/Domain: transmembrane #status predicted <TM7>
F.983-1027/Domain: extracellular #status predicted <EXT>
F.379/Active site: Asp (aspartylphosphate intermediate) #status predicted
F.512/Binding site: ATP (Lys) #status predicted
F.721,725,730/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 1; Length 1027;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PTLREWISFC 14
|||:|
Db 87 PTPPEWVKFC 96

RESULT 22
S03632
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - fruit fly (Drosophila melanogaster)
N./Alternate names: sodium pump alpha chain
C/Species: Drosophila melanogaster
C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C/Accession: S03632; S07049
R./Leibovitz, R.M.; Takeyasu, K.; Fambrough, D.M.
EMBO J. 8, 193-202, 1989
A./Title: Molecular characterization and expression of the (Na+K)-ATPase alpha-subunit fr
A./Reference number: S03632; MUID:89231618; PMID:2549556
A./Accession: S03632
A./Status: not compared with conceptual translation
A./Molecule type: mRNA
A./Residues: 1-1038 <LEB>
A./Cross-references: UNIPROT:P13607; EMBL:X14476
A./Note: the sequence from Fig. 9 is inconsistent with that from Fig. 8 in having 89-Asp,

A>Note: it is uncertain whether Met-1 or Met-40 is the initiator
R.Vareli, A.; Gilmore-Heber, M.; Benz Jr., B.J.
FEBS Lett. 258, 203-207, 1989
A>Title: Amplification of the phosphorylation site - ATP-binding site cDNA fragment of
A:Reference number: S07049; MUID:90092469; PMID:2557235
A:Accession: S07049
A:Molecule type: mRNA
A:Residues: 397-521 <VAR>
A:Cross-references: EMBL:X17471
A>Note: the authors translated the codon ACC for residue 3 as Asn and AAT for residue 89
C:Genetics:
A:Gene: FlyBase:Atp-alpha
A:Cross-references: FlyBase:Fgn0002921
A:Map position: 3R 93B
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keyword: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F:113-135/Domain: transmembrane #status predicted <TM1>
F:146-165/Domain: transmembrane #status predicted <TM2>
F:166-305/Domain: intracellular #status predicted <INT2>
F:306-328/Domain: transmembrane #status predicted <TM3>
F:335-363/Domain: transmembrane #status predicted <TM4>
F:364-801/Domain: intracellular #status predicted <INT3>
F:602-798/Domain: ATPase nucleotide-binding domain homology <ATN>
F:802-825/Domain: transmembrane #status predicted <TM5>
F:864-889/Domain: transmembrane #status predicted <TM6>
F:890-963/Domain: intracellular #status predicted <INT4>
F:967-993/Domain: transmembrane #status predicted <TM7>
F:994-1038/Domain: extracellular #status predicted <EXT>
F:391/Active site: Asp (Aspartylphosphate intermediate) #status predicted
F:523/Binding site: ATP (Lys) #status predicted
F:732,736,741/Active site: Asp, Asp, Lys #status predicted

Query Match 50.6%; Score 43; DB 1; Length 1038;
Best Local Similarity 44.4%; Pred. No. 66;
Matches 8; Conservative 1; Mismatches 3; Indels 6; Gaps 1;
QY 3 DGPFLR-----EWISFC 14
DB 93 DGNLTPPKQTPPEWVKFC 110

RESULT 23
JH0470
Na+/K+-exchanging ATPase (BC 3.6.3.9) alpha chain (clone pATN136) - brine shrimp
C:Species: Artemia franciscana (brine shrimp)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JH0470; S24196
R:Macias, M.T.; Palmero, I.; Sastre, L.
Gene 105, 197-204, 1991
A>Title: Cloning of a cDNA encoding an Artemia franciscana Na/K ATPase alpha-subunit.
A:Reference number: JH0470; MUID:92039032; PMID:1657719
A:Accession: JH0470
A:Molecule type: mRNA
A:Residues: 1-1004 <NAC>
A:Cross-references: UNIPROT:P28774; EMBL:X56650; NID:g10933; PIDD:CA39972.1; PID:g10934
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keyword: ATP; heterodimer; hydrolase; ion transport; phosphoprotein; potassium transp
F:2-1004/Product: Na+/K+-transporting ATPase alpha chain #status predicted <NMT>
F:2-75/Domain: intracellular #status predicted <INT1>
F:76-97/Domain: transmembrane #status predicted <TM1>
F:111-130/Domain: transmembrane #status predicted <TM2>
F:131-271/Domain: intracellular #status predicted <INT2>
F:272-296/Domain: transmembrane #status predicted <TM3>
F:301-329/Domain: transmembrane #status predicted <TM4>
F:330-767/Domain: intracellular #status predicted <INT>
F:368-764/Domain: ATPase nucleotide-binding domain homology <ATN>
F:768-791/Domain: transmembrane #status predicted <TM5>
F:830-855/Domain: transmembrane #status predicted <TM6>
F:856-936/Domain: intracellular #status predicted <INT4>
F:937-955/Domain: transmembrane #status predicted <TM7>
F:956-1004/Domain: extracellular #status predicted <EXT>
F:357/Active site: Asp (aspartylphosphate intermediate) #status predicted
F:489/Binding site: ATP (Lys) #status predicted

F:698,702,707/Active site: Asp, Asp, Lys #status predicted

Query Match 50.0%; Score 42.5; DB 2; Length 1004;
Best Local Similarity 47.4%; Pred. No. 77;
Matches 9; Conservative 0; Mismatches 3; Indels 7; Gaps 1;
QY 3 DGP-----TLREWISFC 14
DB 55 DGNCLTPPKTPPEWVKFC 73

RESULT 24
F6876
hypothetical protein yuJA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: F6876
R:Boletín, A.; Wincker, P.; Manger, S.; Jallón, O.; Malarme, K.; Weissenbach, J.; Ehr1
Genome Res. 11, 731-753, 2001
A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11374771
A:Accession: F6876
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-312 <STO>
A:Cross-references: UNIPROT:Q9CE34; GB:AE005176; PIDD:g12725061; PIDD:AAK06112.1; GSPDB:
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yuJA

Query Match 49.4%; Score 42; DB 2; Length 312;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 4 GPTLRWIS 12
DB 242 GPLKEMIS 250

RESULT 25
D69226
hypothetical protein MTH943 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Dec-2002
C:Accession: D69226
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jilwan, N
kl, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A>Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: D69226
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-522 <MTH>
A:Cross-references: GB:AE000868; GB:AE000666; NID:g2622025; PIDD:AB85441.1; PID:g26220
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH943
A:Start codon: GTG
C:Superfamily: uncharacterized conserved protein

Query Match 49.4%; Score 42; DB 2; Length 522;
Best Local Similarity 70.0%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 ADGPTLRWMI 11
DB 198 ADGTVTWEVI 207

RESULT 26
S62941

probable membrane protein YNL029c - yeast (*Saccharomyces cerevisiae*)
 N:Alternate names: hypothetical protein N2755
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
 C:Accession: S62941; S62951
 R:Anders, B.; Irigui Houssein, I.; Urrestazu, L.A.; Vissers, S.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S62920
 A:Accession: S62941
 A:Molecule type: DNA
 A:Residues: 1-522 <DNA>
 A:Cross-references: UNIPROT:P53966; EMBL:Z71305; NID:g1301864; PID:g1301865; MIPS:YNL029
 A:Experimental source: strain S288C
 R:Duetschhoelt, A.; Floeth, M.; Fritzel, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S62944
 A:Accession: S62951
 A:Molecule type: DNA
 A:Residues: 1-522 <DNA>
 A:Cross-references: EMBL:Z71305; NID:g1301864; PID:g1301865; MIPS:YNL029C
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SGD:KTR5
 A:Cross-references: SGD:S0004974; MIPS:YNL029C
 A:Map position: 14L
 C:Keywords: transmembrane protein
 F:21-37/Domain: transmembrane #status predicted <TMM>

Query Match 49.4%; Score 42; DB 2; Length 522;
 Best Local Similarity 50.0%; Pred. No. 50;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 ADGPTLRWISF 13
 : ||| :|||:
 Db 285 SDDPELRDMWY 236

RESULT 27
 A11544
 conserved hypothetical protein lin0897 [imported] - *Listeria innocua* (strain Clijp11262)
 C:Species: *Listeria innocua*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: A11544
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 Science 294, 849-852, 2001
 D.; Jones, L.M.; Karst, U.
 A:Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Ma
 Ok, C.; Schluter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A:Title: Comparative genomes of *Listeria species*.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: A11544
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-725 <GLA>
 A:Cross-references: UNIPROT:Q92DB8; GB:ML520222; PIDN:CA096129.1; PID:g16413347; GSPDB:G
 A:Experimental source: strain Clijp11262
 C:Genetics:
 A:Gene: lin0897
 C:Superfamily: hypothetical protein ydc1

Query Match 49.4%; Score 42; DB 2; Length 725;
 Best Local Similarity 70.0%; Pred. No. 68;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ADGPTLRWY 11
 : ||| :|||:
 Db 174 SDEPTLRWY 183

RESULT 28
 T12091
 starch phosphorylase (EC 2.4.1.1) H, cytosolic isoform - fava bean

N:Alternate names: alpha 1,4-glucan phosphorylase type H
 C:Species: *Vicia faba* (fava bean)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T12091
 R:Buchner, P.; Borstjuk, L.; Wobus, U.
 Planta 199, 64-73, 1996
 A:Title: Glucan phosphorylases in *Vicia faba* L.: cloning, structural analysis and expres
 A:Reference number: Z17412; MUID:96236831; PMID:8680306
 A:Accession: T12091
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-842 <BUC>
 A:Cross-references: UNIPROT:P53337; EMBL:Z35117; NID:9510931; PIDN:CA84494.1; PID:95109
 A:Experimental source: strain *Vicia faba* var. minor; cultivar Fribio; coveydon, clone VF
 C:Genetics:
 A:Gene: Ph02
 C:Function:
 A:Description: catalyzes the formation of glucose 1-phosphate from polyglucose
 C:Superfamily: glucan phosphorylase
 C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein; pyridoxal phosphate
 F:688/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 49.4%; Score 42; DB 2; Length 842;
 Best Local Similarity 58.3%; Pred. No. 78;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 DGPTLRWISFC 14
 : ||| :|||:
 Db 488 NGITPRRWINFC 499

RESULT 29
 S07755
 hypothetical protein 16 - *Paramecium tetraurelia* mitochondrion
 C:Species: *mitochondrion Paramecium tetraurelia*
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
 C:Accession: S07755
 R:Pritchard, A.E.; Sellhammer, J.J.; Mahalingam, R.; Sable, C.L.; Vennu, S.E.; Cummings,
 Nucleic Acids Res. 18, 173-180, 1990
 A:Title: Nucleotide sequence of the mitochondrial genome of *Paramecium*.
 A:Reference number: S07725; MUID:90174913; PMID:2308823
 A:Accession: S07755
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-189 <PRI>
 A:Cross-references: UNIPROT:P15617; EMBL:X15917; NID:g133256; PID:9578768
 C:Genetics:
 A:Gene: mitochondrion
 A:Genetic code: SGC6
 A:Start codon: ATT
 C:Keywords: mitochondrion

Query Match 48.2%; Score 41; DB 2; Length 189;
 Best Local Similarity 72.7%; Pred. No. 27;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 DGPTLRWISF 13
 : ||| :|||:
 Db 92 DEPTLRWISF 102

RESULT 30
 H70849
 hypothetical protein RV0079 - *Mycobacterium tuberculosis* (strain H37RV)
 C:Species: *Mycobacterium tuberculosis*
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: H70849
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 i; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: H70849
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-273 <COL>
 A:Cross-references: UNIPROT:Q53624; GB:AL021428; GB:AL123456; NID:g3261514; PIDN:CA1626
 A:Experimental source: strain H378V
 C:Genetics:
 A:Gene: RV0079
 C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV0079

Query Match 48.2%; Score 41; DB 2; Length 273;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CADPPTL 7
 |||||
 Db 66 CADPPTL 72

RESULT 31
 E84853
 hypothetical protein At2g42400 (imported) - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: E84853
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bent, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 Natus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: E84853
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1473 <SNO>
 A:Cross-references: UNIPROT:Q9SLB9; GB:AB020293; NID:g4567312; PIDN:AD23723.1; GSPDB:GN
 C:Genetics:
 A:Gene: At2g42400
 A:Map position: 2

Query Match 48.2%; Score 41; DB 2; Length 473;
 Best Local Similarity 54.5%; Pred. No. 66;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DGPTRWISFC 13
 :|||:
 Db 344 EGTIRWLF 354

RESULT 32
 T10947
 starch phosphorylase (EC 2.4.1.1) precursor - sweet potato
 C:Species: Ipomoea batatas (sweet potato)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T10947
 R:Lin, C.T.; Yeh, K.W.; Lee, P.D.; Su, J.C.
 submitted to the EMBL Data Library, July 1991
 A>Description: Primary structure of sweet potato starch phosphorylase deduced from its c
 A:Reference number: Z17224
 A:Accession: T10947
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-955 <LIN>
 A:Cross-references: UNIPROT:P27598; EMBL:M64362; NID:g168275; PID:g168276
 A:Experimental source: cv. Tainong 57; tuberous root
 C:Genetics:
 A:Genome: nuclear
 A>Note: starch phosphorylase
 C:Function:
 A>Description: catalyzes the formation of glucose 1-phosphate from polyglucose
 C:Superfamily: glucan phosphorylase
 C:Keywords: chloroplast; glycocyltransferase; hexosyltransferase; phosphoprotein; pyridic

F:1-43/Domain: transit peptide (chloroplast) #status predicted <TNP>
 F:44-95/Product: starch phosphorylase #status predicted <MAT>
 F:801/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 48.2%; Score 41; DB 2; Length 955;
 Best Local Similarity 58.3%; Pred. No. 13e+02;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DGPTRWISFC 14
 :|||:
 Db 600 NGVTPRWIRFC 611

RESULT 33
 PHPOAG
 starch phosphorylase (EC 2.4.1.1) precursor - potato
 N:Alternate names: alpha-glucan phosphorylase
 C:Species: Solanum tuberosum (potato)
 C>Date: 04-Dec-1986 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
 C:Accession: J00130; A00574; F00139; S15531; S12033
 R:Nakano, K.; Mori, H.; Fukui, T.
 J. Biochem. 106, 691-695, 1989
 A>Title: Molecular cloning of cDNA encoding potato amyloplast alpha-glucan phosphorylase.
 A:Reference number: A91915; MUID:90110071; PMID:2481677
 A:Accession: J00130
 A:Molecule type: mRNA
 A:Residues: 1-966 <NAL>
 A:Cross-references: UNIPROT:P04045; GB:D00520; NID:g3702676; PIDN:BA00407.1; PID:g2179
 R:Nakano, K.; Fukui, T.
 J. Biol. Chem. 261, 8230-8236, 1986
 A>Title: The complete amino acid sequence of potato alpha-glucan phosphorylase.
 A:Reference number: A92591; MUID:86250715; PMID:3722153
 A:Accession: A00574
 A:Molecule type: protein
 A:Residues: 51-966 <NAK>
 R:Brison, N.; Groux, H.; Zollinger, M.; Camirand, A.; Simard, C.
 Plant Cell 1, 559-566, 1989
 A>Title: Maturation and subcellular compartmentation of potato starch phosphorylase.
 A:Reference number: P00139; MUID:92404721; PMID:2535551
 A:Accession: P00139
 A:Molecule type: mRNA
 A:Residues: 1-130 <BRI>
 A:Experimental source: tuber, cv. Kennebec
 R:Brison, N.
 submitted to the EMBL Data Library, April 1990
 A:Reference number: S15531
 A:Accession: S15531
 A:Molecule type: mRNA
 A:Residues: 1158 'D', 160-966 <BR2>
 A:Cross-references: EMBL:X52385; NID:g21578; PIDN:CA36612.1; PID:g21579
 R:Camirand, A.; St-Pierre, B.; Martineau, C.; Brison, N.
 Mol. Gen. Genet. 224, 33-39, 1990
 A>Title: Occurrence of a copia-like transposable element in one of the introns of the p
 A:Reference number: S12033; MUID:91117174; PMID:1703627
 A:Accession: S12033
 A:Molecule type: mRNA
 A:Residues: 416-595 <CAN>
 A:Cross-references: EMBL:X52385
 C:Comment: Phosphorylase, an important allosteric enzyme in carbohydrate metabolism, ca
 gulatory mechanisms and in their natural substrates. However, all known phosphorylaes
 C:Superfamily: glucan phosphorylase
 C:Keywords: allosteric regulation; carbohydrate metabolism; glycocyltransferase; hexosy
 F:1-50/Domain: transit peptide (amyloplast) #status predicted <TNP>
 F:51-966/Product: phosphorylase #status experimental <MAT>
 F:812/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 48.2%; Score 41; DB 1; Length 966;
 Best Local Similarity 58.3%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DGPTRWISFC 14
 :|||:
 Db 611 NGVTPRWIRFC 622

```
RESULT 34
T09210
starch phosphorylase (EC 2.4.1.1) - spinach
M:Alternate names: alpha-glucan phosphorylase
C:Species: Spinacia oleracea (spinach)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 18-Aug-2003
C:Accession: T09210
R:Duvenig, E.; Streub, M.; Willmitzer, L.; Kossmann, J.
submitted to the EMBL Data Library, March 1995
A:Reference number: Z16608
A:Accession: T09210
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-971 <DUM>
A:Cross-references: EMBL:X85181
A:Experimental source: U.S. hybrid 424 Serry-Mores seed company (CA, USA); flower
C:Genetics:
A:Gene: SRP11
C:Function:
A:Description: catalyzes the formation of glucose 1-phosphate from polyglucose
C:Keywords: carbohydrate metabolism; glycosyltransferase; hexosyltransferase; phosphoprop
F:817/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match          48.2%; Score 41; DB 2; Length 971;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 DGPRLREWISFC 14
Db      616 NGVTPRRWIRFC 627

RESULT 35
S47243
starch phosphorylase (EC 2.4.1.1) isoform L precursor, chloroplast - fava bean
M:Alternate names: alpha-1,4 glucan phosphorylase isoform L
C:Species: Vicia faba (fava bean)
C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 18-Aug-2003
C:Accession: S47243
R:Buchner, P.; Borisjuk, L.; Wobus, U.
submitted to the EMBL Data Library, August 1994
A:Description: alpha-1,4 glucan phosphorylases in Vicia faba L.: cDNA-Characterization a
A:Reference number: S47243
A:Accession: S47243
A:Molecule type: mRNA
A:Residues: 1-1000 <BUC>
A:Cross-references: EMBL:Z36880
A:Experimental source: strain Vicia faba var. minor; cultivar Fribo; cotyledon; clone VF
C:Genetics:
A:Gene: Phol
A:Genome: nuclear
C:Superfamily: glucan phosphorylase
C:Keywords: chloroplast; glycosyltransferase; hexosyltransferase; phosphoprotein; pyridic
F:1-61/Domain: transit peptide (chloroplast) #status predicted <TMP>
F:62-1000/Product: starch phosphorylase isoform L #status predicted <MAT>
F:846/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match          48.2%; Score 41; DB 2; Length 1000;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 DGPRLREWISFC 14
Db      645 NGVTPRRWIRFC 656

RESULT 36
T17884
S-layer protein - Bacillus circulans
C:Species: Bacillus circulans
```

```
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T17884
R:Aubert-Pivert, E.; Davies, J.
Gene 147, 1-11, 1994
A:Title: Biosynthesis of butirosin in Bacillus circulans NRRL B3312: identification by
A:Reference number: Z18808; MUID:94374689; PMID:7522196
C:Accession: T17884
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1616 <ANB>
A:Cross-references: UNIPROT:P35824; EMBL:L20421; NID:g304142; PID:g304143; PIDN:AAA62586
C:Genetics:
A:Gene: butB
C:Function:
A:Pathway: butirosin biosynthesis

Query Match          48.2%; Score 41; DB 2; Length 1616;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 DGPRLREWISFC 13
Db      737 DGPRLRDWMEF 747

RESULT 37
A70301
ribosomal protein L22 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 13-Aug-1999
C:Accession: A70301
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: A70301
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <AQF>
A:Cross-references: GB:AE000669; NID:g2982762; PIDN:AA06396.1; PID:g2982770; GB:AE00066
A:Experimental source: strain VFS
C:Genetics:
A:Gene: rplV
C:Superfamily: Escherichia coli ribosomal protein L22

Query Match          47.1%; Score 40; DB 2; Length 98;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      3 DGPRLREWT 11
Db      59 DGPRLKKWI 67

RESULT 38
S21826
T-cell receptor beta chain V region homolog - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S21826
R:George Jr., J.F.; Schroeder Jr., H.W.
submitted to the EMBL Data Library, October 1990
A:Reference number: S21826
A:Accession: S21826
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-152 <GEO>
A:Cross-references: EMBL:X56142; NID:g37500; PIDN:CAA39607.1; PID:g388518
C:Genetics:
A:Introns: 134/3; 139/2
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:56-133/Domain: immunoglobulin homology <IMM>
```

Query Match 47.1%; Score 40; DB 2; Length 152;
 Best Local Similarity 50.0%; Pred. No. 32;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 CAGPRLREWISFC 14
 DB 20 CAGPGLLWVLLC 33

RESULT 39

ICMS2

N;Alternate names: IL-2; T-cell growth factor (TCGF)

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text change 09-Jul-2004

C;Accession: A93550; A54490; A94064; I48597; A01850; I84713

R;Fuse: A.; Fujita, T.; Yasumitsu, H.; Kashima, N.; Hasegawa, K.; Taniguchi, T.

Nucleic Acids Res. 12, 9323-9331, 1984

A;Title: Organization and structure of the mouse interleukin-2 gene.

A;Reference number: A93550; MUID:85087940; PMID:6240025

A;Accession: A93550

A;Molecule type: DNA

A;Residues: 1-169 <RUS>

A;Cross-references: UNIPROT:P04351

R;Degrave, W.; Simons, G.; Devos, R.; Plaetinck, G.; Remaut, E.; Tavernier, J.; Fiers, W.

Mol. Biol. Rep. 11, 57-61, 1986

A;Title: Cloning and structure of a mouse interleukin-2 chromosomal gene.

A;Reference number: A54490; MUID:86118396; PMID:3003564

A;Accession: A54490

A;Molecule type: DNA

A;Residues: 1-169 <DEG>

A;Cross-references: GB:M16760

R;Yokota, T.; Arai, N.; Lee, F.; Rennick, D.; Mosmann, T.; Arai, K.

Proc. Natl. Acad. Sci. U.S.A. 82, 68-72, 1985

A;Title: Use of a cDNA expression vector for isolation of mouse interleukin 2 cDNA clone

A;Reference number: A94064; MUID:85113172; PMID:3918306

A;Accession: A94064

A;Molecule type: mRNA

A;Residues: 1-169 <YOK>

A;Cross-references: GB:K02292; NID:G198330; PIDN:AAA3289.1; PID:9309404

R;Kashima, N.; Nishit-Takaoka, C.; Fujita, T.; Taki, S.; Yamada, G.; Hamuro, J.; Taniguchi

Nature 313, 402-404, 1985

A;Title: Unique structure of murine interleukin-2 as deduced from cloned cDNAs.

A;Reference number: I48597; MUID:85111148; PMID:2578624

A;Accession: I48597

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-169 <RES>

A;Cross-references: EMBL:X01772; GB:K02797; NID:G52663; PIDN:CAA25909.1; PID:9758159

C;Comment: Produced by T-cells in response to antigenic or mitogenic stimulation, this P

C;Genetics:

A;Intons: 63/3; 83/3; 132/3

C;Superfamily: interleukin-2

C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-169/Product: interleukin-2 #status predicted <MAT>

F;22/Binding site: carbohydrate (Thr) (covalent) #status predicted

F;92-140/Disulfide bonds: #status predicted

Query Match 47.1%; Score 40; DB 1; Length 169;

Best Local Similarity 75.0%; Pred. No. 36;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 LREMISFC 14
 DB 153 LRRMIAPC 160

RESULT 40

S37289

Interleukin-2 precursor - mouse
 C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text change 09-Jul-2004

C;Accession: S37289; S27205; S36162; S24936

R;Jodt, U.A.

submitted to the EMBL Data Library, April 1993

A;Reference number: S37289

A;Accession: S37289

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-169 <TOD>

A;Cross-references: UNIPROT:Q8BHA4; EMBL:X73040

R;Mateasanz, F.; Alcina, A.; Pellicer, A.

Biochim. Biophys. Acta 1132, 335-336, 1992

A;Title: A new cDNA sequence for the murine interleukin-2 gene.

A;Reference number: S27205; MUID:93041941; PMID:1420317

A;Accession: S27205

A;Molecule type: mRNA

A;Residues: 1-63 <MTE>

A;Cross-references: EMBL:X66058; NID:G52725; PIDN:CAA46854.1; PID:G52726

R;Gosh, S.; Palmer, S.M.; Rodrigues, N.R.; Cordell, H.J.; Hearne, C.M.; Cornall, R.J.;

Nature Genet. 4, 404-409, 1993

A;Title: Polygenic control of autoimmune diabetes in nonobese diabetic mice.

A;Reference number: S36162; MUID:94004970; PMID:8401590

A;Accession: S36162

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-50 <GHO>

A;Cross-references: EMBL:X73040

C;Superfamily: interleukin-2

C;Keywords: cytokine; glycoprotein; growth factor; lymphokine; T-cell

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-63/Product: interleukin-2 #status predicted <MAT>

Query Match 47.1%; Score 40; DB 2; Length 169;

Best Local Similarity 75.0%; Pred. No. 36;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 LREMISFC 14
 DB 153 LRRMIAPC 160

RESULT 41

E95908

Hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSym

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence revision 24-Aug-2001 #text change 09-Jul-2004

C;Accession: E95908

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Herna

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing end

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: E95908

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-169 <KIR>

A;Cross-references: UNIPROT:Q92W14; GB:A1591985; PIDN:CAC48933.1; PID:G15140418; GSPDB:

A;Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure

hebut, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: SMD20554

A;Genome: plasmid

C;Superfamily: uncharacterized conserved protein

Query Match 47.1%; Score 40; DB 2; Length 169;

Best Local Similarity 53.8%; Pred. No. 36;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:37 ; Search time 52.0719 Seconds
(without alignments)
137.677 Million cell updates/sec

Title: US-10-083-768-12

Perfect score: 85
Sequence: 1 CADGPTLRWISFC 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	62.4	297	2	Q7U0E4
2	50.5	59.4	387	2	Q98A97
3	50.5	59.4	389	2	Q8KJF9
4	48	56.5	1123	2	Q7OC63
5	47.5	55.9	283	2	Q82CW2
6	46	54.1	319	2	Q9RKM5
7	46	54.1	347	2	Q7PPE6
8	45	52.9	108	2	Q7RUA5
9	45	52.9	173	2	Q8C4M6
10	45	52.9	209	2	Q6N1X5
11	45	52.9	309	2	Q8XZM5
12	45	52.9	443	2	Q9P858
13	44	51.8	173	2	Q6QHD2
14	44	51.8	178	2	Q6PLI4
15	44	51.8	209	2	Q9LO59
16	44	51.8	292	2	Q67642
17	44	51.8	298	2	Q86653
18	44	51.8	974	1	PHS2_SOLTU
19	44	51.8	997	2	Q6B1Z6
20	44	51.8	1008	2	Q8AY57
21	44	51.8	1011	2	Q6VYM7
22	44	51.8	1022	1	AT1A_TORCA
23	44	51.8	1023	1	AT1A_HUMAN
24	44	51.8	1025	2	Q7ZTF8
25	44	51.8	1028	1	AT1A_RAT
26	43.5	51.2	405	2	Q9KIE9
27	43.5	51.2	934	2	Q9NEX6
28	43	50.6	127	2	Q9N0Z5
29	43	50.6	171	2	Q8HWK6
30	43	50.6	176	2	Q866A9
31	43	50.6	245	2	Q9M060

32	43	50.6	407	2	Q6NMU4	Q6nm4 drosophila
33	43	50.6	407	2	Q9VK55	Q9vk55 drosophila
34	43	50.6	469	2	Q37839	Q37839 bacterioph
35	43	50.6	490	2	Q04270	Q04270 chlamydom
36	43	50.6	509	2	Q8B1G9	Q8b1g9 mus muscu
37	43	50.6	960	2	Q80U28	Q80u28 mus muscu
38	43	50.6	962	2	Q91YY9	Q91yy9 mus muscu
39	43	50.6	1000	2	Q724I9	Q724i9 homo sapien
40	43	50.6	1009	2	Q96SL3	Q96sl3 electrophor
41	43	50.6	1010	2	AT1A_CHICK	AT1a_chick gallus gall
42	43	50.6	1010	1	AT1A_OREMO	AT1a_oremo oreochromis
43	43	50.6	1012	2	Q6VYM8	Q6vym8 oncorhynch
44	43	50.6	1013	1	AT1A_HUMAN	AT1a_human homo sapien
45	43	50.6	1013	1	AT1A_MOUSE	AT1a_mouse mus muscu
46	43	50.6	1013	1	AT1A_RAT	AT1a_rat mus muscu
47	43	50.6	1017	1	AT1A_CHICK	AT1a_chick gallus gall
48	43	50.6	1017	2	Q9DX34	Q9dx34 brachydanio
49	43	50.6	1017	2	Q9DGL5	Q9dgl5 brachydanio
50	43	50.6	1020	1	AT1A_HUMAN	AT1a_human homo sapien
51	43	50.6	1020	1	AT1A_RAT	AT1a_rat mus muscu
52	43	50.6	1020	2	Q6PIE5	Q6pie5 mus muscu
53	43	50.6	1020	2	Q6PAG0	Q6pag0 xenopus lae
54	43	50.6	1021	1	AT1A_CANFA	AT1a_canfa canis fami
55	43	50.6	1021	1	AT1A_CHICK	AT1a_chick gallus gall
56	43	50.6	1021	1	AT1A_HORSE	AT1a_horse equus cabal
57	43	50.6	1021	1	AT1A_PIG	AT1a_pig sus scrofa
58	43	50.6	1021	1	AT1A_SHEEP	AT1a_sheep ovis aries
59	43	50.6	1022	1	AT1A_ANGAN	AT1a_angan anguilla an
60	43	50.6	1022	2	Q6ZQ49	Q6zq49 mus muscu
61	43	50.6	1022	2	Q90WE7	Q90we7 carassius a
62	43	50.6	1023	1	AT1A_BUPMA	AT1a_bupma bufo marinu
63	43	50.6	1023	1	AT1A_MOUSE	AT1a_mouse mus muscu
64	43	50.6	1023	1	AT1A_OREMO	AT1a_oremo oreochromis
65	43	50.6	1023	1	AT1A_RAT	AT1a_rat mus muscu
66	43	50.6	1023	2	Q9N0Z6	Q9n0z6 oncorhynch
67	43	50.6	1023	2	Q6PI87	Q6pi87 xenopus tro
68	43	50.6	1023	2	Q6P271	Q6p271 brachydanio
69	43	50.6	1023	2	Q7ZSX5	Q7zxs5 xenopus lae
70	43	50.6	1023	2	Q7ZYV1	Q7zyv1 anas platyr
71	43	50.6	1023	2	Q8AY58	Q8ay58 fundulus he
72	43	50.6	1023	2	Q9DEU2	Q9deu2 brachydanio
73	43	50.6	1023	2	Q9DEV2	Q9dev2 brachydanio
74	43	50.6	1024	2	Q90X33	Q90x33 brachydanio
75	43	50.6	1024	2	Q9DEU0	Q9deu0 xenopus lae
76	43	50.6	1025	1	AT1A_XENTLA	AT1a_xentla xenopus lae
77	43	50.6	1025	2	Q6IP41	Q6ip41 oncorhynch
78	43	50.6	1025	2	Q6VYM6	Q6vym6 oncorhynch
79	43	50.6	1025	2	Q9DEU1	Q9deu1 brachydanio
80	43	50.6	1027	1	AT1A_CANTCO	AT1a_cantco catostomus
81	43	50.6	1028	2	Q6VYMS	Q6vym5 oncorhynch
82	43	50.6	1028	2	Q7ZU25	Q7zu25 brachydanio
83	43	50.6	1028	2	Q9DGL6	Q9dgl6 brachydanio
84	43	50.6	1029	1	AT1A_HUMAN	AT1a_human homo sapien
85	43	50.6	1032	1	AT1A_MOUSE	AT1a_mouse mus muscu
86	43	50.6	1053	2	Q8VCE0	Q8vce0 mus muscu
87	43	50.6	2098	2	Q7S687	Q7s687 neurospora
88	42.5	50.0	322	2	Q9U514	Q9u514 attemia par
89	42.5	50.0	384	2	Q9U516	Q9u516 attemia san
90	42.5	50.0	399	2	Q9U605	Q9u605 attemia san
91	42.5	50.0	454	2	Q9TVY2	Q9tvy2 attemia san
92	42.5	50.0	454	2	Q9U606	Q9u606 attemia san
93	42.5	50.0	454	2	Q9U607	Q9u607 attemia san
94	42.5	50.0	454	2	Q9U608	Q9u608 attemia san
95	42.5	50.0	454	2	Q9U609	Q9u609 attemia san
96	42.5	50.0	454	2	Q9U610	Q9u610 attemia san
97	42.5	50.0	454	2	Q9U611	Q9u611 attemia san
98	42.5	50.0	828	2	Q74240	Q74240 chleavia h
99	42.5	50.0	1004	1	AT1B_ARPSF	AT1b_arpsf artemia san
100	42	49.4	168	2	Q9V492	Q9v492 drosophila

ALIGNMENTS

```

RESULT 1
Q7UOE4      PRELIMINARY;      PRT;      297 AA.
AC  Q7UOE4;
DT  01-OCT-2003 (TREMBlrel. 25, Created)
DT  01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DE  01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE  Hypothetical protein.
GN  OrderedLocustNames=RB6375;
OS  Rhodopirellula baltica.
OC  Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC  Planctomycetaceae; Pirellula.
OK  NCBI_TaxID=117;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1;
RX  MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA  Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA  Ludwig W., Gade D., Beck A., Borzym K., Hellmann K., Rabus R.,
RA  Schlesner H., Amann R., Reinhardt R.;
RT  "Complete genome sequence of the marine planctomycete Pirellula sp.
RT  strain 1."
RL  Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR  EMBL; BX294144; CAD74759.1; -.
DR  InterPro; IPR000194; ATPase_a/bcentre.
DR  PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
DR  PROSITE; PS50829; GYP_1.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 297 AA; 31805 MW; 475f670f02c78f9b CRC64;

Query Match
Best Local Similarity 62.4%; Score 53; DB 2; Length 297;
Matches 8; Conservative 72.7%; Pred. No. 0.94;
Mismatch 0; Indels 0; Gaps 0;

QY  2 ADGPTLRKEMIS 12
Db  175 ADGPTLRKEMIS 185

RESULT 2
Q98A97      PRELIMINARY;      PRT;      387 AA.
AC  Q98A97;
DT  01-OCT-2001 (TREMBlrel. 18, Created)
DT  01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT  01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE  M1r6096 protein.
GN  OrderedLocustNames=mlr6096;
OS  Rhizobium loti (Mesorhizobium loti).
OC  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC  Phyllobacteriaceae; Mesorhizobium.
OK  NCBI_TaxID=381;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=MAFF303099;
RX  MEDLINE=21082930; PubMed=11214968;
RA  Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA  Watanabe A., Ideasawa K., Ishikawa A., Kawashima K., Kimura T.,
RA  Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA  Wochizuki Y., Nakayama S., Nakazaki N., Shitipo S., Sugimoto M.,
RA  Takeuchi C., Yamada M., Tabata S.;
RT  "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT  Mesorhizobium loti."
RL  DNA Res. 7:331-338(2000).
DR  EMBL; AP003008; BAB52440.1; -.
DR  HSSP; P77407; 1PQY.
DR  GO; GO:0008152; P:metabolism; IEA.
DR  InterPro; IPR003673; CA1B BAIF.
DR  Pfam; PF02515; CoA_transf_3; 1.
KW  Complete proteome.
SQ  SEQUENCE 387 AA; 42226 MW; 64643BEC8F25518 CRC64;

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Query Match
Best Local Similarity 59.4%; Score 50.5; DB 2; Length 387;
Matches 9; Conservative 42.9%; Pred. No. 3.4;
Mismatch 2; Indels 7; Gaps 1;

QY  1 CADGPTL-----REWISFC 14
Db  243 CADGKEVIFSVQNDREWVFC 263

RESULT 3
Q8KJF9      PRELIMINARY;      PRT;      389 AA.
AC  Q8KJF9;
DT  01-OCT-2002 (TREMBlrel. 22, Created)
DT  01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE  01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE  PUTATIVE RACEMASE/DEHYDRATASE PROTEIN.
GN  Name=msl181;
OS  Rhizobium loti (Mesorhizobium loti).
OC  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC  Phyllobacteriaceae; Mesorhizobium.
OK  NCBI_TaxID=381;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=R7A;
RX  MEDLINE=2199272; PubMed=12003951;
RX  DOI=10.1128/JB.184.11.3086-3095.2002;
RA  Sullivan J.T., Trebatowski J.R., Crickshank R.W., Gouzy J.,
RA  Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rosbach U.,
RA  Stuart G.S., Weaver J.E., Webb J.J., de Bruijn F.J., Ronson C.W.;
RT  "Comparative sequence analysis of the symbiosis island of
RT  Mesorhizobium loti strain R7A."
RL  J. Bacteriol. 184:3086-3095(2002).
DR  EMBL; AL672113; CAD31586.1; -.
DR  HSSP; P77407; 1PQY.
DR  GO; GO:0008152; P:metabolism; IEA.
DR  InterPro; IPR003673; CA1B BAIF.
DR  Pfam; PF02515; CoA_transf_3; 1.
SQ  SEQUENCE 389 AA; 42703 MW; 6678D2C96A7E5204 CRC64;

Query Match
Best Local Similarity 59.4%; Score 50.5; DB 2; Length 389;
Matches 9; Conservative 42.9%; Pred. No. 3.4;
Mismatch 2; Indels 7; Gaps 1;

QY  1 CADGPTL-----REWISFC 14
Db  243 CADGKEVIFSVQNDREWVFC 263

RESULT 4
Q7OC63      PRELIMINARY;      PRT;      1123 AA.
AC  Q7OC63;
DT  01-MAR-2004 (TREMBlrel. 26, Created)
DT  01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT  01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE  AgcC1221.
GN  Name=agcG53078; ORFNames=ENSANG00000018866;
OS  Anopheles gambiae str. PEST.
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OK  NCBI_TaxID=180454;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=PEST;
RA  Anopheles Genome Sequencing Consortium;
RL  Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
CC  -!- CAUTION: The sequence shown here is derived from an
CC  EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL; AAA801008859; EAA08177.1; -.
DR  GO; GO:0005524; F:ATP binding; IEA.

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DR GO; GO:0008988; F:homocysteine S-methyltransferase activity; IEA.
 DR GO; GO:0004672; F:protein kinase activity; IEA.
 DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot Kinase.
 DR InterPro; IPR003726; S_methyl_trans.
 DR Pfam; PF00069; PKinase; 1.
 DR Pfam; PF02574; S_methyl_trans; 1.
 DR ProDom; PD000001; Prot Kinase; 1.
 DR PROSITE; PSS0011; PROTEIN KINASE DOM; 1.
 SO SEQUENCE 1123 AA; 120006 MW; D3CC001D8D482AF CRC64;

Query Match 56.5%; Score 48; DB 2; Length 1123;
 Best Local Similarity 75.0%; Pred. No. 29;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ADGPTLRWISF 13
 Db 969 ADHPVLRWISF 980

RESULT 5
 ID Q82CW2 PRELIMINARY; PRT; 283 AA.
 AC Q82CW2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative ICLR-family transcriptional regulator.
 OS OrderedLocustNames=SAV5226;
 GN Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 NCBI_TaxID=33903;

OX NCB1_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinozaki M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinozaki M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.;
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis.";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL; AP005042; BAC72938.1;
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0006355; P:regulation of transcription; IEA.
 DR InterPro; IPR005471; HTH_ICLR.
 DR InterPro; IPR009058; wing_hlx_DNA_bind.
 DR Pfam; PF01614; ICLR; 1.
 KW Complete proteome.
 SO SEQUENCE 283 AA; 30503 MW; F63B1705578EE67 CRC64;

Query Match 55.9%; Score 47.5; DB 2; Length 283;
 Best Local Similarity 50.0%; Pred. No. 8.1;
 Matches 8; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 CADGPTLRWISF 13
 Db 152 CADGPTLRWISF 167

RESULT 6

Q9RKMS
 ID Q9RKMS PRELIMINARY; PRT; 319 AA.
 AC Q9RKMS;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative Merf family transcriptional regulator.
 GN ORFNames=SCD17.06c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 NCBI_TaxID=1902;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12009593; DOI=10.1038/41741a1;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: Contains 1 HTH merf-type DNA-binding domain.
 DR EMBL; AL939118; CAB56383.1;
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription; IEA.
 DR InterPro; IPR00551; HTH_Merf.
 DR InterPro; IPR009061; Putativ_DNA_bind.
 DR Pfam; PF00376; Merf; 1.
 DR PRINTS; PR00040; HTHMERF.
 DR SMART; SM00422; HTH_MERF.1.
 DR PROSITE; PSS0937; HTH_MERF_2.1.
 KW Complete proteome; DNA-binding.
 SO SEQUENCE 319 AA; 34841 MW; 1F51905A8BA5365E CRC64;

Query Match 54.1%; Score 46; DB 2; Length 319;
 Best Local Similarity 70.0%; Pred. No. 17;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DGPTLRWIS 12
 Db 258 DGPTLRWIS 267

RESULT 7
 ID Q7PP6 PRELIMINARY; PRT; 347 AA.
 AC Q7PP6;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ENSANGP0000020769 (Fragment).
 GN Name=ENSANG000000018280;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008944; EAA10075.2; -.

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DR GO; GO:0008896; F:homocysteine S-methyltransferase activity; IEA.
DR InterPro; IPR003726; S_methyl_trans.
DR Pfam; PF02574; S-methyl_trans; 1.
FT NON TER 1
SQ SEQUENCE 347 AA; 38585 MW; 66FF58A1000CDA4F CRC64;

Query Match 54.1%; Score 46; DB 2; Length 347;
Best Local Similarity 61.5%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CADGPTLRWISF 13
DB 201 CDEPTVRFWISF 213

RESULT 8
O7RUAS PRELIMINARY; PRT; 108 AA.
AC O7RUAS;
DT 01-MAR-2004 (TRENBLREL. 26, Created)
DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)
DE Hypothetical protein B24B19.30.
GN Name=NCU03933.1;
OS Neurospora crassa;
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxId=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR7A4;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehan B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kryzocova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Marino G., Catchside D., Li W., Pratt R.J., Omani S.A.,
RA Desguza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Nativin D.O., Alex L.A., Mannheim G., Ebdole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABX01000719; EAA28336.1; -.
DR Hypothetical protein.
KW SEQUENCE 108 AA; 11994 MW; 093DC0D9617A252E CRC64;
SQ

Query Match 52.9%; Score 45; DB 2; Length 108;
Best Local Similarity 50.0%; Pred. No. 7.9;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CADGPTLRWISF 14
DB 70 CQCPILRWISWMC 83

RESULT 9
O8C4M6 PRELIMINARY; PRT; 173 AA.
AC O8C4M6;
DT 01-MAR-2003 (TRENBLREL. 23, Created)
DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
DE library, clone:Cl30070D15 product:unclassifiable, full insert
DE sequence.

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GN Name=Cl30070B15R1K;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA the FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiji K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akiyama T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hasegaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kanakawa T.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaru-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK081706; BAC38302.1; -.
DR MGI; MGI:2444974; Cl30070B15R1K.
SQ SEQUENCE 173 AA; 19340 MW; 6227DD6725E52FCD CRC64;

Query Match 52.9%; Score 45; DB 2; Length 173;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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OY 4 GPTLRWISFC 14
 DB 75 GVTWREWASWC 85

RESULT 10

06N1X5 PRELIMINARY; PRT; 209 AA.
 ID 06N1X5;
 AC 06N1X5;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=RP44277;
 OS Rhodospseudomonas palustris.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiales; Rhodospseudomonas.
 CX NCBI_TaxID=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
 RA Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
 RA Gibson J.L., Hanson T.E., Bobst C., Torres Y Torres J.L., Peres C.,
 RA Harrison C.F., Gibson J., Harwood C.S.;
 RT "Complete genome sequence of the metabolically versatile
 RT photosynthetic bacterium Rhodospseudomonas palustris.";
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL: BX572606; CAZ9718.1; -.
 DR InterPro; IPR008938; ARM.
 DR InterPro; IPR00357; HEAT.
 DR Pfam; PF02985; HEAT.
 DR KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 209 AA; 23238 MW; 6FE082A84DB040EB CRC64;

Query Match 52.9%; Score 45; DB 2; Length 209;
 Best Local Similarity 50.0%; Pred. No. 16;
 Matches 9; Conservative 2; Mismatches 1; Indels 6; Gaps 1;

OY 1 CADG-----PTLRWIS 12
 DB 98 CADTGYEALPTLRWIS 115

RESULT 11

08XZNS PRELIMINARY; PRT; 309 AA.
 ID 08XZNS;
 AC 08XZNS;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 26, Last annotation update)
 DE PROBABLE TRANSCRIPTION REGULATOR PROTEIN.
 GN Name=BS04642; OrderedLocustNames=RScl360;
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 CX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Broctier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choise N., Chandel-Renard C., Cunac S., Demange N.,
 RA Gaepin C., Lavie M., Moisan A., Robert C., Sautin W., Schlex T.,
 RA Siguer P., Thebault P., Whalen W., Wincker P., Levy M.,
 RA Weissbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
 RL Nature 415:497-502(2002).
 DR EMBL: AL646064; CAD15062.1; -.
 DR HSSP; Q9WKC7; IIXC.
 DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR Pfam; PF00126; HTH 1; 1.
 DR Pfam; PF03466; LysR_substrate; 1.
 DR PROSITE; PS50931; HTH_LYSR; 1.
 KM Complete proteome.
 SQ SEQUENCE 309 AA; 33774 MW; 733551741CE83182 CRC64;

Query Match 52.9%; Score 45; DB 2; Length 309;
 Best Local Similarity 70.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CADGPTLRW 10
 DB 221 CTDGAVLREW 230

RESULT 12

09P858 PRELIMINARY; PRT; 443 AA.
 ID 09P858;
 AC 09P858;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Phaeosphaeria nodorum (Septoria nodorum).
 OC Plasmid pBla1.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
 CX NCBI_TaxID=13684;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BS444;
 RA Rawson J.M.;
 RT "Transposable elements in the phytopathogenic fungus Steganospora
 RT nodorum.";
 RL Thesis (2000), PhD thesis, University of Birmingham, UK.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BS444;
 RA Rawson J.M., Cutler S.B., Caten C.E.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ277966; CAB91876.1; -.
 DR KM Hypothetical protein; Plasmid.
 SQ SEQUENCE 443 AA; 49466 MW; 367E0762EB39E68 CRC64;

Query Match 52.9%; Score 45; DB 2; Length 443;
 Best Local Similarity 58.3%; Pred. No. 36;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 CADGPTLRWIS 12
 DB 170 CSENGTLREWIT 181

RESULT 13

06QHD2 PRELIMINARY; PRT; 173 AA.
 ID 06QHD2;
 AC 06QHD2;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE P32 (Fragment);
 OS Gallid herpesvirus 1.
 OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Iltovirus.
 CX NCBI_TaxID=10386;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP Villareal L.Y., Brandão P.E., Ferreira A.P., Doretto L.J.,
 RA D'Alboux A.N.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY541676; AAG48543.1; -.
 DR InterPro; IPR003363; Herpes_gC.

DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF02400; Herpes_gg; 1.
 FT NON_TER 1
 FT NON_TER 173 173
 SQ SEQUENCE 173 AA; 19130 MW; 5A64A1956CEB9B13 CRC64;

Query Match 51.8%; Score 44; DB 2; Length 173;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CADGPTLRWISFC 14
 DB 120 CLDMPPLRPWTTC 133

RESULT 14

ID 06PL14 PRELIMINARY; PRT; 178 AA.

AC 06PL14;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE P32 (Fragment).
 OS Gallid herpesvirus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Iltovirus.
 OC NCBI_TaxId=10386;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Villarreal L.Y., Brandao P.E., Peguini M.R., Ito N.M., Gama N.,
 RA Ferreira C.A., Ferreira A.J.,
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY598339; AA09767.1; -
 DR InterPro; IPR003363; Herpes_gg.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF02400; Herpes_gg; 1.
 FT NON_TER 1
 FT NON_TER 178 178
 SQ SEQUENCE 178 AA; 19896 MW; 6CC47102594537EF CRC64;

Query Match 51.8%; Score 44; DB 2; Length 178;
 Best Local Similarity 50.0%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CADGPTLRWISFC 14
 DB 120 CLDMPPLRPWTTC 133

RESULT 15

ID 09L059 PRELIMINARY; PRT; 209 AA.

AC 09L059;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein SCO2976.
 GN ORFNames=SCS50.04c;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 OC NCBI_TaxId=1902;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=AJ(2) / M145;
 RA MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieiser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieiser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,

RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor AJ(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL39114; CAB87326.1; -
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 209 AA; 24308 MW; 34B4FECAD96AB7 CRC64;

Query Match 51.8%; Score 44; DB 2; Length 209;
 Best Local Similarity 70.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CADGPTLRW 10
 DB 66 CAQGPALRYW 75

RESULT 16

ID 067642 PRELIMINARY; PRT; 292 AA.

AC 067642;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Glycoprotein G.
 OS Gallid herpesvirus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Iltovirus.
 OC NCBI_TaxId=10386;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=USDA challenge strain;
 RA MEDLINE=97033380; PubMed=8879127;
 RX Wild M.A., Cook S., Cochran M.;
 RT "A genomic map of infectious laryngotracheitis virus and the sequence
 RT and organization of genes present in the unique short and flanking
 RT regions.";
 RL Virus Genes 12:107-116(1996).
 DR EMBL; U28832; AAC55098.1; -
 DR InterPro; IPR003363; Herpes_gg.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF02400; Herpes_gg; 1.
 SQ SEQUENCE 292 AA; 31696 MW; 7B2D3D35DP9F32E8 CRC64;

Query Match 51.8%; Score 44; DB 2; Length 292;
 Best Local Similarity 50.0%; Pred. No. 34;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CADGPTLRWISFC 14
 DB 229 CLDMPPLRPWTTC 242

RESULT 17

ID 086553 PRELIMINARY; PRT; 298 AA.

AC 086553;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE P32 protein.
 GN Name=P32;
 OS Gallid herpesvirus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Iltovirus.
 OC NCBI_TaxId=10386;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=94025939; PubMed=8212855; DOI=10.1016/0168-1702(93)90054-Q;
 RA Konguwan K., Johnson M.A., Pridoux C.T., Sheppard M.;
 RT "Identification of an infectious laryngotracheitis virus gene encoding
 RT an immunogenic protein with a predicted M(r) of 32 kilodaltons.";

RL Virus Res. 29:125-140(1993).
 DR EMBL; S66009; AAB28457.1; -.
 DR InterPro; IPR003363; Herpes_gg.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF02400; Herpes_gg; 1.
 DR SEQUENCE 298 AA; 32325 MW; 737BA28B3CBA4215 CRC64;

Query Match 51.8%; Score 44; DB 2; Length 298;
 Best Local Similarity 50.0%; Pred. No. 35;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CADPRTLRWISFC 14
 DB 228 CLDMPPLRPWTVC 241

RESULT 18
 PHS2_SOLUTU STANDARD; PRT; 974 AA.
 AC P53535;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-1,4 glucan phosphorylase, L-2 isozyme, chloroplast precursor
 DE (EC 2.4.1.1) (Starch phosphorylase L-2).
 GN Name=STP-1;
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OC NCBI_TaxID=4113;
 RP
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Desiree; TISSUE=leaf;
 RC MEDLINE=95201249; PubMed=7894019;
 RX Somewald U., Besner A., Greve B., Steup M.;
 RA "A second L-type isozyme of potato glucan phosphorylase: cloning,
 RT antisense inhibition and expression analysis."
 RL Plant Mol. Biol. 27:567-576(1995).
 CC -1- FUNCTION: Phosphorylase is an important allosteric enzyme in
 carbohydrate metabolism. Enzymes from different sources differ in
 their regulatory mechanisms and in their natural substrates.
 CC However, all known phosphorylases share catalytic and structural
 properties.
 CC -1- CATALYTIC ACTIVITY: {(1,4)-alpha-D-glucosyl}(N) + phosphate =
 CC {(1,4)-alpha-D-glucosyl}(N-1) + alpha-D-glucose 1-phosphate.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- SUBCELLULAR LOCATION: Chloroplast; amyloplast.
 CC -1- TISSUE SPECIFICITY: Leaves.
 CC -1- SIMILARITY: Belongs to the glycogen phosphorylase family.

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 CC -----
 DR EMBL; X73684; CAA52036.1; -.
 DR PIR; S53489; S34189.
 DR HSP; P06738; 1YGP.
 DR InterPro; IPR000811; Glyco_trans_35.
 DR Pfam; PF00343; Phosphorylase; 1.
 DR PIRSF; PIRSF00460; PpyrLase G1gp; 1.
 DR PROSITE; PS00102; PHOSPHORYLASE; 1.
 DR Alloteric enzyme; Amyloplast; Carbohydrate metabolism; Chloroplast;
 KW Glycosyltransferase; Multigene family; Pyridoxal phosphate;
 KW Transferase; Transit peptide.
 FT TRANSIT 1 81
 FT CHAIN 82 974 Alpha-1,4 glucan phosphorylase, L-2
 FT BINDING 820 820 Isozyme.
 FT Pyridoxal phosphate (By similarity).

SQ SEQUENCE 974 AA; 110700 MW; 5FF8A23C237463D8 CRC64;

Query Match 51.8%; Score 44; DB 1; Length 974;
 Best Local Similarity 58.3%; Pred. No. 1,2e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 DGPTLRWISFC 14
 DB 619 NGVTPRRWISFC 630

RESULT 19
 OGB126 PRELIMINARY; PRT; 997 AA.
 ID OGB126;
 AC OGB126;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to CA61451|PPI1869 Candida albicans IPI1869.
 DE ORFNames=DEHA00G14795g;
 GN Debaryomyces hanseolii CBS767.
 OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
 OC NCBI_TaxID=284592;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RC Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marcq C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissiere A., Boyer J., Catolico L., Confariolier F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,
 RA Hantreya F., Hennequin C., Jaumaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicand J.M., Nikoleki M., Ozias S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Sileau A.,
 RA Swenne D., Tekala F., Wesolowski-Jouvel M., Westhof E., Wirth B.,
 RA Zentgraf M., Zivanovic I., Boloitin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RA Genoscope;
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382139; CAG90631.1; -.
 DR InterPro; IPR011046; WD40_like.
 DR SEQUENCE 997 AA; 112803 MW; 3C05D6EAF05875C CRC64;

Query Match 51.8%; Score 44; DB 2; Length 997;
 Best Local Similarity 87.5%; Pred. No. 1,3e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 LREWISFC 14
 DB 956 LREWISFC 963

RESULT 20
 OBAV57 PRELIMINARY; PRT; 1008 AA.
 ID OBAV57;
 AC OBAV57;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Sodium/potassium ATPase alpha subunit isoform 2.
 GN Name=ATP1A2;
 OS Fundulus heteroclitus (Killifish) (Mummichog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OC NCBI_TaxID=8078;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA PubMed=14961245;
RT Sempke J.W., Green H.J., Schulte P.M.;
RT "Molecular Cloning and Characterization of Two Na/K-ATPase Isoforms in
  Fundulus heteroclitus."
RL Mar. Biotechnol. 4:512-519(2002).
DR EMBL; AF057073; AAI8003.1; -.
DR HSSP; P06685; IM07.
DR GO; GO:0005890; C:sodium:potassium-exchanging ATPase complex; ISS.
DR GO; GO:0005391; P:sodium:potassium-exchanging ATPase activity; ISS.
DR GO; GO:0015991; P:ATP hydrolysis coupled proton transport; ISS.
DR GO; GO:0030641; P:hydrogen ion homeostasis; ISS.
DR GO; GO:0006813; P:potassium ion transport; ISS.
DR GO; GO:0006814; P:sodium ion transport; ISS.
DR GO; GO:0030317; P:sperm motility; ISS.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006069; Cation_ATPase.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Dehal_like_hydro.
DR InterPro; IPR008250; E1-E2_ATPase_reg.
DR InterPro; IPR005775; Na/K_ATPase_alph.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PRINTS; PR00121; NAKATPASE.
DR TIGRAMES; TIGR01106; ATPase-ITC-X-K; 1.
DR TIGRAMES; TIGR01494; ATPase_P-type; 4.
DR PROSITE; PS00154; ATPASE_E1-E2; UNKNOWN 1.
SQ SEQUENCE 1008 AA; 111293 MW; EA3AVCEDE8E33B037 CRC64;

Query Match 51.8%; Score 44; DB 2; Length 1008;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14
   |||||
Db 70 PTPPEWIKFC 79

RESULT 21
Q6VYM7 PRELIMINARY; PRT; 1011 AA.
ID 06VYM7;
AC 06VYM7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Na/K ATPase alpha subunit isoform 3. (Salmo gairdneri).
OS Oncorhynchus mykiss (Rainbow trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA PubMed=14610032;
RT "Na(+)/K(+) ATPase alpha-isoform switching in gills of rainbow trout
  (Oncorhynchus mykiss) during salinity transfer."
RL J. Exp. Biol. 206:4475-4486(2003).
DR EMBL; AV319388; AA082787.1; -.
DR HSSP; P04191; 1KTU.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.

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DR GO; GO:0015662; F:ATPase activity, coupled to transmembrane m...; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid...; IEA.
DR GO; GO:0015077; F:monovalent inorganic cation transporter act...; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0015672; P:monovalent inorganic cation transport; IEA.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006069; Cation_ATPase.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Dehal_like_hydro.
DR InterPro; IPR008250; E1-E2_ATPase_reg.
DR InterPro; IPR005775; Na/K_ATPase_alph.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PRINTS; PR00121; NAKATPASE.
DR TIGRAMES; TIGR01106; ATPase-ITC-X-K; 1.
DR PROSITE; PS00154; ATPASE_E1-E2; UNKNOWN 1.
SQ SEQUENCE 1011 AA; 111140 MW; 06D12FA68A23456C CRC64;

Query Match 51.8%; Score 44; DB 2; Length 1011;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14
   |||||
Db 72 PTPPEWIKFC 81

RESULT 22
ID AT1A TORCA STANDARD; PRT; 1022 AA.
AC P05025;
DT 13-AUG-1987 (rel. 05, Last sequence update)
DT 05-JUL-2004 (rel. 44, Last annotation update)
DE Sodium/potassium-transporting ATPase alpha chain precursor
DE (EC 3.6.3.9) (Sodium pump alpha chain) (Na+/K+ ATPase alpha chain).
OS Torpedo californica (Pacific electric ray).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hynostomales; Pristigaster; Batoidae;
OC Torpediniformes; Torpedinidae; Torpedo.
OC NCBI_TaxID=7787;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=85296307; PubMed=2993905;
RA Kawakami K., Noguchi S., Noda M., Takahashi H., Ohra T., Kawamura M.,
RA Nojima H., Nagano K., Hirose T., Inayama S., Hayashida H., Miyata T.,
RA Numa S.;
RT "Primary structure of the alpha-subunit of Torpedo californica (Na+ +
  K+)ATPase deduced from cDNA sequence."
RL Nature 316:733-736(1985).
CC -!- FUNCTION: This is the catalytic component of the active enzyme,
  which catalyzes the hydrolysis of ATP coupled with the exchange of
  sodium and potassium ions across the plasma membrane. This action
  creates the electrochemical gradient of sodium and potassium ions,
  providing the energy for active transport of various nutrients.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + Na(+)(In) + K(+)(Out) = ADP +
  phosphate + Na(+)(Out) + K(+)(In).
CC -!- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
  gamma.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the cation transport ATPases family (P-type
  ATPases). Subfamily IIC.

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DR EMBL; X02810; CAA26578.1; -.

DR PIR; S00503; S00503.

DR HSSP; P06685; 1M07.

DR InterPro; IPR001757; ATPase_E1-E2.

DR InterPro; IPR006069; Cation_ATPase.

DR InterPro; IPR006068; Cation_ATPase_C.

DR InterPro; IPR004014; Cation_ATPase_N.

DR InterPro; IPR005834; Dehalo-like_hydro.

DR InterPro; IPR008250; E1-E2_ATPase_reg.

DR InterPro; IPR005775; Na/K_ATPase_alph.

DR Pfam; PF00689; Cation_ATPase_C; 1.

DR Pfam; PF00690; Cation_ATPase_N; 1.

DR Pfam; PF00122; E1-E2_ATPase; 1.

DR Pfam; PF00702; Hydrolyase; 1.

DR PRINTS; PR00119; CATAPASE.

DR PRINTS; PR00121; NAKATPASE.

DR TIGRFAMs; TIGR01106; ATPase-11C-X-K; 1.

DR TIGRFAMs; TIGR01494; ATPase_P-type; 4.

DR PROSITE; PS00154; ATPASE_E1_E2; 1.

KM ATP-binding; Direct protein sequencing; Hydrolyase; Phosphorylation;

KM Sodium/potassium transport; Transmembrane.

PT PROPER 1 5

FT CHAIN 6 1022

FT DOMAIN 6 87 Sodium/potassium-transporting ATPase

FT TRANSSEM 88 108 Alpha chain.

FT DOMAIN 109 131 Cytoplasmic (Potential).

FT TRANSSEM 132 152 Potential.

FT DOMAIN 153 288 Potential.

FT TRANSSEM 289 308 Cytoplasmic (Potential).

FT DOMAIN 309 320 Potential.

FT TRANSSEM 321 338 Potential.

FT DOMAIN 339 771 Cytoplasmic (Potential).

FT TRANSSEM 772 791 Potential.

FT DOMAIN 792 801 Potential.

FT TRANSSEM 802 822 Potential.

FT DOMAIN 823 842 Cytoplasmic (Potential).

FT TRANSSEM 843 865 Potential.

FT DOMAIN 866 917 Potential.

FT TRANSSEM 918 937 Potential.

FT DOMAIN 938 950 Cytoplasmic (Potential).

FT TRANSSEM 951 969 Potential.

FT DOMAIN 970 984 Potential.

FT TRANSSEM 985 1005 Potential.

FT DOMAIN 1006 1022 Cytoplasmic (Potential).

FT MOD_RES 16 16 Phosphoserine (By PKC) (By similarity).

FT ACT_SITE 376 376 4-aspartylphosphate intermediate (By similarity).

FT MOD_RES 942 942 Phosphoserine (By PKA) (By similarity).

FT BINDING 82 84 Binding of phosphoinositide-3 kinase (By similarity).

FT METAL 716 716 Magnesium (By similarity).

FT METAL 720 720 Magnesium (By similarity).

SO SEQUENCE 1022 AA; 112429 MW; D92FE737847D73C2 CRC64;

Query Match 51.8%; Score 44; DB 1; Length 1022;

Best Local Similarity 70.0%; Pred. No. 1.3e+00;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 PTLREWISFC 14

Db 84 PTPPEWIKFC 93

RESULT 23

AL11 HUMAN STANDARD; PRT; 1023 AA.

ID AC 05023; O16689; O6LDM4; O9UJ20; O9UJ21;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Sodium/potassium-transporting ATPase alpha-1 chain precursor

DE (EC 3.6.3.9) (sodium pump 1) (Na+/K+ ATPase 1).

GN Name=ATP1A1;

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RX MEDLINE=87057096; PubMed=2430951;

RA Kawakami K., Ohta T., Nijima H., Nagano K.;

RT "Primary structure of the alpha-subunit of human Na,K-ATPase deduced from cDNA sequence.";

RL J. Biochem. 100:389-397 (1986).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM LONG).

RC TISSUE=Retinal pigment epithelium;

RX MEDLINE=95237606; PubMed=7536695; DOI=10.1016/0378-1119(94)00812-7;

RA Ruiz A., Bhat S.P., Bok D.;

RT "Characterization and quantification of full-length and truncated Na,K-ATPase alpha 1 and beta 1 RNA transcripts expressed in human retinal pigment epithelium.";

RL Gene 155:179-184 (1995).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM LONG).

RC TISSUE=Brain, Cervix, and Skin;

RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,

RA Brownstein M.J., Udell T.B., Toshylyuk S., Carninci P., Prange C.,

RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smallus D.E.,

RA Schermer A., Schein J.E., Jones S.U.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [4]

RP SEQUENCE OF 471-619 FROM N.A.

RA Ovchinnikov Y.A., Monastyrskaya G.S., Arsenyan S.G., Brode N.E.,

RA Petrunkin K.E., Grishin A.V., Arzamazova N.M., Severtsova I.V.,

RA Modyanov N.N.;

RT "Amino acid sequence of the 17-kilodalton fragment of the cytoplasmic region of the alpha-subunit of Na+,K+-ATPase.";

RL Dokl. Biochem. 288:270-272 (1986).

RN [5]

RP SEQUENCE OF 253-341 AND 420-444 FROM N.A.

RX MEDLINE=8724723; PubMed=3036582; DOI=10.1016/0014-5793(87)80677-4;

RA Sverdlov G.D., Monastyrskaya G.S., Brode N.E., Unshakov Y.A.,

RA Alilikmet R.L., Melkov A.M., Smirnov Y.V., Malyshev I.V.,

RA Dulibova I.E., Petrunkin K.E., Grishin A.V., Kiyetkin N.I.,

RA Kostina M.B., Sverdlov V.E., Modyanov N.N., Ovchinnikov Y.A.;

RT "The family of human Na+,K+-ATPase genes. No less than five genes and/or pseudogenes related to the alpha-subunit.";

RL FEBS Lett. 217:275-278 (1987).

RN [6]

RP SEQUENCE OF 198-943 FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=88068506; PubMed=2891135;

RA Chehab F.F., Kan Y.W., Law M.L., Hartz J., Kao F.T., Blostein R.;

RT "Human placental Na+,K+-ATPase alpha subunit: cDNA cloning, tissue expression, DNA polymorphism, and chromosomal localization.";

Proc. Natl. Acad. Sci. U.S.A. 84:7901-7905(1987).
 (7)
 RN SEQUENCE OF 1-61 FROM N.A.
 RX MEDLINE=90228961; PubMed=1970326;
 RA Shull M.M., Pugh D.G., Lingrel J.B.;
 RT "The human Na,K-ATPase alpha 1 gene: characterization of the 5'-
 flanking region and identification of a restriction fragment length
 polymorphism.";
 RT Genomics 6:451-460(1990).
 RL [8]
 RN SEQUENCE OF 85-148 FROM N.A.
 RP TISSUE=Placenta;
 RA Zhang J.-S., Yang J.X., Fang M.W., Lu S.D.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 (9)
 RN SEQUENCE OF 168-189 AND 213-244 FROM N.A.
 RX MEDLINE=87231946; PubMed=3035563;
 RA Shull M.M., Lingrel J.B.;
 RT "Multiple genes encode the human Na,K-ATPase catalytic subunit.";
 RT Proc. Natl. Acad. Sci. U.S.A. 84:4039-4043(1987).
 (10)
 RN SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
 RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
 RA Hillman R.T., Green R.E., Brenner S.E.;
 RT "An unappreciated role for RNA surveillance.";
 RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
 CC -1- FUNCTION: This is the catalytic component of the active enzyme,
 which catalyzes the hydrolysis of ATP coupled with the exchange of
 sodium and potassium ions across the plasma membrane. This action
 creates the electrochemical gradient of sodium and potassium ions,
 providing the energy for active transport of various nutrients.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + Na(+)(In) + K(+)(Out) = ADP +
 phosphate + Na(+)(Out) + K(+)(In).
 CC -1- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
 gamma.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: Named isoforms=2;
 CC Event=Alternative splicing; Name=Long;
 CC IsoId=P05023-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=P05023-2; Sequence=VSP 000415; VSP 000416;
 CC Note=May be produced at very low levels due to a premature stop
 codon in the mRNA, leading to nonsense-mediated mRNA decay;
 CC -1- PTM: Phosphorylation on Tyr-10 modulates pumping activity (By
 similarity).
 CC -1- SIMILARITY: Belongs to the cation transport ATPases family (P-type
 ATPases). Subfamily IIC.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D00099; BAA00061.1; -
 DR EMBL; U16798; AAC50131.1; -
 DR EMBL; BC003077; AAH03077.1; -
 DR EMBL; BC001330; AAH01330.1; -
 DR EMBL; BC050359; AAH50359.1; -
 DR EMBL; X04297; CAA27840.1; -
 DR EMBL; X03757; CAA27390.1; -
 DR EMBL; M27572; AAA35573.1; -
 DR EMBL; M27579; AAA35574.2; -
 DR EMBL; U03007; AAA51803.1; -
 DR EMBL; L76938; AAA82713.1; -
 DR EMBL; M30310; AAA51801.1; -
 DR EMBL; M30309; AAA51801.1; JOINED.
 DR EMBL; M16793; AAD56251.1; -
 DR EMBL; M16794; AAD56252.1; -
 DR PIR; A24414; A24414.

DR HSP, P06685; I007.
 DR Genew, HGNC:799; ATP1A1.
 DR H-InvDB; HIX0000926; -.
 DR MIM; 182310; -.
 DR GO; GO:0005624; C:membrane fraction; TAS.
 DR GO; GO:0005890; F:sodium/potassium-exchanging ATPase complex; ISS.
 DR GO; GO:0005391; F:sodium/potassium-exchanging ATPase activity; ISS.
 DR GO; GO:0015991; F:ATP hydrolysis coupled proton transport; ISS.
 DR GO; GO:0030641; F:hydrogen ion homeostasis; ISS.
 DR GO; GO:0006813; P:potassium ion transport; ISS.
 DR GO; GO:0006814; P:sodium ion transport; ISS.
 DR GO; GO:0030317; P:sperm motility; ISS.
 DR InterPro; IPR001757; ATPase_E1-E2.
 DR InterPro; IPR006069; Cation_ATPase.
 DR InterPro; IPR006068; Cation_ATPase_C.
 DR InterPro; IPR004014; Cation_ATPase_N.
 DR InterPro; IPR005834; Dehal_like_hydro.
 DR InterPro; IPR008250; E1-E2_ATPase_reg.
 DR InterPro; IPR005775; Na/K_ATPase_alph.
 DR Pfam; PF00689; Cation_ATPase_C; 1.
 DR Pfam; PF00690; Cation_ATPase_N; 1.
 DR Pfam; PF00122; E1-E2_ATPase; 1.
 DR Pfam; PF00702; Hydrolyase; 1.
 DR PRINTS; PR00119; CATATPASE.
 DR PRINTS; PR00121; NAKATPASE.
 DR TIGRfam; TIGR01106; ATPase_IIC-X-K; 1.
 DR TIGRfam; TIGR01494; ATPase_P-type; 5.
 DR PROSITE; PS00154; ATPASE_E1_E2; 1.
 DR K1 Alternative splicing; ATP-binding; Hydrolyase; Magnesium;
 KW Metal-binding; Multigene family; Phosphorylation;
 KW Sodium/potassium transport; Transmembrane.
 FT PROPEP 1 5
 FT CHAIN 6 1023
 FT FT Sodium/potassium-transporting ATPase
 FT FT alpha-1 chain.
 FT DOMAIN 6 87 Cytoplasmic (Potential).
 FT TRANSMEM 88 108 Potential.
 FT DOMAIN 109 131 Lumenal (Potential).
 FT TRANSMEM 132 152 Potential.
 FT TRANSMEM 153 288 Cytoplasmic (Potential).
 FT TRANSMEM 289 308 Potential.
 FT DOMAIN 309 320 Lumenal (Potential).
 FT TRANSMEM 321 338 Potential.
 FT DOMAIN 339 772 Cytoplasmic (Potential).
 FT TRANSMEM 773 792 Potential.
 FT DOMAIN 793 802 Lumenal (Potential).
 FT TRANSMEM 803 823 Potential.
 FT DOMAIN 824 843 Cytoplasmic (Potential).
 FT TRANSMEM 844 866 Potential.
 FT DOMAIN 867 918 Lumenal (Potential).
 FT TRANSMEM 919 938 Potential.
 Query Match 51.8%; Score 44; DB 1; Length 1023;
 Best Local Similarity 70.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 5 PTLREWISKC 14
 DB 84 PTPPEWIKFC 93
 RESULT 24
 ID Q7ZYK8 PRELIMINARY; PRT; 1025 AA.
 AC Q7ZYK8;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Atplaa3-prov protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCB1_TaxID=8355;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueffing T.B., Tothiyuki S., Caminici P., Prange C.,
 RA Raha S.S., Locoellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalska U., Smallus D.E., Schmechel A., Schein J.E.,
 RA Jones S.J., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Embryo;
 RA MEDLINE=22311132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.,
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RT Dev. Dyn. 225:384-391(2002).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Embryo;
 RA Klein S., Strausberg R.,
 RA SubMitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RA EMBL; BC043743; AAA43743.1; -.
 DR HSSP; P06685; IM07.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0015662; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0016820; F:hydrolyase activity, acting on acid anhydrid. . .; IEA.
 DR GO; GO:0015077; F:monovalent inorganic cation transporter act. . .; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR GO; GO:0015672; P:monovalent inorganic cation transport; IEA.
 DR InterPro; IPR001757; ATPase_E1-E2.
 DR InterPro; IPR006069; Cation ATPase.
 DR InterPro; IPR006068; Cation ATPase.
 DR InterPro; IPR004014; Cation ATPase N.
 DR InterPro; IPR005834; Dehal like hydro.
 DR InterPro; IPR008250; E1-E2 ATPase reg.
 DR InterPro; IPR005775; Na/K-ATPase_alph.
 DR Pfam; PF00669; Cation_ATPase_C; 1.
 DR Pfam; PF00122; E1-E2 ATPase; 1.
 DR Pfam; PF00702; Hydrolyase; 1.
 DR PRINTS; PR00119; CATATPASE.
 DR PRINTS; PR00121; NAKATPASE.
 DR TIGRFAMs; TIGR01106; ATPase-ITC-X-K; 1.
 DR TIGRFAMs; TIGR01494; ATPase_P-type; 4.
 DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN 1.
 SQ SEQUENCE 1025 AA; 112954 MW; FAOC02119F5288E CRC64;

RESULT 25
 ID ALA4_RAT
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE (Sodium/potassium-transporting ATPase alpha-4 chain (EC 3.6.3.9)
 OS (Sodium pump 4) (Na+/K+ ATPase 4).
 GN Name=Atpla4; Synonyms=Atpla2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RA MEDLINE=95108076; PubMed=7809153;
 RA Shamraj O.I., Lingrel J.B.,
 RT "A putative fourth Na+,K(+)-ATPase alpha-subunit gene is expressed in
 RT testis";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:12952-12956(1994).
 CC -1- FUNCTION: This is the catalytic component of the active enzyme,
 CC which catalyzes the hydrolysis of ATP coupled with the exchange of
 CC sodium and potassium ions across the plasma membrane. This action
 CC creates the electrochemical gradient of sodium and potassium ions,
 CC providing the energy for active transport of various nutrients.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + Na(+)(In) + K(+)(Out) = ADP +
 CC phosphate + Na(+)(Out) + K(+)(In).
 CC -1- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
 CC gamma.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the cation transport ATPases family (P-type
 CC ATPases). Subfamily IIC.
 CC -----
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 CC -----
 DR EMBL; U15176; AAB81285.1; -.
 DR HSSP; P06685; IM07.
 DR RGD; 61952; Atpla4.
 DR GO; GO:0005890; C:sodium/potassium-exchanging ATPase complex; ISS.
 DR GO; GO:0005391; F:sodium/potassium-exchanging ATPase activity; ISS.
 DR GO; GO:0015391; F:ATP hydrolysis coupled proton transport; ISS.
 DR GO; GO:0030641; P:hydrogen ion homeostasis; ISS.
 DR GO; GO:0006813; P:potassium ion transport; ISS.
 DR GO; GO:0006814; P:sodium ion transport; ISS.
 DR GO; GO:0030317; P:sperm motility; ISS.
 DR InterPro; IPR001757; ATPase_E1-E2.
 DR InterPro; IPR006069; Cation ATPase.
 DR InterPro; IPR006068; Cation ATPase_C.
 DR InterPro; IPR004014; Cation ATPase N.
 DR InterPro; IPR005834; Dehal like hydro.
 DR InterPro; IPR008250; E1-E2 ATPase reg.
 DR InterPro; IPR005775; Na/K-ATPase_alph.
 DR Pfam; PF00669; Cation_ATPase_C; 1.
 DR Pfam; PF00122; E1-E2 ATPase; 1.
 DR Pfam; PF00702; Hydrolyase; 1.
 DR PRINTS; PR00119; CATATPASE.
 DR PRINTS; PR00121; NAKATPASE.
 DR TIGRFAMs; TIGR01106; ATPase-ITC-X-K; 1.
 DR TIGRFAMs; TIGR01494; ATPase_P-type; 4.
 DR PROSITE; PS00154; ATPASE_E1_E2; 1.
 KW ATP-binding; Hydrolyase; Magnesium; Metal-binding; Multigene family;
 KW phosphorylation; Sodium/potassium transport; Transmembrane.

QY 5 PTLREWSIFC 14
 DB 86 PTLPEWIKFC 95

Query Match 51.8%; Score 44; DB 2; Length 1025;
 Best Local Similarity 70.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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FT DOMAIN 1 92 Cytoplasmic (Potential).
FT TRANSMEM 93 113 Potential.
FT DOMAIN 114 137 Luminal (Potential).
FT TRANSMEM 138 158 Potential.
FT DOMAIN 159 294 Cytoplasmic (Potential).
FT TRANSMEM 295 314 Potential.
FT DOMAIN 315 326 Luminal (Potential).
FT TRANSMEM 327 344 Potential.
FT DOMAIN 345 777 Cytoplasmic (Potential).
FT TRANSMEM 778 797 Potential.
FT DOMAIN 798 807 Luminal (Potential).
FT TRANSMEM 808 828 Potential.
FT DOMAIN 829 848 Cytoplasmic (Potential).
FT TRANSMEM 849 871 Potential.
FT DOMAIN 872 923 Luminal (Potential).
FT TRANSMEM 924 943 Potential.
FT DOMAIN 944 956 Cytoplasmic (Potential).
FT TRANSMEM 957 975 Potential.
FT DOMAIN 976 990 Luminal (Potential).
FT TRANSMEM 991 1011 Potential.
FT ACT_SITE 1012 1028 4-asparylphosphate intermediate (By similarity).
FT BINDING 382 382 Binding of phosphoinositide-3 kinase (By similarity).
FT MOD_RES 948 948 Phosphoserine (by PKA) (By similarity).
FT BINDING 87 89 Binding of phosphoinositide-3 kinase (By similarity).
FT METAL 722 722 Magnesium (By similarity).
FT METAL 726 726 Magnesium (By similarity).
SQ SEQUENCE 1028 AA; 114004 MW; 858FE008735D06FA CRC64;

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Query Match
Best Local Similarity 51.8%; Score 44; DB 1; Length 1028;
Matches 7; Conservativity 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 5 PTLREWISFC 14
Db 89 PTPPEWIKFC 98

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RESULT 26
Q9KIE9 PRELIMINARY; PRT; 405 AA.
AC Q9KIE9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE PKbE.
GN Name=fkBE;
OS Streptomyces hygroscopicus subsp. ascomyceticus;
OC Bacteria; Actinobacteria; Actinobacteriales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=132248;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20323220; PubMed=10863099; DOI=10.1016/S0378-1119(00)00171-2;
RA Wu K., Chung L., Revelli W.P., Katz L., Reeves C.D.;
RT "The FK520 gene cluster of Streptomyces hygroscopicus var.
RT ascomyceticus (ATCC 14891) contains genes for biosynthesis of unusual
RT polyketide extender units."
RL Gene 251:81-90(12000)
RL EMBL AF235504; AAF6384.1; -.
DR HSSP; P77407; IPQY.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR003673; CAIB BAIF.
DR Pfam; PF02515; CoA_transf_3; 1.
SQ SEQUENCE 405 AA; 43696 MW; DC2569DFC914AD6F CRC64;

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Query Match
Best Local Similarity 51.2%; Score 43.5; DB 2; Length 405;
Matches 9; Conservativity 1; Mismatches 2; Indels 7; Gaps 1;
Qy 3 DGPTLREWISFC 14

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Db 252 DGQTNLGLQNEREWASFC 270

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RESULT 27
Q9NEX6 PRELIMINARY; PRT; 934 AA.
AC Q9NEX6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein Y105E8A.21.
GN ORFNames=Y105E8A.21;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodietinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL132876; CAC48140.1; -.
DR WormBase; WBGene00013679; Y105E8A.21.
DR WormPep; Y105E8A.21; CE25162.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
KW Hypothetical protein.
SQ SEQUENCE 934 AA; 104855 MW; SED4E1D03DB06F24 CRC64;

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```

Query Match
Best Local Similarity 51.2%; Score 43.5; DB 2; Length 934;
Matches 8; Conservativity 2; Mismatches 3; Indels 1; Gaps 1;

```

```

Qy 1 CADGPTLREW-ISF 13
Db 899 CVDGTTSRDWPVSF 912

```

```

RESULT 28
Q9N0Z5 PRELIMINARY; PRT; 127 AA.
AC Q9N0Z5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Na/K ATPase alpha 2 subunit (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21600302; PubMed=11738066; DOI=10.1016/S0008-6363(01)00412-6;
RA Fransen P., Hendrickx U., Brutsaert D.L., Sys S.U.;
RT "Distribution and role of Na(+)/K(+) ATPase in endocardial
RT endothelium."
RL Cardiovasc. Res. 52:487-499 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX Hendrickx U., Fransen P.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF235025; AAF60311.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015662; F:ATPase activity, coupled to transmembrane m. . .; IEA.

```



```

DR GO; GO:0006812; P.cation transport; IEA.
DR InterPro; IPR004014; Cation_ATPase_N.
DR Pfam; PF00690; Cation_ATPase_N; 1.
FT NON_TER 1
SQ SEQUENCE 127 AA; 14082 MW; 301B90F956954550 CRC64;

Query Match
Best Local Similarity 50.6%; Score 43; DB 2; Length 127;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14
DB 104 PTPPEWVKFC 113

RESULT 29
O8HYW6 PRELIMINARY; PRT; 171 AA.
AC O8HYW6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9)
DE (Fragment).
GN Name=atp1a3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxId=9913;
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal medulla;
RA Benavides A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ496458; CAD4286.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0016820; F:hydrolyase activity; IEA.
DR GO; GO:0005911; F:sodium:potassium-exchanging ATPase activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR006069; Cation_ATPase.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR008250; E1-E2_ATPase_reg.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR PRINTS; PR00121; NAKATPASE.
DR Hydrolase.
KW NON_TER 1
FT NON_TER 171
SQ SEQUENCE 171 AA; 19015 MW; B61570772C03945A CRC64;

Query Match
Best Local Similarity 50.6%; Score 43; DB 2; Length 171;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14
DB 73 PTPPEWVKFC 82

RESULT 30
O866A9 PRELIMINARY; PRT; 176 AA.
AC O866A9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Alpha subunit of equine Na/K ATPase (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxId=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Budik S.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ539381; CAD62375.1; -.
DR HSSP; P08515; 1BGS.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0015662; F:ATPase activity; coupled to transmembrane m. .; IEA.
DR GO; GO:0016820; F:hydrolyase activity; acting on acid anhydrid. . .; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR006069; Cation_ATPase.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR008250; E1-E2_ATPase_reg.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR PRINTS; PR00121; NAKATPASE.
FT NON_TER 1
FT NON_TER 176
SQ SEQUENCE 176 AA; 19615 MW; C5F349EBB74444A8 CRC64;

Query Match
Best Local Similarity 50.6%; Score 43; DB 2; Length 176;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14
DB 68 PTPPEWVKFC 77

RESULT 31
O9M060 PRELIMINARY; PRT; 245 AA.
AC O9M060;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Eukaryotic translation initiation factor 6 (EIF-6)-like protein
DE (A1355620).
GN Name=Flit6.30; Synonyms=At3g55620;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Benes V., Wurmback E., Dzonek H., Anegoe W., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer R.F.X., Quetier F., Salanoubat M.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Shim P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
RA Dale J.M., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
RA Shinzaki K., Davis R.W., Theologis A., Becker J.R.;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinzaki K.,
RA Becker J., Theologis A., Davis R.W.;

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RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AL161667; CAB81587.1; -.
DR EMBL: BT009656; AAP75806.1; -.
DR EMBL: AY128351; AAM91554.1; -.
DR PIR: T47701; T47701.
DR HSSP: O12522; 1G62.
DR GO: GO:0003744; P:translation initiation factor activity; IEA.
DR GO: GO:0006413; P:translational initiation; IEA.
DR InterPro: IPR002769; eIF6.
DR Pfam: PF01912; eIF-6; 1.
DR ProDom: PD006880; eIF6; 1.
DR SMART: SM00654; eIF6; 1.
DR TIGRFAMs: TIGR00323; eIF-6; 1.
DR Initiation factor.
SQ SEQUENCE 245 AA; 26482 MW; 73369A2A657F390D CRC64;

Query Match
Best Local Similarity 50.6%; Score 43; DB 2; Length 245;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ADGPTLRWISFC 14
Db 194 AAGMTVNDWTSFC 206

RESULT 32
Q6NMU4 PRELIMINARY; PRT; 407 AA.
AC Q6NMU4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
AT161019D.
GN Name=CG15483;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Ceiniker S.;
RA Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: BT011561; AAS15697.1; -.
DR InterPro: IPR000345; CYC heme BS.
DR PROSITE: PS00190; CYTOCHROME C; UNKNOWN 1.
SQ SEQUENCE 407 AA; 46390 MW; BFA2D74079EE09 CRC64;

Query Match
Best Local Similarity 50.6%; Score 43; DB 2; Length 407;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CADGPTLRWIS 12
Db 280 CHRGPNLEWIN 291

RESULT 33
Q9VK55 PRELIMINARY; PRT; 407 AA.
AC Q9VK55;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2004 (TREMBlrel. 26, Last annotation update)
DE CG15483-PA.
GN ORFNames=CG15483;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaralides P.G., Scherer S.E., Li P.W., Hoekins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle J.K., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Abil U.F., Aghayani A., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Baxendale J., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockler P., Brotter P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heitman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.U., Wei M.H., Ibegam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon R., Nusken D.R., Pacleb J.M.,
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkas R., Tecce C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgerl, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Ceiniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hogson A.,
RA George R.A., Hoekins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svrtkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svrtkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Ceiniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426093; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Ceiniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
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RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003637; AAF53224.1; -.
DR FlyBase; FBgn0032457; CG15483.
DR InterPro; IPR000345; CyC_heme_BS.
DR PROSITE; PS00190; CYTOCHROME_C_UNGROWN_1.
SQ SEQUENCE 407 AA; 46420 MW; BFAC2105079EE508 CRC64;

Query Match
Best Local Similarity 50.6%; Score 43; DB 2; Length 407;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CADPTLRWIS 12
DB 280 CHRGPILREWIN 291

RESULT 34
Q37839 PRELIMINARY; PRT; 469 AA.
AC Q37839;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ORF469 protein.
GN Name=ORF469;
OS Bacteriophage R4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=10732;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsumura M., Noguchi T., Aida T., Asayama M., Takahashi H., Shirai M.;
RT "A gene essential for the site-specific excision of actinophage R4 prophage genome from the chromosome of a lysogen.";
RL J. Gen. Appl. Microbiol. 41:53-61(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96236063; PubMed=8655526;
RA Matsumura M., Noguchi T., Yamaguchi D., Aida T., Asayama M., Takahashi H., Shirai M.;
RT "The arg gene (ORF469) encodes a site-specific recombinase responsible for integration of the R4 phage genome.";
RL J. Bacteriol. 178:3374-3376(1996).
DR EMBL; D38173; BAA07372.1; -.
DR GO; GO:0000150; P:recombinase activity; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR011109; Recombinase.
DR InterPro; IPR006119; Recombinase.
DR Pfam; PF07508; Recombinase; 1.
DR Pfam; PF00239; Resolvase; 1.
SQ SEQUENCE 469 AA; 50656 MW; B3C37E3E2A43853C CRC64;

Query Match
Best Local Similarity 50.6%; Score 43; DB 2; Length 469;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14
DB 429 PTRRAWVDFC 438

RESULT 35
Q04270 PRELIMINARY; PRT; 490 AA.
AC Q04270;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)

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DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phosphatidylinositol 3-kinase (Fragment).
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CW-15;
RX MEDLINE=98281574; PubMed=9620264; DOI=10.1023/A:1005973423723;
RA Molendijk A.J., Irvine R.F.;
RT "Inositide signalling in Chlamydomonas: characterization of a phosphatidylinositol 3-kinase gene.";
RL Plant Mol. Biol. 37:53-66(1998).
DR EMBL; U97663; AAC50018.1; -.
DR PIR; T09084; T09084.
DR GO; GO:0005942; C:phosphoinositide 3-kinase complex; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016303; F:phosphatidylinositol 3-kinase activity; IEA.
DR InterPro; IPR008973; C2_GaIR.
DR InterPro; IPR002420; PI3K_C2.
DR Pfam; PF00792; PI3K_C2; 1.
KM Kinase.
FT NON TER
SQ SEQUENCE 490 AA; 46593 MW; E60A14E45E84D48 CRC64;

Query Match
Best Local Similarity 50.6%; Score 43; DB 2; Length 490;
Matches 8; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 3 DGPTLR--EWISFC 14
DB 250 DGTARWDEWLTFC 263

RESULT 36
Q081G9 PRELIMINARY; PRT; 509 AA.
AC Q081G9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:EI30306P09 product:NA.K-ATPASE ALPHA 1 ISOFORM (EC 3.6.1.37) homolog.
DE DE 3.6.1.37) homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Eyeball;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Eyeball;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Eyeball;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Eyeball;
RX MEDLINE=20493974; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Eyeball;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RX Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama Y., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwaigi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Eyeball;
RC Adachi J., Aizawa K., Akimura T., Aikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuto M., Hanagaki T., Hara A., Haashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hitozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kanukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Konda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Niemi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Tova T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK053751; BAC35507.1; -.
DR HSSP; P06685; IM07.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0015662; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0016820; F:hydrolyase activity; acting on acid anhydrid. . .; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006069; Cation ATPase.
DR InterPro; IPR004014; Cation ATPase_N.
DR InterPro; IPR008250; E1-E2_ATPase_Reg.
DR Pfam; PF00690; Cation_ATPase_N.1.
DR PRINTS; PR00122; E1-E2_ATPase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PRINTS; PR00121; NAKATPASE.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 2.
DR PROSITE; PS00154; ATPASE_E1-E2; UNKNOWN_1.
SQ SEQUENCE 509 AA; 55779 MM; 132C342CA9000E97 CRC64;

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Query Match 50.6%; Score 43; DB 2; Length 509;
Best Local Similarity 60.0%; Pred. No. 93;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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OY 5 PTLRWISFC 14
DB 74 PTLRWVFC 83

RESULT 37
O80U28 PRELIMINARY; PRT; 960 AA.
AC O80U28;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

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DE Atplaz2 protein (Fragment).
GN Name=Atplaz2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603999;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RC Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041774; AAH41774.1; -.
DR HSSP; P06685; IM07.
DR MGD; MGI:88106; Atplaz2.
DR GO; GO:0005890; C:sodium:potassium-exchanging ATPase complex; ISS.
DR GO; GO:0005391; F:sodium:potassium-exchanging ATPase activity; ISS.
DR GO; GO:0015991; P:ATP hydrolysis coupled proton transport; ISS.
DR GO; GO:000641; P:hydrogen ion homeostasis; ISS.
DR GO; GO:0001504; P:neurotransmitter uptake; IMP.
DR GO; GO:0006813; P:potassium ion transport; ISS.
DR GO; GO:0006814; P:sodium ion transport; ISS.
DR GO; GO:0030317; P:sperm motility; ISS.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006069; Cation ATPase.
DR InterPro; IPR004014; Cation ATPase_N.
DR InterPro; IPR008250; Denal_Ilike_Hydro.
DR InterPro; IPR005834; Denal_Ilike_Hydro.
DR InterPro; IPR008250; E1-E2_ATPase_Reg.
DR InterPro; IPR005775; Na/K_ATPase_alph.
DR Pfam; PF00689; Cation ATPase_C; 1.
DR Pfam; PF00690; Cation ATPase_C; 1.
DR Pfam; PF00690; Cation ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolyase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PRINTS; PR00121; NAKATPASE.
DR TIGRFAMs; TIGR01406; ATPase-ITC_X-K; 1.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 4.
DR PROSITE; PS00154; ATPASE_E1-E2; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 960 AA; 105641 MM; EA838C86819D0C45 CRC64;

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Query Match 50.6%; Score 43; DB 2; Length 960;
Best Local Similarity 60.0%; Pred. No. 18+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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OY 5 PTLRWISFC 14
DB 22 PTLRWVFC 31

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RESULT 38
ID Q91YV9 PRELIMINARY; PRT; 962 AA.
AC Q91YV9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013561; AAI13561.1; -.
DR HSSP; P06685; 1MO7.
DR GO; GO:0005890; C:sodium:potassium-exchanging ATPase complex; ISS.
DR GO; GO:0005391; F:sodium:potassium-exchanging ATPase activity; ISS.
DR GO; GO:0015991; P:ATP hydrolysis coupled proton transport; ISS.
DR GO; GO:0030641; P:hydrogen ion homeostasis; ISS.
DR GO; GO:0006813; P:potassium ion transport; ISS.
DR GO; GO:0006814; P:sodium ion transport; ISS.
DR GO; GO:0030317; P:sperm motility; ISS.
DR pfam; PF00689; Cation_ATPase_C; 1.
DR pfam; PF00689; Cation_ATPase_N; 1.
DR pfam; PF00122; El-E2_ATPase; 1.
DR pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PRINTS; PR00121; NAKATPASE.
DR TIGRFAWS; TIGR01106; ATPase-ITC-X-K; 1.
DR TIGRFAWS; TIGR01494; ATPase-P-type; 4.
DR PROSITE; PS00154; ATPASE_EI_E2; UNKNOWN_1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 962 AA; 105826 MW; AB00A952F990AE45 CRC64;

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Query Match 50.6%; Score 43; DB 2; Length 962;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy 5 PTLREWSIFC 14
Db 24 PTLPEWVKFC 33

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RESULT 39
ID Q7Z4I9 PRELIMINARY; PRT; 1000 AA.
AC Q7Z4I9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ATPase Na+/K+ transporting alpha 4.
GN Name=ATP1A4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Hlivko J.T., James P.F.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF506797; AAC07964.1; -.
DR HSSP; P06685; 1MO8.
DR GO; GO:0005890; C:sodium:potassium-exchanging ATPase complex; ISS.
DR GO; GO:0005391; F:sodium:potassium-exchanging ATPase activity; ISS.
DR GO; GO:0015991; P:ATP hydrolysis coupled proton transport; ISS.
DR GO; GO:0030641; P:hydrogen ion homeostasis; ISS.
DR GO; GO:0006813; P:potassium ion transport; ISS.
DR GO; GO:0006814; P:sodium ion transport; ISS.
DR GO; GO:0030317; P:sperm motility; ISS.
DR InterPro; IPR001757; ATPase_EI_E2.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Dehal_like_hydro.
DR InterPro; IPR008250; El-E2_ATPase_reg.
DR InterPro; IPR005775; Na/K_ATPase_alph.
DR pfam; PF00689; Cation_ATPase_C; 1.
DR pfam; PF00689; Cation_ATPase_N; 1.
DR pfam; PF00122; El-E2_ATPase; 1.
DR pfam; PF00702; Hydrolase; 1.
DR TIGRFAWS; TIGR01106; ATPase-ITC-X-K; 1.
DR TIGRFAWS; TIGR01494; ATPase-P-type; 3.
DR PROSITE; PS00154; ATPASE_EI_E2; UNKNOWN_1.
SQ SEQUENCE 1000 AA; 110943 MW; 5A9EBA0B24D482D1 CRC64;

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Query Match 50.6%; Score 43; DB 2; Length 1000;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy 5 PTLREWSIFC 14
Db 63 PTLPEWVKFC 72

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RESULT 40
ID Q98SL3 PRELIMINARY; PRT; 1009 AA.
AC Q98SL3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sodium/potassium pump alpha subunit.
OS Electrophorus electricus (Electric eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC Electrophoridae; Electrophorus.
NCBI_TaxID=8005;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Electric organ;
RX MEDLINE=98068871; PubMed=9405797;
RA Kaya S., Yokoyama A., Imagawa T., Taniguchi K., Froehlich J.P.,
RA Albers R.W.;
RT "Cloning of the eel electroplex Na+(K+)-ATPase alpha subunit.";
RL Ann. N. Y. Acad. Sci. 834:129-131(1997).
RN [2]

```

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RP SEQUENCE FROM N.A.
RC TISSUE-Electric organ;
RA Kaya S., Yokoyama A., Imagawa T., Taniguchi K., Froehlich J.P.,
RA Albers R.W.;
RU Submitted (Mar-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL, AF358351; NAK27722.1; -.
DR HSSP, P06685; IM07.
DR GO, GO:0016021; C:Integral to membrane; IEA.
DR GO, GO:0005524; F:ATP binding; IEA.
DR GO, GO:0015662; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO, GO:0016787; F:hydrolyase activity; IEA.
DR GO, GO:0016820; F:hydrolyase activity, acting on acid anhydrid. . .; IEA.
DR GO, GO:0015077; F:monovalent inorganic cation transporter act. . .; IEA.
DR GO, GO:0008152; P:metabolism; IEA.
DR GO, GO:0015672; P:monovalent inorganic cation transport; IEA.
DR InterPro: IPR001757; ATPase_E1-E2.
DR InterPro: IPR006069; Cation_ATPase.
DR InterPro: IPR006068; Cation_ATPase_C.
DR InterPro: IPR004014; Cation_ATPase_N.
DR InterPro: IPR005834; Dehal_like_hydro.
DR InterPro: IPR008250; E1-E2_ATPase_reg.
DR InterPro: IPR005775; Na/K_ATPase_alph.
DR Pfam: PF00689; Cation_ATPase_C; 1.
DR Pfam: PF00690; Cation_ATPase_N; 1.
DR Pfam: PF00122; E1-E2_ATPase; 1.
DR Pfam: PF00702; Hydrolyase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PRINTS; PR00121; NAKATPASE.
DR TIGRFAMs; TIGR01106; ATPase-IIC_X-K; 1.
DR TIGRFAMs; TIGR01494; ATPase_E1-E2; UNKNOWN_1.
DR PROSITE; PS00154; ATPASE_E1-E2; UNKNOWN_1.
SQ SEQUENCE 1009 AA; 110950 MW; F37C781A4487577 CRC64;

Query Match 50.6%; Score 43; DB 2; Length 1009;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLREWISFC 14
Db 70 PTPPEWVKFC 79

RESULT 41
ID A1A3 CHICK STANDARD; PRT; 1010 AA.
AC P24758;
DT 01-MAR-1992 (Rel. 21, Last sequence created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sodium/potassium-transferring ATPase alpha-3 chain (EC 3.6.3.9)
DE (Sodium pump 3) (Na+/K+ ATPase 3) (Alpha(III)).
GN Name=ATP1A3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCB1_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91023019; PubMed=2171348;
RA Takeyasu K., Lemae V., Fambrough D.M.;
RT "Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms in evolution.";
RL Am. J. Physiol. 259:C619-C630(1990).
CC -I- FUNCTION: This is the catalytic component of the active enzyme,
CC which catalyzes the hydrolysis of ATP coupled with the exchange of
CC sodium and potassium ions across the plasma membrane. This action
CC creates the electrochemical gradient of sodium and potassium ions,
CC providing the energy for active transport of various nutrients.
CC -I- CATALYTIC ACTIVITY: ATP + H(2)O + Na(+) (In) + K(+) (Out) = ADP +
CC phosphate + Na(+) (Out) + K(+) (In).
CC -I- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
CC gamma.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.

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CC -I- SIMILARITY: Belongs to the cation transport ATPases family (P-type
CC ATPases). Subfamily IIC.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; M59960; AAA48982.1; -.
DR PIR; B37227; B37227.
DR HSSP; P06685; IM07.
DR GO; GO:0005890; C:sodium/potassium-exchanging ATPase complex; ISS.
DR GO; GO:0005391; F:sodium/potassium-exchanging ATPase activity; ISS.
DR GO; GO:0015991; P:ATP hydrolysis coupled proton transport; ISS.
DR GO; GO:0030641; P:hydrogen ion homeostasis; ISS.
DR GO; GO:0006813; P:potassium ion transport; ISS.
DR GO; GO:0006814; P:sodium ion transport; ISS.
DR GO; GO:0030317; P:sperm motility; ISS.
DR InterPro: IPR001757; ATPase_E1-E2.
DR InterPro: IPR006069; Cation_ATPase.
DR InterPro: IPR006068; Cation_ATPase_C.
DR InterPro: IPR004014; Cation_ATPase_N.
DR InterPro: IPR005834; Dehal_like_hydro.
DR InterPro: IPR008250; E1-E2_ATPase_reg.
DR InterPro: IPR005775; Na/K_ATPase_alph.
DR Pfam: PF00689; Cation_ATPase_C; 1.
DR Pfam: PF00690; Cation_ATPase_N; 1.
DR Pfam: PF00122; E1-E2_ATPase; 1.
DR Pfam: PF00702; Hydrolyase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PRINTS; PR00121; NAKATPASE.
DR TIGRFAMs; TIGR01106; ATPase-IIC_X-K; 1.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 5.
DR PROSITE; PS00154; ATPASE_E1-E2; 1.
DR ATP-binding; Hydrolyase; Magnesium; Metal-binding; Multigene family;
KW phosphorylation; Sodium/potassium transport; Transmembrane.
KM DOMAIN 1 74
FT DOMAIN 1 74
FT TRANSMEM 75 95
FT DOMAIN 96 118
FT TRANSMEM 119 139
FT DOMAIN 140 275
FT TRANSMEM 276 295
FT DOMAIN 296 307
FT TRANSMEM 308 325
FT DOMAIN 326 759
FT TRANSMEM 760 779
FT DOMAIN 780 789
FT TRANSMEM 790 810
FT DOMAIN 811 830
FT TRANSMEM 831 853
FT DOMAIN 854 905
FT TRANSMEM 906 925
FT DOMAIN 926 938
FT TRANSMEM 939 957
FT DOMAIN 958 972
FT TRANSMEM 973 993
FT DOMAIN 994 1010
FT ACT_SITE 363 363
FT MOD_RES 930 930
FT BINDING 69 71
FT METAL 704 704
FT METAL 708 708
SQ SEQUENCE 1010 AA; 111284 MW; 71526BC25633BFA6 CRC64;

Query Match 50.6%; Score 43; DB 1; Length 1010;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

Qy 5 PTLREWISFC 14
Db 71 PTLPEWVKFC 80

RESULT 42

ALM3_OREMO STANDARD; PRT; 1010 AA.

AC P58312; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sodium/potassium-transferring ATPase alpha-3 chain (EC 3.6.3.9)
GN Name=ATP1A3; Oreochochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Perciformes; Labroidae; Cichlidae; Oreochochromis.
OC NCBI_TaxID=8127;
OX [1]
RN SEQUENCE FROM N.A.

RA Peng H.H., Leu J.H., Huang C.J., Hwang P.P.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of sodium and potassium ions across the plasma membrane. This action creates the electrochemical gradient of sodium and potassium ions, providing the energy for active transport of various nutrients.

-1- CATALYTIC ACTIVITY: ATP + H(2)O + Na(+) (In) + K(+) (Out) = ADP + phosphate + Na(+) (Out) + K(+) (In).

-1- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and gamma.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily 11C.

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CC -----
EMBL: AF109409; AAF75108.1; -

DR HSSP; P06685; IM07.

DR InterPro; IPR001757; ATPase_E1-E2.

DR InterPro; IPR006069; Cation ATPase.

DR InterPro; IPR006068; Cation ATPase_C.

DR InterPro; IPR004014; Cation ATPase_N.

DR InterPro; IPR005834; Dehalo-like_hydro.

DR InterPro; IPR008250; E1-E2_ATPase_reg.

DR InterPro; IPR005775; Na/K_ATPase_alph.

DR Pfam; PF00689; Cation_ATPase_C; 1.

DR Pfam; PF00122; E1-E2_ATPase; 1.

DR Pfam; PF00702; Hydrolyase; 1.

DR PRINTS; PR00119; CATATPASE.

DR PRINTS; PR00121; NAKATPASE.

DR TIGRFAMs; TIGR01106; ATPase-IIIC-X-K; 1.

DR TIGRFAMs; TIGR01494; ATPase_P-type; 5.

DR POSITe; PS00154; ATPase_E1-E2; 1.

KM ATP-binding; Hydrolyase; Magnesium; Metal-binding; Multigene family; Cytoplasmic (Potential); Transmembrane.

FT DOMAIN 1 74 Cytoplasmic (Potential).

FT TRANSSEM 75 95 Potential.

FT DOMAIN 96 118 Lumenal (Potential).

FT TRANSSEM 119 139 Potential.

FT DOMAIN 140 275 Cytoplasmic (Potential).

FT TRANSSEM 276 295 Potential.

FT DOMAIN 296 307 Lumenal (Potential).

FT TRANSSEM 308 325 Potential.
FT DOMAIN 326 759 Cytoplasmic (Potential).
FT TRANSSEM 760 779 Potential (Potential).
FT DOMAIN 780 789 Lumenal (Potential).
FT TRANSSEM 790 810 Potential.
FT DOMAIN 811 830 Cytoplasmic (Potential).
FT TRANSSEM 831 853 Potential.
FT DOMAIN 854 905 Lumenal (Potential).
FT TRANSSEM 906 925 Potential.
FT DOMAIN 926 938 Cytoplasmic (Potential).
FT TRANSSEM 939 957 Potential.
FT DOMAIN 958 972 Lumenal (Potential).
FT TRANSSEM 973 993 Potential.
FT DOMAIN 994 1010 Cytoplasmic (Potential).
FT ACT_SITE 10 13 Poly-phosphatase intermediate (By 4-azepylphosphate intermediate (By similarity).
FT MOD_RES 930 930 Phosphoserine (By PKA) (By similarity).
FT BINDING 69 71 Binding of phosphoinositide-3 kinase (By similarity).

FT METAL 704 704 Magnesium (By similarity).
FT METAL 708 708 Magnesium (By similarity).
SQ SEQUENCE 1010 AA; 111506 MW; 9FEDB07C7547F0D1 CRC64;

Query Match 50.6%; Score 43; DB 1; Length 1010;
Best Local Similarity 60.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 3;

Qy 5 PTLREWISFC 14
Db 71 PTLPEWVKFC 80

RESULT 43

06VYM8 PRELIMINARY; PRT; 1012 AA.

ID 06VYM8;

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Na(+)/K(+) ATPase alpha subunit isoform 2.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Oncorhynchus.

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Oncorhynchus.

OC Protactinopterygii; Salmoniformes; Salmoniformes; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]
RN SEQUENCE FROM N.A.

RP TISSUE=Muscle;

RC PubMed=14610032;

RA Richards J.G., Sempke J.W., Bystriansky J.S., Schulte P.M.;

RT "Na(+)/K(+) ATPase alpha-isoform switching in gills of rainbow trout (Oncorhynchus mykiss) during salinity transfer."

RT J. Exp. Biol. 206:4475-4486(2003).

DR EMBL; AY119387; AA082786.1; -

DR GO; GO:0016021; C: integral to membrane; IEA.

DR GO; GO:0005524; F: ATP binding; IEA.

DR GO; GO:0015662; F: ATPase activity, coupled to transmembrane m. . .; IEA.

DR GO; GO:0016787; F: hydrolyase activity; IEA.

DR GO; GO:0016820; F: hydrolyase activity, acting on acid anhydrid. . .; IEA.

DR GO; GO:0015077; F: monovalent inorganic cation transporter act. . .; IEA.

DR GO; GO:0008152; F: metabolism; IEA.

DR GO; GO:0015672; P: monovalent inorganic cation transport; IEA.

DR InterPro; IPR001757; ATPase_E1-E2.

DR InterPro; IPR006069; Cation ATPase.

DR InterPro; IPR006068; Cation ATPase_C.

DR InterPro; IPR004014; Cation ATPase_N.

DR InterPro; IPR005834; Dehalo-like_hydro.

DR InterPro; IPR008250; E1-E2_ATPase_reg.

DR InterPro; IPR005775; Na/K_ATPase_alph.

DR Pfam; PF00689; Cation_ATPase_C; 1.

DR Pfam; PF00690; Cation_ATPase_N; 1.

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DR Pfam: PF00122; E1-E2, ATPase; 1.
DR Pfam: PF00702; Hydrolyase; 1.
DR PRINTS; PRO0119; CATATPASE.
DR PRINTS; PRO0121; NAKATPASE.
DR TIGRFAmE; TIGR01106; ATPase-ITC X-K; 1.
DR PROSITE; PS00030; ATPase_E1_E2; UNKNOWN_1.
DR PROSITE; PS00030; RRM_RNF_1; UNKNOWN_1.
SQ SEQUENCE 1012 AA; 111220 MW; FF93D65A24A06258 CRC64;

Query Match
Best Local Similarity 50.6%; Score 43; DB 2; Length 1012;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTLRWISFC 14
Db 74 PTPPEWVKFC 83

RESULT 44
ID ALA3_HUMAN STANDARD; PRT; 1013 AA.
AC P13637; Q16732; Q16735; Q969K5;
DT 01-JAN-1990 (Rel. 13, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Sodium/potassium-coupling ATPase alpha-3 chain (EC 3.6.3.9)
DE (Sodium pump 3) (Na+/K+ ATPase 3) (Alpha(III)).
GN Name=ATP1A3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8255304; PubMed=2838329; DOI=10.1016/0014-5793(88)81361-9;
RA Ovcshnikov Y.A., Monastyrskaya G.S., Brode N.E., Unshkaryov Y.A.,
RA Melkov A.M., Smirnov Y.V., Malyshev I.V., Altkmetes R.L.,
RA Kostina M.B., Dulubova I.E., Kiyatkin N.I., Grishin A.V.,
RA Modyanov N.N., Sverdlov E.D.;
RA "Family of human Na+, K+-ATPase genes. Structure of the gene for the
RA catalytic subunit (alpha III-form) and its relationship with
RA structural features of the protein.";
RL FEBS Lett. 233:87-94(1988).

[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX PubMed=2834163;
RA Sverdlov E.D., Monastyrskaya G.S., Brode N.E., Unshkaryov Y.A.,
RA Melkov A.M., Smirnov Y.V., Malyshev I.V., Altkmetes R.L.,
RA Kostina M.B., Dulubova I.E., Kiyatkin N.I., Grishin A.V.,
RA Modyanov N.N., Ovcshnikov Y.A.;
RA "Family of human Na(+),K(+)-ATPase genes. Structure of the gene of
RA isoform alpha-III.";
RL Dokl. Akad. Nauk SSSR 297:1488-1494(1987).

[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Mullaly S.J.,
RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[4]
RN SEQUENCE OF 120-387; 494-538 AND 545-1013 FROM N.A.
RX MEDLINE=87162481; PubMed=3030810; DOI=10.1016/0014-5793(87)81467-9;
RA Ovcshnikov Y.A., Monastyrskaya G.S., Brode N.E., Altkmetes R.L.,
RA Unshkaryov Y.A., Melkov A.M., Smirnov Y.V., Malyshev I.V.,
RA Dulubova I.E., Petrunkhin K.E., Gryshin A.V., Sverdlov E.E.,
RA Kiyatkin N.I., Kostina M.B., Modyanov N.N., Sverdlov E.D.;
RA "The family of human Na+,K+-ATPase genes. A partial nucleotide
RA sequence related to the alpha-subunit.";
RL FEBS Lett. 213:73-80(1987).

[5]
RN ERRATUM.
RP Ovcshnikov Y.A., Monastyrskaya G.S., Brode N.E., Altkmetes R.L.,
RA Unshkaryov Y.A., Melkov A.M., Smirnov Y.V., Malyshev I.V.,
RA Dulubova I.E., Petrunkhin K.E., Gryshin A.V., Sverdlov E.E.,
RA Kiyatkin N.I., Kostina M.B., Modyanov N.N., Sverdlov E.D.;
RL FEBS Lett. 214:375-375(1987).

[6]
RN SEQUENCE OF 243-434 FROM N.A.
RX MEDLINE=87247232; PubMed=3035582; DOI=10.1016/0014-5793(87)80677-4;
RA Sverdlov E.D., Monastyrskaya G.S., Brode N.E., Unshkaryov Y.A.,
RA Altkmetes R.L., Melkov A.M., Smirnov Y.V., Malyshev I.V.,
RA Dulubova I.E., Petrunkhin K.E., Gryshin A.V., Kiyatkin N.I.,
RA Kostina M.B., Sverdlov E.E., Modyanov N.N., Ovcshnikov Y.A.;
RA "The family of human Na+,K+-ATPase genes. No less than five genes
RA and/or pseudogenes related to the alpha-subunit.";
RL FEBS Lett. 217:275-278(1987).

-1- FUNCTION: This is the catalytic component of the active enzyme,
which catalyzes the hydrolysis of ATP coupled with the exchange of
sodium and potassium ions across the plasma membrane. This action
creates the electrochemical gradient of sodium and potassium ions,
providing the energy for active transport of various nutrients.
-1- CATALYTIC ACTIVITY: ATP + H(2)O + Na(+) (in) + K(+) (out) = ADP +
phosphate + Na(+) (out) + K(+) (in).
-1- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and
gamma.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: Belongs to the cation transport ATPases family (P-type
ATPases). Subfamily IIC.

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DR EMBL; M37457; AAA51798.1; -;
DR EMBL; M37436; AAA51798.1; JOINED.
DR EMBL; M37437; AAA51798.1; JOINED.
DR EMBL; M37438; AAA51798.1; JOINED.
DR EMBL; M37439; AAA51798.1; JOINED.
DR EMBL; M37440; AAA51798.1; JOINED.
DR EMBL; M37441; AAA51798.1; JOINED.
DR EMBL; M37442; AAA51798.1; JOINED.
DR EMBL; M37443; AAA51798.1; JOINED.
DR EMBL; M37444; AAA51798.1; JOINED.
DR EMBL; M37445; AAA51798.1; JOINED.
DR EMBL; M37447; AAA51798.1; JOINED.
DR EMBL; M37448; AAA51798.1; JOINED.
DR EMBL; M37449; AAA51798.1; JOINED.
DR EMBL; M37450; AAA51798.1; JOINED.
DR EMBL; M37451; AAA51798.1; JOINED.
DR EMBL; M37452; AAA51798.1; JOINED.
DR EMBL; M37453; AAA51798.1; JOINED.
DR EMBL; M37454; AAA51798.1; JOINED.

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DR	EMBL	X12912	CAA31390.1	JOINED.	
DR	EMBL	X12913	CAA31390.1	JOINED.	
DR	EMBL	X12914	CAA31390.1	JOINED.	
DR	EMBL	X12915	CAA31390.1	JOINED.	
DR	EMBL	X12916	CAA31390.1	JOINED.	
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DR	EMBL	X12919	CAA31390.1	JOINED.	
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DR	EMBL	X12921	CAA31390.1	JOINED.	
DR	EMBL	X12922	CAA31390.1	JOINED.	
DR	EMBL	X12923	CAA31390.1	JOINED.	
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DR	EMBL	M35821	AAA52286.1	JOINED.	
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DR	EMBL	M27573	AAA58380.1	JOINED.	
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DR	EMBL	BC009394	AAH09394.1	-	
DR	EMBL	BC015566	AAH15566.1	-	
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DR	GO	GO:0005351	F:sodium/potassium-exchanging ATPase activity	ISS.	
DR	GO	GO:0015991	P:ATP hydrolysis coupled proton transport	ISS.	
DR	GO	GO:0030641	P:hydrogen ion homeostasis	ISS.	
DR	GO	GO:0006813	P:potassium ion transport	ISS.	
DR	GO	GO:0006147	P:sodium ion transport	ISS.	
DR	GO	GO:0030317	P:sperm motility	ISS.	
DR	GO	GO:0006810	P:transport	IAS.	
DR	InterPro	IPR001757	ATPase_E1-E2.		
DR	InterPro	IPR006069	Cation ATPase.		
DR	InterPro	IPR006068	Cation ATPase C.		
DR	InterPro	IPR004014	Cation ATPase N.		
DR	InterPro	IPR005834	DnaI_like_hydro.		
DR	InterPro	IPR008250	E1-E2 ATPase reg.		
DR	InterPro	IPR005775	Na/K ATPase alph.		
DR	Pfam	PF00689	Cation ATPase C	1.	
DR	Pfam	PF00690	Cation ATPase N	1.	
DR	Pfam	PF00122	E1-E2 ATPase	1.	
DR	Pfam	PF00702	Hydrolase	1.	
DR	PRINTS	PR00119	CATRAPASE.		
DR	PRINTS	PR00121	NAKATAPASE.		
DR	TIGRFAMs	TIGR01106	ATPase-IIIC_X-K	1.	
DR	TIGRFAMs	TIGR01494	ATPase_P-type	5.	
DR	PROSITE	PS00154	ATPase_E1-E2	1.	
KW	ATP-binding	Hydrolase	Magnesium	Metal-binding	Multigene family
KW	Phosphorylation	Sodium/potassium	transpot	Transmembrane	
FT	DOMAIN		1	77	
FT	TRANSMEM		78	98	
FT	DOMAIN		99	121	
FT	TRANSMEM		122	142	
FT	DOMAIN		143	278	
FT	TRANSMEM		279	298	
FT	DOMAIN		299	310	
FT	TRANSMEM		311	328	
FT	DOMAIN		329	762	
FT	TRANSMEM		763	782	
FT	DOMAIN		783	792	

FT	TRANSMEM	793	813	Potential.
Query Match		50.6*	Score 43;	DB 1; Length 1013;
Best Local Similarity		60.0*	Pred. No. 1.9e+02;	
Matches	6; Conservative	1;	Mismatches	3; Indels 0; Gaps 0;
Oy	5	PTLRWISFC 14		
Db	74	PTLRWISFC 83		
RESULT 45				
AL13_MOUSE	STANDARD;	PRT;	1013	AA.
ID	AL13_MOUSE			
AC	Q6P1C6			
DT	25-OCT-2004 (Rel. 45, Created)			
DT	25-OCT-2004 (Rel. 45, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Sodium/potassium-transporting ATPase alpha-3 chain (EC 3.6.3.9)			
DE	(Sodium pump 3) (Na+/K+ ATPase 3) (Alpha(III)).			
GN	Name=ATP1a3;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
TI	TISSUE=Eye;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diachenko L., Marsina K., Farmer A.A., Rubin G.W., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,			
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Mullaly S.J.,			
RA	Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.B.,			
RA	Schmehrer A., Schein J.B., Jones S.J.W., Matra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-1- FUNCTION: This is the catalytic component of the active enzyme,			
CC	which catalyzes the hydrolysis of ATP coupled with the exchange of			
CC	sodium and potassium ions across the plasma membrane. This action			
CC	creates the electrochemical gradient of sodium and potassium ions,			
CC	providing the energy for active transport of various nutrients (By			
CC	similarity).			
CC	-1- CATALYTIC ACTIVITY: ATP + H(2)O + Na(+) (In) + K(+) (Out) = ADP +			
CC	phosphate + Na(+) (Out) + K(+) (In).			
CC	-1- SUBUNIT: Composed of three subunits: alpha (catalytic), beta and			
CC	gamma (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: Belongs to the cation transport ATPases family (P-type			
CC	ATPases). Subfamily IIC.			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	-----			
DR	EMBL; BC034645; AAH34645.1; -			
DR	EMBL; BC037206; AAH37206.1; -			

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DR EMBL; BC042894; AAH42894.1; -.
DR MGD; MGI:88107; AcpIa3.
DR InterPro; IPR001757; ATPase_E1-E2.
DR InterPro; IPR006069; Cation_ATPase.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Denal_like_hydro.
DR InterPro; IPR008250; E1-E2_ATPase_reg.
DR InterPro; IPR005775; Na/K_ATPase_alph.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; E1-E2_ATPase; 1.
DR Pfam; PF00702; HydroIase; 1.
DR PRINTS; PR00119; CATATPASE.
DR PRINTS; PR00121; NAKATPASE.
DR TIGRFAMs; TIGR01106; ATPase-11C-X-K; 1.
DR PROSITE; PS00154; ATPASE_E1_E2; 1.
KM ATP-binding; Hydrolase; Magnesium; Metal-binding; Multigene family;
KW Phosphorylation; Sodium/potassium transport; Transmembrane.
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FT TRANSMEM 78 98 Potential.
FT DOMAIN 99 121 Lumenal (Potential).
FT TRANSMEM 122 142 Potential.
FT DOMAIN 143 278 Cytoplasmic (Potential).
FT TRANSMEM 279 298 Potential.
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FT TRANSMEM 311 328 Potential.
FT DOMAIN 329 762 Cytoplasmic (Potential).
FT TRANSMEM 763 782 Potential.
FT DOMAIN 783 792 Lumenal (Potential).
FT TRANSMEM 793 813 Potential.
FT DOMAIN 814 833 Cytoplasmic (Potential).
FT TRANSMEM 834 856 Potential.
FT DOMAIN 857 908 Lumenal (Potential).
FT TRANSMEM 909 928 Potential.
FT DOMAIN 929 941 Cytoplasmic (Potential).
FT TRANSMEM 942 960 Potential.
FT DOMAIN 961 975 Lumenal (Potential).
FT TRANSMEM 976 996 Potential.
FT DOMAIN 997 1013 4-Aspartylphosphate intermediate (By
FT ACT_SITE 366 366 similarity).
FT MOD_RES 933 933 Phosphoserine (by PKA) (By similarity).
FT BINDING 72 74 Binding of phosphoinositide-3 kinase (By
FT METAL 707 707 similarity).
FT METAL 711 711 Magnesium (By similarity).
SQ SEQUENCE 1013 AA; 111690 MW; 72F051406284E8A8A CRC64;

Query Match 50.6%; Score 43; DB 1; Length 1013;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 5 PTLREWISFC 14
DB 74 PTPPEWVKFC 83

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Search completed: September 1, 2005, 16:21:16
 Job time : 54.0719 secs

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OM protein - protein search, using sw model

Run on: September 1, 2005, 15:48:02 ; Search time 64.3597 Seconds
(without alignments)
84.131 Million cell updates/sec

Title: US-10-083-768-13

Perfect score: 73
Sequence: 1 IEGLPTIRQMLARA 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:.*
1: geneseq19808:.*
2: geneseq19908:.*
3: geneseq20008:.*
4: geneseq20018:.*
5: geneseq20028:.*
6: geneseq20038:.*
7: geneseq20048:.*
8: geneseq20058:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	14	AAW09463	AAW09463 Thrombopo
2	73	100.0	14	AAW09468	AAW09468 Thrombopo
3	73	100.0	14	AAW33030	AAW33030 Thrombopo
4	73	100.0	14	AAW33034	AAW33034 Thrombopo
5	73	100.0	14	AAW36774	AAW36774 Thrombopo
6	73	100.0	14	AD124843	AD124843 AF 12505
7	73	100.0	14	AA196515	AA196515 Thrombopo
8	73	100.0	14	AAAB16962	AAAB16962 Thrombopo
9	73	100.0	14	AAU25827	AAU25827 Human thr
10	73	100.0	14	AAU26004	AAU26004 Human thr
11	73	100.0	14	ABR72853	ABR72853 TPO mimet
12	73	100.0	14	ABR51669	ABR51669 Thrombopo
13	73	100.0	14	AAE18011	AAE18011 Human lig
14	73	100.0	14	ABG71747	ABG71747 TPO recep
15	73	100.0	14	ABR62907	ABR62907 Erythrope
16	73	100.0	14	ADC33697	ADC33697 Erythrope
17	73	100.0	14	ADN59652	ADN59652 Thrombopo
18	73	100.0	14	ADL27293	ADL27293 Amino aci
19	73	100.0	14	ADM72483	ADM72483 TPO mimet
20	73	100.0	14	ADQ16584	ADQ16584 Agonist T
21	73	100.0	15	AAW35416	AAW35416 Thrombopo
22	73	100.0	15	AAW36776	AAW36776 Thrombopo
23	73	100.0	15	AAW66712	AAW66712 Peptide c
24	73	100.0	15	AAAB20684	AAAB20684 Thrombocy
25	73	100.0	15	AAU25996	AAU25996 Human thr

26	73	100.0	15	AAU25831	AAU25831 Human thr
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37	73	100.0	16	AAW19534	AAW19534 Thrombopo
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40	73	100.0	16	AAW66709	AAW66709 Peptide c
41	73	100.0	16	AAW66713	AAW66713 Peptide c
42	73	100.0	16	AAW66733	AAW66733 Peptide c
43	73	100.0	16	AAW66716	AAW66716 Peptide c
44	73	100.0	16	AAU26005	AAU26005 Human thr
45	73	100.0	16	AAU26043	AAU26043 Human thr
46	73	100.0	16	AAU25832	AAU25832 Human thr
47	73	100.0	16	ADM72532	ADM72532 TPO mimet
48	73	100.0	16	ADM72484	ADM72484 TPO mimet
49	73	100.0	16	AAAB16957	AAAB16957 PBGLated
50	73	100.0	18	AAAB16956	AAAB16956 PBGLated
51	73	100.0	18	ABP51687	ABP51687 TPO mimet
52	73	100.0	18	ABP51689	ABP51689 TPO mimet
53	73	100.0	18	ABP51688	ABP51688 TPO mimet
54	73	100.0	18	ABP51677	ABP51677 TPO mimet
55	73	100.0	18	ABP51684	ABP51684 TPO mimet
56	73	100.0	18	ABP51683	ABP51683 TPO mimet
57	73	100.0	18	ABP51674	ABP51674 TPO mimet
58	73	100.0	18	ABP51686	ABP51686 TPO mimet
59	73	100.0	18	ABP51685	ABP51685 TPO mimet
60	73	100.0	18	ABP51691	ABP51691 TPO mimet
61	73	100.0	18	ABP51673	ABP51673 TPO mimet
62	73	100.0	18	ABP51690	ABP51690 TPO mimet
63	73	100.0	18	ABP51680	ABP51680 TPO mimet
64	73	100.0	18	ABP51675	ABP51675 TPO mimet
65	73	100.0	18	ABP51692	ABP51692 TPO mimet
66	73	100.0	18	ADN59812	ADN59812 Thrombopo
67	73	100.0	18	ADQ16611	ADQ16611 TPO mimet
68	73	100.0	18	ADQ16619	ADQ16619 TPO mimet
69	73	100.0	18	ADQ16621	ADQ16621 TPO mimet
70	73	100.0	18	ADQ16641	ADQ16641 TPO mimet
71	73	100.0	18	ADQ16646	ADQ16646 TPO mimet
72	73	100.0	18	ADQ16607	ADQ16607 TPO mimet
73	73	100.0	18	ADQ16615	ADQ16615 TPO mimet
74	73	100.0	18	ADQ16625	ADQ16625 TPO mimet
75	73	100.0	18	ADQ16617	ADQ16617 TPO mimet
76	73	100.0	18	ADQ16629	ADQ16629 TPO mimet
77	73	100.0	18	ADQ16613	ADQ16613 TPO mimet
78	73	100.0	18	ADQ16623	ADQ16623 TPO mimet
79	73	100.0	18	ADQ16605	ADQ16605 TPO mimet
80	73	100.0	18	ADQ16609	ADQ16609 TPO mimet
81	73	100.0	18	ADQ16639	ADQ16639 TPO mimet
82	73	100.0	19	AAAB18003	AAAB18003 FC-TWP pe
83	73	100.0	20	AAAB17929	AAAB17929 TPO-mimet
84	73	100.0	20	ABR73403	ABR73403 TPO mimet
85	73	100.0	20	ADN59687	ADN59687 TWP pepti
86	73	100.0	22	ADQ16714	ADQ16714 Immunoglo
87	73	100.0	22	ADQ16713	ADQ16713 Immunoglo
88	73	100.0	22	ADQ16709	ADQ16709 Immunoglo
89	73	100.0	22	ADQ16706	ADQ16706 Immunoglo
90	73	100.0	22	ADQ16699	ADQ16699 TPO mimet
91	73	100.0	22	ADQ16712	ADQ16712 Immunoglo
92	73	100.0	22	ADQ16711	ADQ16711 Immunoglo
93	73	100.0	22	ADQ16708	ADQ16708 Immunoglo
94	73	100.0	22		
95	73	100.0	22		
96	73	100.0	22		
97	73	100.0	22		
98	73	100.0	22		

99 73 100.0 22 8 ADQ16710
100 73 100.0 28 3 AAb17285

Adq16710 Immunoglob
Aab17285 TPO-mimetic

ALIGNMENTS

RESULT 1
AAW09463

ID AAW09463 standard; protein; 14 AA.

AC AAW09463;

DT 10-SEP-1997 (first entry)

DE Thrombopoietin receptor binding compound peptide.

XX Haematology; thrombocytopenia; TPO; TR; proliferation;

KM bone marrow transfusion; chemotherapy; radiation therapy.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..14

FT /note= "Preferably linkages are selected from: -
CH2OC(O)NR-; phosphonate; -CH2S(O)2NR-; -CH2NR-; -C(O)NR6
; -NHC(O)NH; where R is hydrogen or lower alkyl and R6 is
lower alkyl"

FT Modified-site

FT 1 /note= "Preferably N-terminus is selected from: -NR1; -
NRC(O)R; -NRC(O)OR; -NRS(O)2R; -NHC(O)NHR; succinimide;
benzylloxycarbonyl-NH; benzylloxycarbonyl-NH with 1-3
substitutions on the phenyl ring selected from lower
alkyl, lower alkoxy, chloro, bromo; where R and R1 are
independently selected from hydrogen and lower alkyl"

FT Modified-site

FT 14 /note= "Preferably C-terminus is -C(O)R2 where R2 is
selected from hydroxy, lower alkoxy, and -NR3R4, where R3
and R4 are independently selected from hydrogen and lower
alkyl, and where the nitrogen atom of the -NR3R4 group
can optionally be the amine group of the N-terminus of
the peptide forming a cyclic peptide"

XX W09640189-A1.

XX PD 19-DEC-1996.

XX PF 05-JUN-1996; 96WO-US008998.

XX PR 07-JUN-1995; 95US-00472371.

XX PR 07-JUN-1995; 95US-00473604.

XX PR 07-JUN-1995; 95US-00476168.

XX PR 07-JUN-1995; 95US-00478128.

XX PR 07-JUN-1995; 95US-00484090.

XX PR 07-JUN-1995; 95US-00485301.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;

XX PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX PS WPI, 1997-051883/05.

XX PT Thrombopoietin receptor-binding/activating peptide(s) and peptide

XX PT mimetic(s) - useful in treatment of haematological disorders, esp.

XX CC thrombocytopenia resulting from chemotherapy, etc.

XX CC Claim 18; Page 89; 106pp; English.

XX CC The present sequence is a compound which binds to thrombopoietin (TPO)

XX CC receptor (TR). It has a molecular weight of < 8000 Da, and a binding

XX CC affinity to TR as expressed by an IC50 of no more than about 100 nM. The

XX CC compound (especially if modified, see features table) can be used for

CC treating patients suffering from haematological disorders and
CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
CC marrow transfusions. The peptide may also be used to maintain the
CC proliferation and growth of TPO-dependent cell lines and for use in
CC biological research, for detecting TPO receptors on living cells

XX Sequence 14 AA;

Query Match 100.0%; Score 73; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 1,4e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEPTLRQWLARA 14

Db 1 IEPTLRQWLARA 14

RESULT 2
AAW09468

ID AAW09468 standard; protein; 14 AA.

AC AAW09468;

DT 10-SEP-1997 (first entry)

DE Thrombopoietin receptor binding compound peptide (part of a dimer).

XX Haematology; thrombocytopenia; TPO; TR; proliferation;

KM bone marrow transfusion; chemotherapy; radiation therapy.

OS Synthetic.

XX Key Location/Qualifiers

FT Cross-links 14

FT /note= "Linked to the omega lys from AAW19534"

XX W09640189-A1.

XX PD 19-DEC-1996.

XX PF 05-JUN-1996; 96WO-US008998.

XX PR 07-JUN-1995; 95US-00472371.

XX PR 07-JUN-1995; 95US-00473604.

XX PR 07-JUN-1995; 95US-00476168.

XX PR 07-JUN-1995; 95US-00478128.

XX PR 07-JUN-1995; 95US-00484090.

XX PR 07-JUN-1995; 95US-00485301.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;

XX PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX PS WPI, 1997-051883/05.

XX PT Thrombopoietin receptor-binding/activating peptide(s) and peptide

XX PT mimetic(s) - useful in treatment of haematological disorders, esp.

XX CC thrombocytopenia resulting from chemotherapy, etc.

XX CC Claim 30; Page 91; 106pp; English.

XX CC The present sequence is a compound which binds to thrombopoietin (TPO)

XX CC receptor (TR). It is part of a dimer linked by the omega amino acid to

XX CC the omega amino acid in the sequence in AAW19534. The compound can be

XX CC used for treating patients suffering from haematological disorders and

XX CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone

XX CC marrow transfusions. The peptide may also be used to maintain the

XX CC proliferation and growth of TPO-dependent cell lines and for use in

XX CC biological research, for detecting TPO receptors on living cells

XX Sequence 14 AA;

Query Match 100.0%; Score 73; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IEGPTLRQWLAAARA 14
 |||||
 1 IEGPTLRQWLAAARA 14

RESULT 3
 AAM33030
 ID AAM33030 standard; peptide; 14 AA.

AC AAM33030;

DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.

OS Synthetic.

PN MO9640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

PI Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

DR WPI; 1997-052226/05.

PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

PS Claim 19; Page 89; 106pp; English.

XX The present peptide binds the thrombopoietin receptor (TR), has a
 CC molecular weight of less than 8000 Da and a TR binding affinity as
 CC expressed by an IC50 of no more than about 100 microm. It can be used to
 CC treat disorders which are susceptible to treatment with a thrombopoietin
 CC agonist, preferably haematological disorders and thrombocytopenia
 CC resulting from chemotherapy, radiation therapy or bone marrow
 CC transfusions. It can also be used diagnostically, e.g. to investigate the
 CC mechanism of thrombopoietin signal transduction and receptor activation,
 CC or to maintain the proliferation and growth of thrombopoietin dependent
 CC cell lines

SQ Sequence 14 AA;

Query Match 100.0%; Score 73; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IEGPTLRQWLAAARA 14
 |||||
 1 IEGPTLRQWLAAARA 14

RESULT 4
 AAM33034
 ID AAM33034 standard; peptide; 14 AA.

XX AAM33034;

DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.

OS Synthetic.

PN MO9640750-A1.

PD 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

PI Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

DR WPI; 1997-052226/05.

PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

PS Claim 30; Page 91; 106pp; English.

XX The present peptide binds the thrombopoietin receptor (TR), has a
 CC molecular weight of less than 8000 Da and a TR binding affinity as
 CC expressed by an IC50 of no more than about 100 microm. It can be used to
 CC treat disorders which are susceptible to treatment with a thrombopoietin
 CC agonist, preferably haematological disorders and thrombocytopenia
 CC resulting from chemotherapy, radiation therapy or bone marrow
 CC transfusions. It can also be used diagnostically, e.g. to investigate the
 CC mechanism of thrombopoietin signal transduction and receptor activation,
 CC or to maintain the proliferation and growth of thrombopoietin dependent
 CC cell lines

SQ Sequence 14 AA;

Query Match 100.0%; Score 73; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IEGPTLRQWLAAARA 14
 |||||
 1 IEGPTLRQWLAAARA 14

RESULT 5
 AAM36774
 ID AAM36774 standard; peptide; 14 AA.

AC AAM36774;

DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 14
 FT /note="NH2-Ala"
 XX
 PM WO9640750-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009623.
 XX
 PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Dower WJ, Barrett RM, Gwirla SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wighton NC;
 DR WPI; 1997-052226/05.
 XX
 PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX
 PS Example 9; Page 77; 106pp; English.
 XX
 CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 XX
 SQ Sequence 14 AA;
 XX
 QY
 DB 1 IEPTLRQWLARA 14
 1 IEPTLRQWLARA 14
 1 IEPTLRQWLARA 14
 XX
 RESULT 6
 AD124843
 ID AD124843 standard; peptide; 14 AA.
 XX
 AC AD124843;
 XX
 DT 15-APR-2004 (first entry)
 XX
 DE AF 12505 as active moiety for pharmacologically active peptide.
 XX
 KW pharmacologically active peptide conjugate; enzymatic cleavage; pain;
 KW HIV; cancer; diabetes; incontinence; hypertension; amnesia;
 KW Alzheimer's disease; fever; depression; sex hormone regulation;
 KW eating disorder; schizophrenia; osteoporosis; insomnia;
 KW Central nervous system disorder; contraceptive.
 XX
 OS Synthetic.
 XX
 PM WO9946283-A1.
 XX

PD 16-SEP-1999.
 XX
 PF 09-MAR-1999; 99WO-DK000118.
 XX
 PR 09-MAR-1998; 98DK-00000317.
 XX
 PA (ZEAL-) ZEALAND PHARM AS.
 XX
 PI Larsen BD;
 DR WPI; 1999-561659/47.
 XX
 PT New peptide conjugates used for treating, e.g. pain, HIV, depression,
 PT schizophrenia, osteoporosis or insomnia.
 XX
 PS Claim 24; Page 90; 113pp; English.
 XX
 CC The invention relates to a novel pharmacologically active peptide
 CC conjugate having a reduced tendency towards enzymatic cleavage comprises
 CC X and Z, where: (a) X is a pharmacologically active peptide sequence; and
 CC (b) Z is a stabilizing peptide sequence of 4-20 amino acid units
 CC covalently bound to X, where each amino acid unit in the stabilizing
 CC peptide sequence, Z being selected from Ala, Leu, Ser, Thr, Tyr, Asn,
 CC Gln, Asp, Glu, Lys, Arg, His, Met, Orn, and amino acid units of formula -
 CC NH-C(R1)(R2)-C(=O)- (1), where: R1 and R2 are H, 1-6C alkyl, phenyl, and
 CC phenyl-methyl, where 1-6C-alkyl is optionally substituted with 1-3
 CC substituents selected from halogen, hydroxy, amino, cyano, nitro,
 CC sulfono, and carboxy, and phenyl and phenyl-methyl are optionally
 CC substituted with 1-3 substituents selected from 1-6C-alkyl, 2-6C-alkenyl,
 CC halogen, hydroxy, amino, cyano, nitro, sulfono, and carboxy, or R 1 and R
 CC 2 together with the C atom to which they are bound form a cyclopentyl,
 CC cyclohexyl or cycloheptyl ring, e.g. 2,4-diaminobutanoic acid and 2,3-
 CC diaminopropanoic acid; the ratio between the half-life of the peptide
 CC conjugate and the half-life of the corresponding active peptide sequence,
 CC X, when treated with carboxypeptidase A or leucine aminopeptidase in
 CC about 50 mM phosphate buffer solution at about pH 7.4 and about 37 deg C
 CC or in serum or plasma is at least about 2 (preferably at least about 10),
 CC or when the pharmacologically active peptide X is not orally absorbed,
 CC the conjugate is absorbed, or a salt, with the proviso that the
 CC pharmacologically active peptide conjugate is not selected from sequences
 CC (AD124843)-(AD124841). The peptide conjugates can be used for treating
 CC e.g. pain, HIV, cancer, diabetes, incontinence, hypertension, amnesia,
 CC Alzheimer's disease, fever, depression, sex hormone regulation, eating
 CC disorders, schizophrenia, osteoporosis or insomnia. They can also be used
 CC for treating e.g. CNS disorders and as contraceptives. The conjugated
 CC peptides are less susceptible to degradation by proteases compared to the
 CC corresponding free pharmacologically active peptides. This sequence
 CC represents a pharmacologically active peptide as the X part of the
 CC peptide of the invention.
 XX
 SQ Sequence 14 AA;
 XX
 QY
 DB 1 IEPTLRQWLARA 14
 1 IEPTLRQWLARA 14
 1 IEPTLRQWLARA 14
 XX
 RESULT 7
 AAY96515
 ID AAY96515 standard; peptide; 14 AA.
 XX
 AC AAY96515;
 XX
 DT 04-SEP-2000 (first entry)
 XX
 DE Thrombopoietin mimetic peptide.
 XX
 KW Thrombopoietin; mimetic; TMP; TPO; platelet; megakaryocyte; production;
 KW anti-human immunodeficiency virus; anti-HIV; anti-anemic; dermatological;

KM		immunosuppressive; anti-inflammatory.
XX		Synthetic.
OS		
XX		
FT	Key	Location/Qualifiers
FT	Modified-site	14
FT		/note= "subunits in the dimer are covalently bonded at each carboxy terminus through peptide linkage with NH ₂ -CH ₂ -4-CH (CONH ₂)-NH-CO-(CH ₂) ₂ -NH ₂ "
PN		WO200024770-A2.
PX		04-MAY-2000.
PD		
PP	22-OCT-1999;	99WO-US024834.
PR	23-OCT-1998;	98US-010534BP.
XX		(AMGE-) AMGEN INC.
PA		Liu C, Feige U, Cheetham J;
PI		WPI; 2000-365108/31.
DR		
XX		
FT		Thrombopoietic peptides which activate mpl receptors and increase the production of platelets or platelet precursors, useful for treatment of diseases which involve thrombocytopenia.
PT		
PS	Claim 7; Page 60; 91pp; English.	
XX		
CC		A compound which binds to an mpl receptor comprising a thrombopoietin mimetic peptide (TMP) dimer joined by a linker (TWP_1-(L_1)_nTWP_2), is new. TWP 1 and TWP 2 are amino acid sequences varying from at least 10 to 14 residues in length comprising X-2-X-1-0, X-2-X-1-1, X-2-X-1-2, X-2-X-1-3, X-2-X-1-4, X-1-X-1-0, X-1-X-1-1, X-1-X-1-2, X-1-X-1-3 and X-1-X-1-4. X_1 = I, A, V, L, S or R; X_2 = E, D, K or V; X_3 = G or A; X_4 = P; X_5 = T or S; X_6 = L, I, V, A or F; X_7 = R or K; X_8 = Q, N, or E; X_9 = W, Y or F; X_1-0 = L, I, V, A, F, M, or K; X_1-1 = A, I, V, L, F, S, T, K, H, or B; X_1-2 = A, I, V, L, F, M, S, or Q; X_1-3 = R, K, T, V, N, O or G; X_1-4 = A, I, V, L, F, T, R, E, or G; L_1 = linker comprising 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate the c-mpl receptor which mediates the activity of endogenous thrombopoietin. The TWPs are useful for increasing the production of platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which is useful for treatment of diseases which involve thrombocytopenia, e.g. aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency virus associated ITP, and systemic lupus erythematosus
CC		
CC		
CC		
CC		
CC		
CC		
CC		
XX	Sequence 14 AA;	
SQ		
	Query Match	100.0%; Score 73; DB 3; Length 14;
	Best Local Similarity	100.0%; Pred. No. 1,4e-05;
	Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 IEGPLRLQMLAARA 14 	
DB	1 IEGPLRLQMLAARA 14	
RESULT 8		
AAB16962		
ID	AAB16962 standard; peptide; 14 AA.	
AC	AAB16962;	
XX		
XX		
DT	31-OCT-2000 (first entry)	
XX		
DE	TPO-mimetic peptide TMP SEQ ID NO:13.	
XX		
KM	Modified peptide; therapeutic agent; fusion; FC domain; cancer; autoimmune disease; cytostatic; antineoplastic; thrombolytic; VEGF; immunosuppressive; EGF; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;	
KW		

KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical.
OS Synthetic.
XX
XX WO200024782-A2.
XX
XX PD 04-MAY-2000.
XX
XX PF 25-OCT-1999; 99WO-US025044.
XX
XX PR 23-OCT-1998; 98US-0105371P.
XX PR 22-OCT-1999; 99US-00428082.
XX
XX PA (AMGE-) AMGEN INC.
XX
XX PI Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
XX
XX PT Novel composition of matter comprising an Fc domain and pharmacologically
XX active peptides, useful for treating cancer and autoimmune diseases.
XX
XX Claim 19; Page 189; 608pp; English.

The present invention describes composition of matter (1) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (1) is: (X1)-a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each independently selected from -(L1)-C-P1, -(L1)-C-P1-(L2)d-P2, -(L1)-C-P1-(L2)d-P2-(L3)e-P3, or -(L1)-C-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2, P3, and P4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can have cytosolic, antisecretory, thrombolytic and immunosuppressive activities. DNAs, vectors and host cells from the present invention can be used for producing pharmaceutical compositions. The compositions are useful for treating cancer, asthma, thrombosis, or autoimmune diseases. The use of an Fc domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AA69443 to AA69526 and AB16955 to AB18003 represent nucleotide and amino acid sequences used in the exemplification of the present invention

Sequence 14 AA;

SQ

Query Match	Best Local Similarity	Score 73;	DB 3;	Length 14;
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY 1 IEGPTLRWLARA 14				
Ddb 1 IEGETLRWLARA 14				

RESULT 9
AAU25827
ID AAU25827 standard; peptide; 14 AA.
XX
XX AAU25827;
XX
XX DT 17-DEC-2001 (first entry)
XX
DE Human thrombopoietin receptor (TPO-R) activator peptide #13.
XX
XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
XX haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA,
XX bone marrow transplantation; haematological disorder; platelet disorder;
XX enzyme-linked immunosorbent assay; in situ staining; biological fluid;
XX tissue homogenate; fluorescence-activated cell sorting; Western blotting;
XX in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
XX

OS	Homo sapiens.
XX	
FN	US6251864-B1.
PD	26-JUN-2001.
XX	
PF	01-MAR-2000; 2000US-00516704.
XX	
PR	07-JUN-1995; 95US-00478128.
PR	07-JUN-1995; 95US-00485301.
PR	07-JUN-1996; 96WO-US009623.
PR	15-AUG-1996; 96US-00699027.
XX	
PA	(GLAXO) GLAXO GROUP LTD.
P1	Dower WJ, Barrett RW, Cwirla SE, Gates CM, Schatz RJ;
P1	Balsubramanian P, Wagsstrom CR, Hendren RW, Deprince RB, Poddaturi S;
P1	Yin Q;
DR	WPI; 2001-564142/63.
XX	
PT	Activating thrombopoietin receptors in cells, used to treat
PT	thrombocytopenia and hematological disorders, comprises contacting cells
PT	with peptides and peptide mimetics attached to hydrophilic polymers.
XX	
PS	Disclosure; Col 69-70; 128pp; English.
XX	
CC	Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
CC	bind to and activate the human thrombopoietin receptor (TPO-R). Methods
CC	of activating thrombopoietin receptors in cells comprise contacting the
CC	cells with effective amounts of peptides and peptide mimetics attached to
CC	hydrophilic polymers. The methods are used to treat thrombocytopenia such
CC	as that due to chemotherapy, radiation therapy or bone-marrow
CC	transplantation and to prevent thrombocytopenia in patients at risk.The
CC	sequences are used to treat and prevent haematological disorders
CC	including thrombocytopenia and platelet disorders. They are used in vitro
CC	as unique tools for understanding the biological role of thrombopoietin
CC	(TPO) and to develop other compounds that bind to and activate the TPO
CC	receptor. The peptides can be used to detect TPO receptors on living
CC	cells and fixed cells, in biological fluids, in tissue homogenates, and
CC	in purified or natural biological materials. They may also be used for in
CC	situ staining, fluorescence-activated cell sorting, Western blotting and
CC	enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
CC	be used for in vitro expansion of megakaryocytes and their committed
CC	progenitors alone or in conjunction with additional cytokines
XX	
SQ	Sequence 14 AA:
Query Match	100.0%; Score 73; DB 4; Length 14;
Best Local Similarity	100.0%; Pred No. 1.4e-05;
Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1 IEGPTLRQWLARA 14
Db	1 IEGPTLRQWLARA 14
RESULT 10	
AAU26004	
ID	AAU26004 standard; peptide; 14 AA.
XX	
AC	AAU26004;
XX	
DT	17-DEC-2001 (first entry)
XX	
DE	Human thrombopoietin receptor (TPO-R) activator peptide #190.
XX	
KM	Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
KM	haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
KM	bone marrow transplantation; haematological disorder; platelet disorder;
KM	enzyme-linked immunosorbent assay; in situ staining; biological fluid;
KM	tissue homogenate; fluorescence-activated cell sorting; Western blotting;
KM	in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.

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XX OS Homo sapiens.
XX XX
XX XX US6251864-B1.
XX PD
XX XX 26-JUN-2001.
XX PF
XX XX 01-MAR-2000; 2000US-00516704.
XX PR 07-JUN-1995; 95US-004678128.
XX PR 07-JUN-1995; 95US-00465101.
XX PR 07-JUN-1996; 96MO-US0006623.
XX PR 15-AUG-1996; 96US-00659027.
XX XX
XX PA (GLAXO ) GLAXO GROUP LTD.
XX PI
XX PI Downer MJ, Barrett RM, Cwirla SE, Gates CM, Schatz PJ;
XX PI Balasubramanian P, Wagstrom CR, Hendren RM, Deprince RB, Podduri S;
XX PI Yin Q;
XX DR WPI; 2001-564142/63.
XX XX
XX PT Activating thrombopoietin receptors in cells, used to treat
XX PT thrombocytopenia and hematological disorders, comprises contacting cells
XX PT with peptides and peptide mimetics attached to hydrophilic polymers.
XX PS
XX PS Disclosure; Col 147; 128pp; English.
XX XX
XX XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
XX CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
XX CC of activating thrombopoietin receptors in cells comprise contacting the
XX CC cells with effective amounts of peptides and peptide mimetics attached to
XX CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
XX CC as that due to chemotherapy, radiation therapy or bone-marrow
XX CC transplantation and to prevent thrombocytopenia in patients at risk.The
XX CC sequences are used to treat and prevent hematological disorders
XX CC including thrombocytopenia and platelet disorders. They are used in vitro
XX CC as unique tools for understanding the biological role of thrombopoietin
XX CC (TPO) and to develop other compounds that bind to and activate the TPO
XX CC receptor. The peptides can be used to detect TPO receptors on living
XX CC cells and fixed cells, in biological fluids, in tissue homogenates, and
XX CC in purified or natural biological materials. They may also be used for in
XX CC situ staining, fluorescence-activated cell sorting, Western blotting and
XX CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
XX CC be used for in vitro expansion of megakaryocytes and their committed
XX CC progenitors alone or in conjunction with additional cytokines
XX CC
XX SQ Sequence 14 AA;
XX XX
XX Query Match 100.0%; Score 73; DB 4; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 1,4e-05;
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX QY 1 IEPTTLRWLAARA 14
XX |||||
XX 1 IEPTTLRWLAARA 14
XX Db
XX
XX RESULT 11
XX ABB72853
XX ID ABB72853 standard; peptide; 14 AA.
XX AC
XX AC ABB72853;
XX XX
XX XX 05-APR-2002 (first entry)
XX XX
XX XX TPO mimetic peptide SEQ ID NO:13.
XX DE
XX XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
XX KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
XX KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
XX KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
XX KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
XX KW

```


KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianemic; anorectic; antifertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurologic degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200183525-A2.
 PN 08-NOV-2001.
 PD 02-MAY-2001; 2001WO-US014310.
 PF 03-MAY-2000; 2000US-00563286.
 PR (AMGE-) AMGEN INC.
 PA Feige U, Liu C, Cheatham JC, Boone TC, Gudas JM;
 PI WPI; 2002-130313/17.
 DR Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 XX
 PS Claim 39; Page 43; 176pp; English.
 XX
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianemic, anorectic, antifertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertibility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 14 AA;
 QY
 Db 1 IEGETLRQWLAAARA 14
 1 IEGETLRQWLAAARA 14
 Query Match 100.0%; Score 73; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Thrombopoietin (TPO) agonist mimetic peptide SEQ ID NO:1.
 XX TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
 KW complementarity determining region; immunoglobulin; antianemic;
 KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200246238-A2.
 PN 13-JUN-2002.
 PD 05-DEC-2001; 2001WO-US047656.
 PF 05-DEC-2000; 2000US-0251448P.
 PR 04-MAY-2001; 2001US-0288889P.
 PR 29-MAY-2001; 2001US-0294068P.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 PI Bowdish KS, Barbas-Frederickson S, Renshaw M;
 DR WPI; 2002-566610/60.
 DR A novel immunogen molecule comprising a region in which amino acid
 PT residues corresponding to at least a portion of the complementary
 PT determining region are replaced or fused with an erythropoietin or
 PT thrombopoietin mimetic.
 XX
 PS Claim 16; Page 6; 113pp; English.
 XX
 CC The present invention describes an immunoglobulin molecule or its fragment
 CC (I) comprising a region where amino acid residues corresponding to at
 CC least a portion of the complementary determining region (CDR) are
 CC replaced or fused with biologically active peptides e.g. a peptide
 CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
 CC that is flanked with proline at its carboxy terminus. (I) has
 CC antianemic, haemostatic and nephrotropic activities, and can be used as
 CC a stimulator of proliferation, differentiation and maturation of
 CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
 CC for stimulating proliferation, differentiation or growth of
 CC promegakaryocytes or megakaryocytes, where (I) is contacted with
 CC promegakaryocytes or megakaryocytes, which results in increased platelet
 CC production. (I) with a region where amino acid residues corresponding to
 CC a portion of CDR is replaced with an EPO mimetic, or which has one or
 CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
 CC production of red blood cells, where (I) is contacted with haematopoietic
 CC stem cells or their progenitors. (I) is useful for diagnostics or
 CC therapeutics, in cell isolation strategies, and for treating patients
 CC suffering from deficiency in cell populations caused by disease,
 CC disorders or treatments related to the suppression of haematopoiesis.
 CC ABO73288 to ABO73377 and ABP51669 to ABP51696 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 14 AA;
 QY
 Db 1 IEGETLRQWLAAARA 14
 1 IEGETLRQWLAAARA 14
 Query Match 100.0%; Score 73; DB 5; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 ABP51669
 ID ABP51669 standard; peptide; 14 AA.
 XX
 AC ABP51669;
 XX
 DT 01-OCT-2002 (first entry)
 XX

RESULT 13
 AAE18011
 ID AAE18011 standard; peptide; 14 AA.
 XX
 AC AAE18011;
 XX
 DT 07-MAY-2002 (first entry)
 XX

	OS	Synthetic.	T-helper cell; B-helper cell; synthebody; pharmaceutical; vaccine;
KW	XX	WO200278612-A2.	proliferation; growth; differentiation; haematopoietic cell;
KM	XX	10-OCT-2002.	platelet progenitor cell; immune disorder; thrombocytopenia;
KM	XX	02-APR-2002; 2002WO-US010301.	dissminated intravascular coagulation; stem cell; transplantation;
KW	XX	02-APR-2001; 2001US-0281183P.	gene therapy; diagnostic; haemostatic; immunomodulator; anticoagulant.
XX	XX	(PURD) PURDUE PHARMA LP.	
PA	P1	Soltis DA, Burch RM, Ogert RA;	
XX	XX	WPI, 2003-040615/03.	
DR	XX		
XX	XX		
PT	PT	New thrombopoietin synthebodyes, useful for stimulating proliferation,	
PT	PT	growth, or differentiation of hematopoietic cells, for treating or	
XX	XX	preventing hematopoietic or immune disorders, e.g. thrombocytopenia.	
PS	PS	Claim 62; Page 71; 97pb; English.	
CC	CC	The invention discloses a variant of an immunoglobulin (Ig) variable	
CC	CC	heavy or light chain domain that comprises at least one complementarily	
CC	CC	determining region (CDR) and framework regions flanking the CDR. The CDR	
CC	CC	also has added or substituted to it, at least one binding sequence which	
CC	CC	is heterologous to the CDR and is an antigenic, agonistic sequence from a	
CC	CC	thrombopoietin (TPO) receptor binding sequence. The antigenic sequence	
CC	CC	can be a binding sequence heterologous to the CDR, a cytotoxic T-	
CC	CC	lymphocyte (CTL)-epitope sequence, a T-helper cell sequence, a B-helper	
CC	CC	cell sequence or a combination of each. The variant or thrombopoietin	
CC	CC	synthebody, pharmaceutical and vaccine compositions are useful for	
CC	CC	stimulating proliferation, growth or differentiation of haematopoietic	
CC	CC	cells, particularly platelet progenitor cells. The variants are also	
CC	CC	useful for treating or preventing haematopoietic or immune disorders	
CC	CC	resulting from chemotherapy, radiation therapy, or bone marrow	
CC	CC	transfusions (e.g. thrombocytopenia or dissminated intravascular	
CC	CC	coagulation). Compositions comprising the synthebodyes can be used for	
CC	CC	the mobilisation, amplification and ex vivo expansion of stem cells and	
CC	CC	committed precursor cells for autologous and allogeneic transplantation	
CC	CC	as well as for the expansion of stem cells for gene therapy. They are	
CC	CC	also useful as diagnostic or analytical reagents for studying the	
CC	CC	function of thrombopoietin and its receptor in vivo or in vitro. The	
CC	CC	sequence presented is the TPO receptor (MPL) agonist peptide, AF12505	
XX	SQ	Sequence 14 AA;	
		Query Match 100.0%; Score 73; DB 6; Length 14;	
		Best Local Similarity 100.0%; Pred. No. 1.4e-05;	
		Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY		1 IEGPTLRQMTLAARA 14 	
D6		1 IEGPTLRQMTLAARA 14 	
		RESULT 15	
ID		ABR62907 standard; peptide; 14 AA.	
XX		ABR62907;	
AC		04-DEC-2003 (first entry)	
XX		Thrombopoietin mimetic peptide AP12505.	
DT		Thrombopoietin; mimetic; thrombocytopenia; antibody targeting.	
DE			
XX			

XX OS Synthetic.
 XX PN WO2003059251-A2.
 XX PD 24-JUL-2003.
 XX PF 22-OCT-2002; 2002WO-US033991.
 XX PR 22-OCT-2001; 2001US-0344614P.
 XX PR 19-SRP-2002; 2002US-0412455P.
 XX PA (SCRI) SCRIPPS RES INST.
 XX PI Barbas CF, Rader C, Sinha SC, Lerner R;
 XX DR WPI; 2003-636673/60.
 XX PT Antibody targeting compound useful e.g. for diagnostic immunoassays and
 XX PT treating microbial diseases comprises targeting or biological agent
 XX PT covalently linked to combining site of the antibody.
 XX PS Example 7; Page 62; 56pp; English.
 XX CC The present sequence is that of thrombopoietin (TPO) mimetic peptide
 CC AFI2305, which mimics the activity of recombinant TPO. The invention
 CC provides antibody targeting compounds that are used to reprogram the
 CC specificity of an antibody. The antibody targeting compound is linked to
 CC the combining site of the antibody, such that the modified antibody takes
 CC on the binding specificity of the targeting agent. In an example from the
 CC invention, a TPO receptor targeting antibody compound was prepared by
 CC covalently linking peptide AFI2305 to aldolase monoclonal antibody 38C2.
 CC The TPO receptor targeting antibody compound can be used to treat
 CC thrombocytopaenia resulting from chemotherapy and bone marrow
 CC transplantation
 XX SQ Sequence 14 AA;
 XX
 XX Query Match 100.0%; Score 73; DB 7; Length 14;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IEGPTLRQWLARA 14
 Db 1 IEGPTLRQWLARA 14
 Db
 XX RESULT 16
 XX ID ADC33697 standard; peptide; 14 AA.
 XX AC ADC33697;
 XX DT 18-DEC-2003 (first entry)
 XX DE Erythropoietin receptor/erythropoietin consensus peptide SEQ ID NO:1.
 XX KM chimeric retrovirus envelope protein; ecotropic envelope protein;
 XX KM cytoskeletal; gene therapy; cancer.
 XX OS Synthetic.
 XX OS WO2003076596-A2.
 XX PN 18-SEP-2003.
 XX PD 07-MAR-2003; 2003WO-US007323.
 XX PR 08-MAR-2002; 2002US-0362655P.
 XX PR (UYMA-) UNIV MASSACHUSETTS.
 XX PA Green MR, Gollan TJ;
 XX PI

XX DR WPI; 2003-722332/68.
 XX DX
 XX PT New chimeric retrovirus envelope protein comprising an ecotropic envelope
 XX PT protein and a heterologous short peptide ligand inserted within the
 XX PT ecotropic envelope protein useful for treating cancer.
 XX PS Disclosure; SEQ ID NO 1; 42pp; English.
 XX CC The present invention describes a chimeric retrovirus envelope protein
 CC (1) comprising an ecotropic envelope protein and a heterologous short
 CC peptide ligand inserted within the ecotropic envelope protein. Also
 CC described: (1) a nucleic acid molecule comprising a sequence encoding the
 CC recombinant chimeric envelope protein; (2) a vector comprising a nucleic
 CC acid sequence encoding the chimeric envelope protein; (3) a recombinant
 CC retroviral particle comprising a chimeric envelope protein comprising a
 CC heterologous short peptide ligand; (3) altering retroviral tropism; (4)
 CC identifying a nucleic acid sequence encoding the chimeric envelope
 CC protein that alters viral tropism; (5) delivering a nucleic acid sequence
 CC to a cell; and (6) treating cancer. (1) has cytostatic activity and can
 CC be used in gene therapy. The chimeric retrovirus envelope protein is
 CC useful for treating cancer, which comprises providing a cancer cell, e.g.
 CC human cancer cell and infecting the cancer cell with a virus, e.g.
 CC retrovirus comprising the chimeric envelope protein comprising a
 CC heterologous short peptide ligand and a therapeutically useful gene, e.g.
 CC encoding thymidine kinase. The present sequence represents an
 CC erythropoietin receptor/erythropoietin consensus peptide, which is given
 CC in the exemplification of the present invention.
 XX SQ Sequence 14 AA;
 XX
 XX Query Match 100.0%; Score 73; DB 7; Length 14;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IEGPTLRQWLARA 14
 Db 1 IEGPTLRQWLARA 14
 Db
 XX RESULT 17
 XX ID ADN59652 standard; peptide; 14 AA.
 XX AC ADN59652;
 XX DT 01-JUL-2004 (first entry)
 XX DE Thrombopoietin mimetic peptide (TMP), seq id 1.
 XX KM Haemostatic; antihaemic; immunosuppressive; platelet;
 XX KM transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
 XX KM TMP; c-mpl receptor; platelet precursor; megakaryocyte;
 XX KM thrombocytopaenia; aplastic anaemia; autoimmune thrombocytopaenia;
 XX KM autoimmune haemolytic anaemia; Hughes' s syndrome;
 XX KM lupoid thrombocytopaenia.
 XX OS Homo sapiens.
 XX OS WO2003031589-A2.
 XX PN 17-APR-2003.
 XX PD 11-OCT-2002; 2002WO-US032552.
 XX PR 11-OCT-2001; 2001US-0328666P.
 XX PR 10-OCT-2002; 2002US-00269806.
 XX PA (AMGE-) AMGEN INC.
 XX PA Min H, Sitney KC, Hartley C;
 XX PI WPI; 2003-403101/38.
 XX DR

XX Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
PT which stimulate the production of platelets and/or the production of
PT platelet precursors, useful for treating thrombocytopenia.
XX
25 Disclosure; SEQ ID NO 1; 126pp; English.

The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that binds to the c-mpl (mpl) receptor, and which stimulates the production of platelets and/or the production of platelet precursors, is new. Further disclosed is a composition of matter (II) that binds to an mpl receptor, and a pharmaceutical composition comprising (II) and a carrier. The pharmaceutical composition of the invention is useful for treating thrombocytopenia in an animal, and for increasing megakaryocytes or platelets in a patient. The TMP of the invention is useful for treating conditions involving a megakaryocyte and/or platelet deficiency, e.g., disease conditions involving thrombocytopenia such as aplastic anaemia, autoimmune thrombocytopenia, drug induced immune thrombocytopenia, autoimmune haemolytic anaemia, Hughes's syndrome and lupoid thrombocytopenia. The TMP of the invention is also useful for maintaining the viability or storage life of platelets and/or megakaryocytes and its derived cells. The compounds demonstrate an improved ability to bind to and/or trigger transmembrane signal through, i.e. activating, the mpl receptor the compounds have superior thrombopoietic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelets and/or megakaryocytic activity, i.e. the ability to stimulate, in vivo and in vitro, the production of platelet precursors. Further, certain of the compounds also exhibit superior therapeutic properties, such as improved plasma half-life, biological activity and in vivo circulation time. The current sequence represents a TMP of the invention

Query Match	100.0%	Score 73;	DB 7;	Length 14;
Best Local Similarity	100.0%	Pred. No.	1.4e-05;	
Matches 14; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

```
QY      1 IEGPTLRQWLAARA 14
        |||||
Db      1 IEGPTLRQWLAARA 14
```

RESULT 18
ADL27293

AC ADL27293;

DT 03-JUN-2004 (first entry)

DE Amino acid sequence of a thrombopoietin agonist peptide.

KW fusion protein; C4bp; alpha chain; systemic lupus erythematosus.

05 Homo sapiens.

OS Synthetic.

PN WO2004020639-A2.

PD 11-MAR-2004

PF 12-AUG-2003; 2003WO-EP008928.

PR 14-AUG-2002; 2002EP-00292043.

PA (AVID-) AVIDIS SA.

PI Garnier L, Hill F, Julien M;

DR WPI; 2004-239202/22.

PT Obtaining a recombinant fusion protein, useful for treating lupus,

PT comprises providing a prokaryotic host cell carrying a nucleic acid
PT encoding the recombinant protein operably linked to a promoter functional
PT in the prokaryotic cell.

PS Claim 8; Page 48; 69pp; English.

CC The specification describes a method for obtaining a recombinant fusion
CC protein comprising a scaffold of a C-terminal core protein of C4bp alpha
CC chain, where the recombinant fusion protein is capable of forming
CC multimers in soluble form in a prokaryotic host cell. The method
CC comprises providing a prokaryotic host cell carrying a nucleic acid
CC encoding the recombinant protein operably linked to a promoter functional
CC in the prokaryotic cell, culturing the host cell under conditions where
CC the recombinant protein is expressed, and recovering the recombinant
CC protein where the protein is recovered in multimeric form without
CC performing a scaffold refolding step. The protein is useful for treating
CC systemic lupus erythematosus. The present sequence represents a
CC thrombopoietin agonist peptide, which is used to produce fusion proteins
CC of the invention.

Query Match	100.0%	Score 73;	DB 8;	length 14;
Best Local Similarity	100.0%;	Pred. No. 1.4e-05;		
Matches 14; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0.

```
QY      1 IEGPTLRQWLAARA 14
         |||||
Db      1 IEGPTLRQWLAARA 14
```

RESULT 19

ID ADM72483 standard; peptide; 14 AA

AC ADM72483;

DT 17-JUN-2004 (first entry)

DE TPO mimetic peptide fragment.

KW TPO; haematopoietic stem cell; thrombopoietin; haemostatic;
KW stem cell therapy; HSC; transplantation; engraftment; mimetic.
KW

OS Synthetic.

PN WO2004026332-A1.

PD 01-APR-2004.

PF 18-SEP-2003; 2003WO-US029701

PR 18-SEP-2002; 2002US-0411700P

XX

XX

XX

XX

PT Increasing hematopoietic stem cell production in subject, useful in
PT reducing the incidence of delayed primary engraftment, comprises
PT administering a Thrombopoietin mimetic compound e.g., a peptide to a
PT subject.

PS Disclosure; Fig 2; 32pp; English

CC The invention relates to a method (M1) for increasing haematopoietic stem
CC cell production in a subject which involves administering a
CC Thrombopoietin (TPO) mimetic compound to the subject. Also included is
CC another method (M2) of providing haematopoietic stem cells to a subject
CC which involves administering a TPO mimetic compound to a subject to

CC enhance expansion of a stem cell population within bone marrow and/or
 CC mobilize stem cells in peripheral circulation, harvesting one or more of
 CC the bone marrow stem cells or the stem cells in the peripheral
 CC circulation, and transplanting the harvested stem cells into the subject.
 CC A method (M3) is also provided for reducing a time to engraftment
 CC following reinfusion of stem cells in a subject, involves administering a
 CC TPO mimetic compound to the subject, enhancing the expansion of the stem
 CC cell population within bone marrow and/or mobilizing the stem cells in
 CC peripheral circulation, harvesting one or more of the bone marrow stem
 CC cells or one or more of the stem cells in the peripheral circulation, and
 CC transplanting the one or more harvested stem cells into the subject. TPO
 CC mimetic compounds are disclosed as peptides, including cyclic or modified
 CC peptides. (M1) is useful for increasing haematopoietic stem cell
 CC production in a subject e.g., human. (M3) is useful for reducing time to
 CC engraftment following reinfusion of stem cells, reducing the incidence of
 CC delayed primary engraftment, reducing the incidence of secondary failure
 CC of platelet production and reducing the time of platelet and/or
 CC neutrophil engraftment following reinfusion of stem cells in a subject.
 CC (M1) is also useful for increasing the number of stem cells from a donor
 CC whose cells are then used for rescue of recipient subject. Also useful in
 CC the treatment of thrombocytopenia. (M1) enables transplantation to
 CC proceed in patients who would not otherwise be considered as candidates
 CC because of unacceptably high risk of failed engraftment, reduces the
 CC number of aphereses required to generate a minimum acceptable harvest,
 CC reduces the incidence of primary and secondary failure of engraftment by
 CC increasing the number of haematopoietic stem cells (HSCs) available for
 CC transplantation and reduces the time required for primary engraftment.
 CC The present sequence represents an example of TPO mimetic peptide
 CC fragment.

XX Sequence 14 AA;

Query Match 100.0%; Score 73; DB 8; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLARA 14
 |||||
 1 IEGPTLRQWLARA 14

RESULT 20

ADQ16584 ID ADQ16584 standard; peptide; 14 AA.

XX AC ADQ16584;

XX DT 09-SEP-2004 (first entry)

DE Agonist TPO mimetic peptide SEQ ID NO:1.

XX immunoglobulin; complementarity determining region; CDR; peptide mimetic;

KM erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;

KW immunotherapy; thrombocytopenia.

OS Unidentified.

XX WO2004050017-A2.

PD 17-JUN-2004.

XX 17-NOV-2003; 2003WO-US036894.

XX PR 02-DEC-2002; 2002US-00307724.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Frederickson S, Renshaw M;

XX WPI; 2004-460973/43.

PT New immunoglobulin molecule comprising a region, where two
 complementary determining regions (CDRs) are replaced with EPO mimetic

PT or a TPO mimetic, useful for treating thrombocytopenia.
 XX Claim 8; SEQ ID NO 1; 107pp; English.

XX The invention relates to a novel immunoglobulin molecule or its fragment
 CC comprising a region where amino acid residues corresponding to at least a
 CC portion of a two complementarity determining regions (CDRs) are replaced
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 CC invention has immunosuppressive activity, and may have a use in
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow
 CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide.

XX Sequence 14 AA;

Query Match 100.0%; Score 73; DB 8; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLARA 14
 |||||
 1 IEGPTLRQWLARA 14

RESULT 21

AAW35416 ID AAW35416 standard; peptide; 15 AA.

XX AC AAW35416;

XX DT 11-MAR-1998 (first entry)

DE Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;

KW haematological disorder; thrombocytopenia; chemotherapy;

KW radiation therapy; bone marrow transfusion; diagnosis;

XX signal transduction; receptor activation; cell culture.

OS Synthetic.

XX Key Location/Qualifiers

FT Cross-links 1 /note="linked via disulfide bond to Cys1 of identical
 FT peptide" peptide" 15
 FT Modified-site 15 /note="NH2-Ala"

XX WO9640750-A1.

XX PD 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009623.

XX PR 07-JUN-1995; 95US-00478128.

XX PR 07-JUN-1995; 95US-00485301.

XX (GLAXO) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cairlia SE, Duffin DJ, Gates CM, Johnson SS;

XX Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX Example 9; Page 73; 106pp; English.

CC The present peptide, which binds the thrombopoietin receptor (TR), can be

CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 73; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEPTLRQWLAAARA 14
 |||||
 Db 2 IEPTLRQWLAAARA 15

RESULT 22
 AAM36776
 ID AAM36776 standard; peptide; 15 AA.
 XX
 AC AAM36776;

DT 11-MAR-1998 (first entry)
 XX
 DE Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;
 KM haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.

OS Synthetic.

XX Key Location/Qualifiers

FT Cross-links 1 /note="linked via disulfide bond to Cys1 of identical
 FT peptide"
 FT Modified-site 15 /note="NH2-Ala"

PN WO9640750-A1.

PD 19-DEC-1996.

PR 07-JUN-1996; 96WO-US009623.

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1995; 95US-00485301.

PA (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

DR WPI; 1997-052226/05.

PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of hematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

PS Example 9; Page 77; 106pp; English.

CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 73; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEPTLRQWLAAARA 14
 |||||
 Db 2 IEPTLRQWLAAARA 15

RESULT 23
 AAM66712
 ID AAM66712 standard; peptide; 15 AA.
 XX
 AC AAM66712;

DT 01-DEC-1998 (first entry)

DE Peptide chain of compound which binds to the thrombopoietin receptor.
 XX thrombopoietin receptor; haematological disorder; screening; agonist;
 KW assay; megakaryocyte; blood disorder; thrombocytopenia; TPO.

OS Synthetic.

XX Key Location/Qualifiers

FT Region 1..14
 FT Modified-site 15 /note="thrombopoietin receptor agonist"

FT /note="Epsilon amino group of Lys¹⁵ in its amide form, is
 FT attached to another peptide chain identical to the region
 FT (residues 1 to 14) of this peptide"

PN WO9825965-A2.

PD 18-JUN-1998.

PR 09-DEC-1997; 97WO-EP006850.

PR 11-DEC-1996; 96US-00764640.

PA (GLAXO) GLAXO GROUP LTD.

PI Dower WJ, Barrett RM, Cwiria SE, Gates CM, Schatz PJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RM, Depierre RB, Podduturi S;
 PI Yin Q;

DR WPI; 1998-377261/32.

PT New peptide compound(s) which can bind and activate thrombopoietin
 PT receptor - may be used in treating haematological disorders and in
 PT methods for screening for new thrombopoietin receptor agonists.

PS Claim 2; Page 60; 78pp; English.

CC The invention relates to peptide compounds composed of two peptide chains
 CC attached to each of the amino groups of a single lys in the amide form.
 CC The compounds are of formula (Pept1)(Pept2)K(NH2), where Pept1 is of
 CC formula: X1-I-E-X2-P-T-L-X3-X4-X5-L-X6-X7-X8-X9'-X10'; and Pept2 is of
 CC formula: X1-I-E-X2-P-T-L-X3-X4-X5-L-X6-X7-X8-X9'-X10'. X1 = H or acyl; X2
 CC = Gly or Sar (sarcosine); X3 = Arg, Ala, Nle (norleucine) or N-
 CC acetyllysine; X4 = Gln or Glu; X5 = Trp, L-1-naphthylalanine or Phe; X6 =
 CC Ala, 5-aminopentanoic acid or 2-aminobutyric acid; X7 = Ala,
 CC diphenylalanine, or is absent; X8 = Arg, P- amino-phenylalanine, N-
 CC acetyl-lysine, or is absent; X9, X9' = Ala, beta Ala, N-methyl-alanine,
 CC Sar, or is absent; X10, X10' = beta Ala or is absent. The new peptides
 CC are capable of binding to, and activating, the thrombopoietin (TPO)
 CC receptor. They may be used in vitro as tools for understanding the
 CC biological role of TPO. They may be used as competitive binders in assays
 CC to screen for new TPO receptor agonists. They may be used as reagents for
 CC detecting TPO receptors in living cells, biological fluids, etc. They may

CC be used to maintain growth and proliferation of TPO-dependent cells and
 CC for in vitro expansion of megakaryocytes. They may be used to activate
 CC TPO receptors in vivo, e.g., to treat blood disorders or
 CC thrombocytopenia associated with bone marrow transplants, radiotherapy
 CC or chemotherapy. The present sequence represents a specific example of
 CC (Pep)K(NH2)

XX Sequence 15 AA;

Query Match 100.0%; Score 73; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
 1 IEGPTLRQWLAAARA 14

Db

RESULT 24
 AAB20684 standard; peptide; 15 AA.

XX AAB20684;

DT 20-DEC-2000 (first entry)

XX Thrombocyte generation promoting peptide.

XX Thrombocyte; promotion; generation.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 15 /note="optionally amidated; optionally attached to the C
 FT -terminal cysteine of a similar peptide"

PN CNI254718-A.

XX 31-MAY-2000.

XX 20-NOV-1998; 98CN-00125011.

XX 20-NOV-1998; 98CN-00125011.

XX (BIOL-) INST BIOLOGICAL ENG CHINESE ACAD MILITAR.

PI Cheng D, Li C, Huang P;

XX WPI; 2000-533568/49.

PT Active peptide.

PS Claim 1; Page 1; Spp; Chinese.

XX The present invention discloses an active peptide which promotes
 CC thrombocyte generation. The active peptide can be synthesised by a
 CC polypeptide solid-phase synthesis method, and has the monomer sequence of
 CC IEGPTLRQWLAAARA and the amidated peptide chain structure of
 CC IEGPTLRQWLAAARAC-NH2. Its activity is increased by 20 times for its
 CC monomer, or by 10 times for the amidated peptide chain compared with the
 CC monomer, or by 100 times for its dimer compared with its monomer

XX Sequence 15 AA;

Query Match 100.0%; Score 73; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
 1 IEGPTLRQWLAAARA 14

Db 1 IEGPTLRQWLAAARA 14

RESULT 25
 AAU25996 standard; peptide; 15 AA.

XX AAU25996;

DT 17-DEC-2001 (first entry)

XX Human thrombopoietin receptor (TPO-R) activator peptide #182.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 XX haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; laci gene.

XX Homo sapiens.

XX US6251864-B1.

XX 26-JUN-2001.

XX 01-MAR-2000; 2000US-00516704.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

XX 07-JUN-1996; 96WO-US009623.

XX 15-AUG-1996; 96US-00699027.

XX (GLAXO) GLAXO GROUP LTD.

XX Power WJ, Barrett RW, Cwiria SE, Gabes CM, Schatz PJ,

PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprience RB, Podduturi S,

PI Yin Q;

XX WPI; 2001-564142/63.

XX Disclosures; Col 143-144; 128pp; English.

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent haematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines

XX Sequence 15 AA;

Query Match 100.0%; Score 73; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
 1 IEGPTLRQWLAAARA 15

Db 2 IEGPTLRQWLAAARA 15

RESULT 26
AAU25831
ID AAU25831 standard; peptide; 15 AA.
XX
AC AAU25831;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human thrombopoietin receptor (TPO-R) activator peptide #17.
XX
KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
KW bone marrow transplantation; haematological disorder; platelet disorder;
KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
XX
OS Homo sapiens.
XX
PN US6251864-B1.
XX
PD 26-JUN-2001.
XX
PF 01-MAR-2000; 2000US-00516704.
XX
PR 07-JUN-1995; 95US-00478128.
XX
PR 07-JUN-1995; 95US-00485301.
XX
PR 07-JUN-1996; 96WO-US009623.
XX
PR 15-AUG-1996; 96US-00699027.
XX
PA (GLAXO) GLAXO GROUP LTD.
XX
PI Dower WJ, Barrett RM, Cwirla SE, Gates CM, Schatz PJ,
PI Balasubramanian P, Magstrom CR, Hendren RM, Deprience RB, Podduturi S;
PI Yin Q;
XX
DR WPI; 2001-564142/63.
XX
PT Activating thrombopoietin receptors in cells, used to treat
PT thrombocytopenia and hematological disorders, comprises contacting cells
PT with peptides and peptide mimetics attached to hydrophilic polymers.
XX
PS Claim 1; Col 69-70; 128pp; English.
XX
CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
CC of activating thrombopoietin receptors in cells comprise contacting the
CC cells with effective amounts of peptides and peptide mimetics attached to
CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
CC as that due to chemotherapy, radiation therapy or bone-marrow
CC transplantation and to prevent thrombocytopenia in patients at risk. The
CC sequences are used to treat and prevent haematological disorders
CC including thrombocytopenia and platelet disorders. They are used in vitro
CC as unique tools for understanding the biological role of thrombopoietin
CC (TPO) and to develop other compounds that bind to and activate the TPO
CC receptor. The peptides can be used to detect TPO receptors on living
CC cells and fixed cells, in biological fluids, in tissue homogenates, and
CC in purified or natural biological materials. They may also be used for in
CC situ staining, fluorescence-activated cell sorting, Western blotting and
CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
CC be used for in vitro expansion of megakaryocytes and their committed
CC progenitors alone or in conjunction with additional cytokines
XX
SO Sequence 15 AA:

Query Match 100.0%; Score 73; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IEGPTLRQWLAAARA 14
|||||

DB 1 IEGPTLRQWLAAARA 14
RESULT 27
ABP51670
ID ABP51670 standard; peptide; 15 AA.
XX
AC ABP51670;
XX
DT 01-OCT-2002 (first entry)
XX
DE Thrombopoietin (TPO) agonist mimetic peptide SEQ ID NO:2.
XX
KW TPO; EPO; thrombopoietin; erythropoietin; antibody; CDR region;
KW complementarity determining region; immunoglobulin; antianemic;
KW haemostatic; nephrotropic; haematopoietic cell; haematopoiesis.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO200246238-A2.
XX
PD 13-JUN-2002.
XX
PF 05-DEC-2001; 2001WO-US047656.
XX
PR 05-DEC-2000; 2000US-0251448P.
XX
PR 04-MAY-2001; 2001US-0288889P.
XX
PR 29-MAY-2001; 2001US-0294068P.
XX
PA (ALEXON) PHARM INC.
XX
PI Bowdish KS, Barbass-Frederickson S, Renshaw M;
XX
DR WPI; 2002-566610/60.
XX
PT A novel immunogen molecule comprising a region in which amino acid
PT residues corresponding to at least a portion of the complementary
PT determining region are replaced or fused with an erythropoietin or
PT thrombopoietin mimetic.
XX
PS Claim 19; Page 6; 113pp; English.
XX
CC The present invention describes an immunoglobulin molecule or its fragment
CC (I) comprising a region where amino acid residues corresponding to at
CC least a portion of the complementary determining region (CDR) are
CC replaced or fused with biologically active peptides e.g. a peptide
CC mimetic such as an erythropoietin (EPO) or thrombopoietin (TPO) mimetic,
CC that is flanked with proline at its carboxy terminus. (I) has
CC antianemic, haemostatic and nephrotropic activities, and can be used as
CC a stimulator of proliferation, differentiation and maturation of
CC haematopoietic cells, and a stimulator of haematopoiesis. (I) is useful
CC for stimulating proliferation, differentiation or growth of
CC promegakaryocytes or megakaryocytes, where (I) is contacted with
CC promegakaryocytes or megakaryocytes, which results in increased platelet
CC production. (I) with a region where amino acid residues corresponding to
CC a portion of CDR is replaced with an EPO mimetic, or which has one or
CC more of its CDRs fused to an EPO mimetic, is useful for increasing the
CC production of red blood cells, where (I) is contacted with haematopoietic
CC stem cells or their progenitors. (I) is useful for diagnostics or
CC therapeutics, in cell isolation strategies, and for treating patients
CC suffering from deficiency in cell populations caused by disease.
CC disorders or treatments related to the suppression of haematopoiesis.
CC ABQ73288 to ABQ73377 and ABP51669 to ABP51696 represent sequences used in
CC the exemplification of the present invention
XX
SO Sequence 15 AA:

Query Match 100.0%; Score 73; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IEGPTLRQWLAAARA 14
|||||

DB 1 IEGPTLRQWLAAARA 14

RESULT 28
ABR62908
ID ABR62908 standard; peptide; 15 AA.

AC ABR62908;

DT 04-DEC-2003 (first entry)

DE Thrombopoietin mimetic peptide AFI2505.

KM Thrombopoietin; mimetic; thrombocytopenia; antibody targeting.

XX Synthetic.

PN WO2003059251-A2.

PD 24-JUL-2003.

PF 22-OCT-2002; 2002WO-US033991.

PR 22-OCT-2001; 2001US-0344614P.

PR 19-SEP-2002; 2002US-0412455P.

PA (SCRI) SCRIIPS RES INST.

PI Barbas CF, Rader C, Sinha SC, Lerner R;

DR MPI; 2003-636673/60.

PT Antibody targeting compound useful e.g. for diagnostic immunoassays and
PT creating microbial diseases comprises targeting or biological agent
PT covalently linked to combining site of the antibody.

XX Example 7; Page 62; 56pp; English.

XX The present sequence is that of thrombopoietin (TPO) mimetic peptide
CC AFI2505, modified to include an N-terminal Cys residue. AFI2505 mimics
CC the activity of recombinant TPO. The invention provides antibody
CC targeting compounds that are used to reprogram the specificity of an
CC antibody. The antibody targeting compound is linked to the combining
CC site of the antibody, such that the modified antibody takes on the binding
CC specificity of the targeting agent. In an example from the invention, a
CC TPO receptor targeting antibody compound was prepared by covalently
CC linking Cys-modified peptide AFI2505 to aldolase monoclonal antibody 38C2
CC using a maleimide-diketone linker. The resulting TPO receptor targeting
CC antibody compound can be used to treat thrombocytopenia resulting from
CC chemotherapy and bone marrow transplantation

XX Sequence 15 AA;

Query Match 100.0%; Score 73; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
2 IEGPTLRQWLAAARA 15

DB 2 IEGPTLRQWLAAARA 15

RESULT 29

ADM72485
ID ADM72485 standard; peptide; 15 AA.

AC ADM72485;

DT 17-JUN-2004 (first entry)

DE TPO mimetic peptide fragment.

KM TPO; haematopoietic stem cell; thrombopoietin; haemostatic;
KM stem cell therapy; HSC; transplantation; engraftment; mimetic.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 15
FT /label= bAla
FT /note= "beta-alanine"

PN WO2004026332-A1.

PD 01-APR-2004.

PF 18-SEP-2003; 2003WO-US029701.

PR 18-SEP-2002; 2002US-0411700P.

PR 18-SEP-2002; 2002US-0411779P.

PA (THRE-) 3-DIMENSIONAL PHARM INC.

PI Kaushansky K, Macdonald BR;

DR MPI; 2004-283153/26.

PT Increasing hematopoietic stem cell production in subject, useful in
PT reducing the incidence of delayed primary engraftment, comprises
PT administering a Thrombopoietin mimetic compound e.g., a peptide to a
PT subject.

XX Disclosure; Fig 2; 32pp; English.

XX The invention relates to a method (M1) for increasing haematopoietic stem
CC cell production in a subject which involves administering a
CC Thrombopoietin (TPO) mimetic compound to the subject. Also included is
CC another method (M2) of providing haematopoietic stem cells to a subject
CC which involves administering a TPO mimetic compound to a subject to
CC enhance expansion of a stem cell population within bone marrow and/or
CC mobilize stem cells in peripheral circulation, harvesting one or more of
CC the bone marrow stem cells or the stem cells in the peripheral
CC circulation, and transplanting the harvested stem cells into the subject.
CC A method (M3) is also provided for reducing a time to engraftment
CC following reinfusion of stem cells in a subject, involves administering a
CC TPO mimetic compound to the subject, enhancing the expansion of the stem
CC cell population within bone marrow and/or mobilizing the stem cells in
CC peripheral circulation, harvesting one or more of the bone marrow stem
CC cells or one or more of the stem cells in the peripheral circulation, and
CC transplanting the one or more harvested stem cells into the subject. TPO
CC mimetic compounds are disclosed as peptides, including cyclic or modified
CC peptides. (M1) is useful for increasing haematopoietic stem cell
CC production in a subject e.g., human. (M3) is useful for reducing time to
CC engraftment following reinfusion of stem cells, reducing the incidence of
CC delayed primary engraftment, reducing the incidence of secondary failure
CC of platelet production and reducing the time of platelet and/or
CC neutrophil engraftment following reinfusion of stem cells in a subject.
CC (M1) is also useful for increasing the number of stem cells from a donor
CC whose cells are then used for rescue of recipient subject. Also useful in
CC the treatment of thrombocytopenia. (M1) enables transplantation to
CC proceed in patients who would not otherwise be considered as candidates
CC because of unacceptably high risk of failed engraftment, reduces the
CC number of adherences required to generate a minimum acceptable harvest,
CC reduces the incidence of primary and secondary failure of engraftment by
CC increasing the number of haematopoietic stem cells (HSCs) available for
CC transplantation and reduces the time required for primary engraftment.
CC The present sequence represents an example of TPO mimetic peptide
CC fragment.

XX Sequence 15 AA;

Query Match 100.0%; Score 73; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLARA 14
 |||||
 Db 1 IEGPTLRQWLARA 14

RESULT 30
 ADM72479
 ID ADM72479 standard; peptide, 15 AA.
 XX
 AC ADM72479;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE TPO mimetic peptide fragment.
 XX
 XX TPO; haematopoietic stem cell; thrombopoietin; haemostatic;
 KM stem cell therapy; HSC; transplantation; engraftment; mimetic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 15
 FT /note= "beta-alanine"
 XX
 PN WO2004026332-A1.
 XX
 PD 01-APR-2004.
 XX
 PF 18-SEP-2003; 2003WO-US029701.
 XX
 PR 18-SEP-2002; 2002US-0411700P.
 PR 18-SEP-2002; 2002US-0411779P.
 XX
 PA (THRE-) 3-DIMENSIONAL PHARM INC.
 XX
 PI Kaushansky K, Macdonald BR;
 DR WPI; 2004-283153/26.
 XX
 PT Increasing hematopoietic stem cell production in subject, useful in
 PT reducing the incidence of delayed primary engraftment, comprises
 PT administering a Thrombopoietin mimetic compound e.g., a peptide to a
 PT subject.
 XX
 PS Disclosure; Fig 2; 32pp; English.
 XX
 CC The invention relates to a method (M1) for increasing haematopoietic stem
 CC cell production in a subject which involves administering a
 CC Thrombopoietin (TPO) mimetic compound to the subject. Also included is
 CC another method (M2) of providing haematopoietic stem cells to a subject
 CC which involves administering a TPO mimetic compound to a subject to
 CC enhance expansion of a stem cell population within bone marrow and/or
 CC mobilize stem cells in peripheral circulation, harvesting one or more of
 CC the bone marrow stem cells or the stem cells in the peripheral
 CC circulation, and transplanting the harvested stem cells into the subject.
 CC A method (M3) is also provided for reducing a time to engraftment
 CC following reinfusion of stem cells in a subject, involves administering a
 CC TPO mimetic compound to the subject, enhancing the expansion of the stem
 CC cell population within bone marrow and/or mobilizing the stem cells in
 CC peripheral circulation, harvesting one or more of the bone marrow stem
 CC cells or one or more of the stem cells in the peripheral circulation, and
 CC transplanting the one or more harvested stem cells into the subject. TPO
 CC mimetic compounds are disclosed as peptides, including cyclic or modified
 CC peptides. (M1) is useful for increasing haematopoietic stem cell
 CC production in a subject e.g., human. (M3) is useful for reducing time to
 CC engraftment following reinfusion of stem cells, reducing the incidence of
 CC delayed primary engraftment, reducing the incidence of secondary failure
 CC of platelet production and reducing the time of platelet and/or
 CC neutrophil engraftment following reinfusion of stem cells in a subject.
 CC (M1) is also useful for increasing the number of stem cells from a donor
 CC whose cells are then used for rescue of recipient subject. Also useful in
 CC the treatment of thrombocytopenia. (M1) enables transplantation to
 CC proceed in patients who would not otherwise be considered as candidates

CC because of unacceptably high risk of failed engraftment, reduces the
 CC number of aphereses required to generate a minimum acceptable harvest,
 CC reduces the incidence of primary and secondary failure of engraftment by
 CC increasing the number of haematopoietic stem cells (HSCs) available for
 CC transplantation and reduces the time required for primary engraftment.
 CC The present sequence represents an example of TPO mimetic peptide
 CC fragment.
 XX
 SQ Sequence 15 AA;
 XX
 XX

Query Match 100.0%; Score 73; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLARA 14
 |||||
 Db 1 IEGPTLRQWLARA 14

RESULT 31
 ADM72478
 ID ADM72478 standard; peptide, 15 AA.
 XX
 AC ADM72478;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE TPO mimetic peptide fragment.
 XX
 XX TPO; haematopoietic stem cell; thrombopoietin; haemostatic;
 KM stem cell therapy; HSC; transplantation; engraftment; mimetic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 15
 FT /note= "Iys (15) is linked to one copy of the TPO mimetic
 FT peptide through the alpha amino group and to a second
 FT copy of the peptide (not shown) via the omega amino
 FT group"
 XX
 PN WO2004026332-A1.
 XX
 PD 01-APR-2004.
 XX
 PF 18-SEP-2003; 2003WO-US029701.
 XX
 PR 18-SEP-2002; 2002US-0411700P.
 PR 18-SEP-2002; 2002US-0411779P.
 XX
 PA (THRE-) 3-DIMENSIONAL PHARM INC.
 XX
 PI Kaushansky K, Macdonald BR;
 DR WPI; 2004-283153/26.
 XX
 PT Increasing hematopoietic stem cell production in subject, useful in
 PT reducing the incidence of delayed primary engraftment, comprises
 PT administering a Thrombopoietin mimetic compound e.g., a peptide to a
 PT subject.
 XX
 PS Disclosure; Fig 2; 32pp; English.
 XX
 CC The invention relates to a method (M1) for increasing haematopoietic stem
 CC cell production in a subject which involves administering a
 CC Thrombopoietin (TPO) mimetic compound to the subject. Also included is
 CC another method (M2) of providing haematopoietic stem cells to a subject
 CC which involves administering a TPO mimetic compound to a subject to
 CC enhance expansion of a stem cell population within bone marrow and/or
 CC mobilize stem cells in peripheral circulation, harvesting one or more of
 CC the bone marrow stem cells or the stem cells in the peripheral
 CC circulation, and transplanting the harvested stem cells into the subject.
 CC A method (M3) is also provided for reducing a time to engraftment

PN WO2004026332-A1.
XX
XX 01-APR-2004.
XX
XX 18-SEP-2003; 2003WO-US029701.
XX
XX 18-SEP-2002; 2002US-0411700P.
XX
XX 18-SEP-2002; 2002US-0411779P.
XX
XX (THRE-) 3-DIMENSIONAL PHARM INC.
XX
XX Kaushansky K, Macdonald BR;
XX
XX WPI; 2004-283153/26.
XX
XX Increasing hematopoietic stem cell production in subject, useful in
PT reducing the incidence of delayed primary engraftment, comprises
PT administering a Thrombopoietin mimetic compound e.g., a peptide to a
PT subject.
XX
XX Disclosure; Fig 2; 32pp; English.
XX
XX The invention relates to a method (M1) for increasing haematopoietic stem
XX cell production in a subject which involves administering a
XX Thrombopoietin (TPO) mimetic compound to the subject. Also included is
XX another method (M2) of providing haematopoietic stem cells to a subject
XX which involves administering a TPO mimetic compound to a subject to
XX enhance expansion of a stem cell population within bone marrow and/or
XX mobilize stem cells in peripheral circulation, harvesting one or more of
XX the bone marrow stem cells or the stem cells in the peripheral
XX circulation, and transplanting the harvested stem cells into the subject.
XX A method (M3) is also provided for reducing a time to engraftment
XX following reinfusion of stem cells in a subject, involves administering a
XX TPO mimetic compound to the subject, enhancing the expansion of the stem
XX cell population within bone marrow and/or mobilizing the stem cells in
XX peripheral circulation, harvesting one or more of the bone marrow stem
XX cells or one or more of the stem cells in the peripheral circulation, and
XX transplanting the one or more harvested stem cells into the subject. TPO
XX mimetic compounds are disclosed as peptides, including cyclic or modified
XX peptides. (M1) is useful for increasing haematopoietic stem cell
XX production in a subject e.g., human. (M3) is useful for reducing time to
XX engraftment following reinfusion of stem cells, reducing the incidence of
XX delayed primary engraftment, reducing the incidence of secondary failure
XX of platelet production and reducing the time of platelet and/or
XX neutrophil engraftment following reinfusion of stem cells in a subject.
XX (M1) is also useful for increasing the number of stem cells from a donor
XX whose cells are then used for rescue of recipient subject. Also useful in
XX the treatment of thrombocytopenia. (M1) enables transplantation to
XX proceed in patients who would not otherwise be considered as candidates
XX because of unacceptably high risk of failed engraftment, reduces the
XX number of aphereses required to generate a minimum acceptable harvest,
XX reduces the incidence of primary and secondary failure of engraftment by
XX increasing the number of haematopoietic stem cells (HSCs) available for
XX transplantation and reduces the time required for primary engraftment.
XX The present sequence represents an example of TPO mimetic peptide
XX fragment.
XX
XX Sequence 15 AA;
SQ

Query Match 100.0%; Score 73; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
| | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | |
Db 1 IEGPTLRQWLAAARA 14

RESULT 34
ADM72523
ID ADM72523 standard; peptide; 15 AA.
XX
XX ADM72523;

XX 17-JUN-2004 (first entry)
DT
XX
XX TPO mimetic peptide fragment.
DE
XX
XX TPO; haematopoietic stem cell; thrombopoietin; haemostatic;
KW stem cell therapy; HSC; transplantation; engraftment; mimetic.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 15
FT /note= "beta-alanine"
FT
XX
XX WO2004026332-A1.
XX
XX 01-APR-2004.
XX
XX 18-SEP-2003; 2003WO-US029701.
XX
XX 18-SEP-2002; 2002US-0411700P.
XX
XX 18-SEP-2002; 2002US-0411779P.
XX
XX (THRE-) 3-DIMENSIONAL PHARM INC.
XX
XX Kaushansky K, Macdonald BR;
XX
XX WPI; 2004-283153/26.
XX
XX Increasing hematopoietic stem cell production in subject, useful in
PT reducing the incidence of delayed primary engraftment, comprises
PT administering a Thrombopoietin mimetic compound e.g., a peptide to a
PT subject.
XX
XX Disclosure; Fig 2; 32pp; English.
XX
XX The invention relates to a method (M1) for increasing haematopoietic stem
XX cell production in a subject which involves administering a
XX Thrombopoietin (TPO) mimetic compound to the subject. Also included is
XX another method (M2) of providing haematopoietic stem cells to a subject
XX which involves administering a TPO mimetic compound to a subject to
XX enhance expansion of a stem cell population within bone marrow and/or
XX mobilize stem cells in peripheral circulation, harvesting one or more of
XX the bone marrow stem cells or the stem cells in the peripheral
XX circulation, and transplanting the harvested stem cells into the subject.
XX A method (M3) is also provided for reducing a time to engraftment
XX following reinfusion of stem cells in a subject, involves administering a
XX TPO mimetic compound to the subject, enhancing the expansion of the stem
XX cell population within bone marrow and/or mobilizing the stem cells in
XX peripheral circulation, harvesting one or more of the bone marrow stem
XX cells or one or more of the stem cells in the peripheral circulation, and
XX transplanting the one or more harvested stem cells into the subject. TPO
XX mimetic compounds are disclosed as peptides, including cyclic or modified
XX peptides. (M1) is useful for increasing haematopoietic stem cell
XX production in a subject e.g., human. (M3) is useful for reducing time to
XX engraftment following reinfusion of stem cells, reducing the incidence of
XX delayed primary engraftment, reducing the incidence of secondary failure
XX of platelet production and reducing the time of platelet and/or
XX neutrophil engraftment following reinfusion of stem cells in a subject.
XX (M1) is also useful for increasing the number of stem cells from a donor
XX whose cells are then used for rescue of recipient subject. Also useful in
XX the treatment of thrombocytopenia. (M1) enables transplantation to
XX proceed in patients who would not otherwise be considered as candidates
XX because of unacceptably high risk of failed engraftment, reduces the
XX number of aphereses required to generate a minimum acceptable harvest,
XX reduces the incidence of primary and secondary failure of engraftment by
XX increasing the number of haematopoietic stem cells (HSCs) available for
XX transplantation and reduces the time required for primary engraftment.
XX The present sequence represents an example of TPO mimetic peptide
XX fragment.
XX
XX Sequence 15 AA;
SQ

Query Match 100.0%; Score 73; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
 |||||
 1 IEGPTLRQWLAAARA 14

DB 1 IEGPTLRQWLAAARA 14

RESULT 35
 ADM72482
 ID ADM72482 standard; peptide; 15 AA.
 AC ADM72482;
 AD 17-JUN-2004 (first entry)
 DT XX
 DE TPO mimetic peptide fragment.
 XX
 KW TPO; haematopoietic stem cell; thrombopoietin; haemostatic;
 KM stem cell therapy; HSC; transplantation; engraftment; mimetic.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Modified-site 15
 FT /note= "lys (15) is linked to one copy of the TPO mimetic
 FT peptide through the alpha amino group and to a second
 FT copy of the peptide (not shown) via the omega amino
 FT group"
 PN WO2004026332-A1.
 PD 01-APR-2004.
 PF 18-SEP-2003; 2003WO-US029701.
 PR 18-SEP-2002; 2002US-0411700P.
 PR 18-SEP-2002; 2002US-0411779P.
 XX
 PA (THRE-) 3-DIMENSIONAL PHARM INC.
 PI Kaushansky K, Macdonald BR;
 DR WPI; 2004-283153/26.
 XX
 PT Increasing hematopoietic stem cell production in subject, useful in
 PT reducing the incidence of delayed primary engraftment, comprises
 PT administering a Thrombopoietin mimetic compound e.g., a peptide to a
 PT subject.
 XX
 PS Disclosure; Fig 2; 32pp; English.

CC The invention relates to a method (M1) for increasing haematopoietic stem
 CC cell production in a subject which involves administering a
 CC Thrombopoietin (TPO) mimetic compound to the subject. Also included is
 CC another method (M2) of providing haematopoietic stem cells to a subject
 CC which involves administering a TPO mimetic compound to a subject to
 CC enhance expansion of a stem cell population within bone marrow and/or
 CC mobilize stem cells in peripheral circulation, harvesting one or more of
 CC the bone marrow stem cells or the stem cells in the peripheral
 CC circulation, and transplanting the harvested stem cells into the subject.
 CC A method (M3) is also provided for reducing a time to engraftment
 CC following reinfusion of stem cells in a subject, involves administering a
 CC TPO mimetic compound to the subject, enhancing the expansion of the stem
 CC cell population within bone marrow and/or mobilizing the stem cells in
 CC peripheral circulation, harvesting one or more of the bone marrow stem
 CC cells or one or more of the stem cells in the peripheral circulation, and
 CC transplanting the one or more harvested stem cells into the subject. TPO
 CC mimetic compounds are disclosed as peptides, including cyclic or modified
 CC peptides. (M1) is useful for increasing haematopoietic stem cell
 CC production in a subject e.g., human. (M3) is useful for reducing time to
 CC engraftment following reinfusion of stem cells, reducing the incidence of

CC delayed primary engraftment, reducing the incidence of secondary failure
 CC of platelet production and reducing the time of platelet and/or
 CC neutrophil engraftment following reinfusion of stem cells in a subject.
 CC (M1) is also useful for increasing the number of stem cells from a donor
 CC whose cells are then used for rescue of recipient subject. Also useful in
 CC the treatment of thrombocytopenia. (M1) enables transplantation to
 CC proceed in patients who would not otherwise be considered as candidates
 CC because of unacceptably high risk of failed engraftment, reduces the
 CC number of aphereses required to generate a minimum acceptable harvest,
 CC increases the incidence of primary and secondary failure of engraftment by
 CC transplanting the number of haematopoietic stem cells (HSCs) available for
 CC The present sequence represents an example of TPO mimetic peptide
 CC fragment.

SQ Sequence 15 AA;

Query Match 100.0%; Score 73; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
 |||||
 1 IEGPTLRQWLAAARA 14

DB 1 IEGPTLRQWLAAARA 14

RESULT 36
 ADQ16585
 ID ADQ16585 standard; peptide; 15 AA.
 AC ADQ16585;
 AD 09-SEP-2004 (first entry)
 DT XX
 DE TPO mimetic peptide SEQ ID NO:2.
 XX
 KW immunoglobulin; complementarity determining region; CDR; peptide mimetic;
 KM erythropoietin; EPO; thrombopoietin; TPO; immunosuppressive;
 XX immunotherapy; thrombocytopenia.
 XX
 OS Unidentified.
 XX
 PN WO2004050017-A2.
 PD 17-JUN-2004.
 PF 17-NOV-2003; 2003WO-US036894.
 PR 02-DIC-2002; 2002US-00307724.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 PI Bowdish KS, Frederickson S, Renshaw M;
 DR WPI; 2004-460973/43.
 XX
 PT New immunoglobulin molecule comprising a region, where two
 PT complementarity determining regions (CDRs) are replaced with EPO mimetic
 PT or a TPO mimetic, useful for treating thrombocytopenia.
 XX
 PS Disclosure; SEQ ID NO 2; 107pp; English.

CC The invention relates to a novel immunoglobulin molecule or its fragment
 CC comprising a region where amino acid residues corresponding to at least a
 CC portion of a two complementarity determining regions (CDRs) are replaced
 CC with a peptide mimetic selected from an erythropoietin (EPO) mimetic and
 CC a thrombopoietin (TPO) mimetic. An immunoglobulin molecule of the
 CC invention has immunosuppressive activity, and may have a use in
 CC immunotherapy. The immunoglobulin molecule is useful for diagnosing or
 CC treating thrombocytopenia as a result of chemotherapy, bone marrow
 CC transplantation, or chronic diseases such as idiopathic thrombocytopenia.
 CC The present sequence represents a TPO mimetic peptide.

SQ Sequence 15 AA;

Query Match 100.0%; Score 73; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
 |||||
 DB 1 IEGPTLRQWLAAARA 14

RESULT 37

AAW19534 standard; protein; 16 AA.

AAW19534;

10-SEP-1997 (first entry)

Thrombopoietin receptor binding compound peptide (part of a dimer).

Haematology; thrombocytopenia; TPO; TR; proliferation;

bone marrow transfusion; chemotherapy; radiation therapy.

Synthetic.

Key Location/Qualifiers

Modified-site 15 /label= bala

Cross-links 16 /note= "linked to the omega Ala in AAW09468"

Modified-site 16 /note= "In amide form"

WO9640189-A1.

19-DEC-1996.

05-JUN-1996; 96WO-US008998.

07-JUN-1995; 95US-00472371.

07-JUN-1995; 95US-00473604.

07-JUN-1995; 95US-00476168.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00484090.

07-JUN-1995; 95US-00485301.

(GLAXO) GLAXO GROUP LTD.

Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

Mathaeakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

MPI; 1997-051883/05.

Thrombopoietin receptor-binding/activating peptide(s) and peptide

mimetic(s) - useful in treatment of haematological disorders, esp.

thrombocytopenia resulting from chemotherapy, etc.

Claim 30; Page 91; 106pp; English.

SQ Sequence 16 AA;

Query Match 100.0%; Score 73; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
 |||||
 DB 1 IEGPTLRQWLAAARA 14

RESULT 38

AAW33035 standard; peptide; 16 AA.

AAW33035;

11-MAR-1998 (first entry)

Thrombopoietin receptor binding peptide.

Thrombopoietin receptor; binding peptide; treatment; agonist;

haematological disorder; thrombocytopenia; chemotherapy;

radiation therapy; bone marrow transfusion; diagnosis;

signal transduction; receptor activation; cell culture.

Synthetic.

Key Location/Qualifiers

Cross-links 14 /note= "epsilon amino group of Lys16 linked to terminal

Modified-site 15 carboxy group of AAW33034"

WO9640750-A1.

19-DEC-1996.

07-JUN-1996; 96WO-US009623.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00485301.

(GLAXO) GLAXO GROUP LTD.

Dower WJ, Barrett RM, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

Mathaeakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

MPI; 1997-052226/05.

Peptides and peptide mimetics which bind to and activate the

thrombopoietin receptor - useful in treatment of haematological

disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

Claim 30; Page 91; 106pp; English.

The present peptide binds the thrombopoietin receptor (TR), has a

molecular weight of less than 8000 Da and a TR binding affinity as

expressed by an IC50 of no more than about 100 microm. It can be used to

treat disorders which are susceptible to treatment with a thrombopoietin

agonist, preferably haematological disorders and thrombocytopenia

resulting from chemotherapy, radiation therapy or bone marrow

transfusions. It can also be used diagnostically, e.g. to investigate the

mechanism of thrombopoietin signal transduction and receptor activation,

or to maintain the proliferation and growth of thrombopoietin dependent

cell lines

SQ Sequence 16 AA;

Query Match 100.0%; Score 73; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAARA 14
 |||||
 DB 1 IEGPTLRQWLAAARA 14

RESULT 39

AAW36775 standard; peptide; 16 AA.

AAW36775;

11-MAR-1998 (first entry)

Thrombopoietin receptor binding peptide.

Thrombopoietin receptor; binding peptide; treatment; agonist;

haematological disorder; thrombocytopenia; chemotherapy;

radiation therapy; bone marrow transfusion; diagnosis;

signal transduction; receptor activation; cell culture.

Synthetic.

Key Disulfide-bond 1.16
Modified-site 16 /note="NH2-Cys"

MO9640750-A1.

19-DEC-1996.

07-JUN-1996; 96WC-US009623.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00485301.

(GLAXO) GLAXO GROUP LTD.

Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

WPI; 1997-052226/05.

Peptides and peptide mimetics which bind to and activate the

thrombopoietin receptor - useful in treatment of haematological

disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

Example 9; Page 77; 106pp; English.

The present peptide, which binds the thrombopoietin receptor (TR), can be

used to treat disorders which are susceptible to treatment with a

thrombopoietin agonist, preferably haematological disorders and

thrombocytopenia resulting from chemotherapy, radiation therapy or bone

marrow transfusions. It can also be used diagnostically, e.g. to

investigate the mechanism of thrombopoietin signal transduction and

receptor activation, or to maintain the proliferation and growth of

thrombopoietin dependent cell lines

Sequence 16 AA;

Query Match 100.0%; Score 73; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.6e-05; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IEPTLRQWLARA 14

2 IEPTLRQWLARA 15

Thrombopoietin receptor binding peptide.

Thrombopoietin receptor; binding peptide; treatment; agonist;

haematological disorder; thrombocytopenia; chemotherapy;

radiation therapy; bone marrow transfusion; diagnosis;

signal transduction; receptor activation; cell culture.

Synthetic.

Key Disulfide-bond 1.16
Modified-site 16 /note="NH2-Cys"

MO9640750-A1.

19-DEC-1996.

07-JUN-1996; 96WC-US009623.

07-JUN-1995; 95US-00478128.

07-JUN-1995; 95US-00485301.

(GLAXO) GLAXO GROUP LTD.

Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;

Matheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

WPI; 1997-052226/05.

Peptides and peptide mimetics which bind to and activate the

thrombopoietin receptor - useful in treatment of haematological

disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

Example 9; Page 76; 106pp; English.

The present peptide, which binds the thrombopoietin receptor (TR), can be

used to treat disorders which are susceptible to treatment with a

thrombopoietin agonist, preferably haematological disorders and

thrombocytopenia resulting from chemotherapy, radiation therapy or bone

marrow transfusions. It can also be used diagnostically, e.g. to

investigate the mechanism of thrombopoietin signal transduction and

receptor activation, or to maintain the proliferation and growth of

thrombopoietin dependent cell lines

Sequence 16 AA;

Query Match 100.0%; Score 73; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.6e-05; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IEPTLRQWLARA 14

2 IEPTLRQWLARA 15

Peptide chain of compound attached to hydrophilic polymer.

thrombopoietin receptor; haematological disorder; screening; agonist;

assay; megakaryocyte; blood disorder; thrombocytopenia; IFO.

Synthetic.

Key Location/Qualifiers

RESULT 43
 AAW6733 standard; peptide; 16 AA.
 ID AAW6733;
 AC AAW6733;
 XX
 DT 01-DEC-1998 (first entry)
 DE Peptide chain of compound which binds to the thrombopoietin receptor.
 XX thrombopoietin receptor; haematological disorder; screening; agonist;
 KM assay; megakaryocyte; blood disorder; thrombocytopaenia; TPO.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..15
 FT /note= "thrombopoietin receptor agonist"
 FT Modified-site 1
 FT /note= "Cys is disulphide bonded to Cys1 of another
 FT peptide chain identical to the region (residues 1-15) of
 FT the present peptide"
 FT Modified-site 16
 FT /note= "Epsilon amino group of Lys, in its amide form, is
 FT attached to another peptide chain identical to the region
 FT (residues 1 to 14) of this peptide"
 XX
 PN WO9825965-A2.
 XX 18-JUN-1998.
 PD 09-DEC-1997; 97WO-EP006850.
 PF 11-DEC-1996; 96US-00764640.
 PR (GLAX) GLAXO GROUP LTD.
 XX
 PA Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RM, Degrince RB, Poddaturi S;
 PI Yin Q;
 XX WPI; 1998-377261/32.
 DR
 XX
 PT New peptide compound(s) which can bind and activate thrombopoietin
 PT receptor - may be used in treating haematological disorders and in
 PT methods for screening for new thrombopoietin receptor agonists.
 XX
 PS Claim 12; Page 64; 78pp; English.
 XX
 PS The invention relates to new peptides which are capable of binding to,
 CC and activating, the thrombopoietin (TPO) receptor. They may be used in
 CC vitro as tools for understanding the biological role of TPO. They may be
 CC used as competitive binders in assays to screen for new TPO receptor
 CC agonists. They may be used as reagents for detecting TPO receptors in
 CC living cells, biological fluids, etc. They may be used to maintain growth
 CC and proliferation of TPO-dependent cells and for in vitro expansion of
 CC megakaryocytes. They may be used to activate TPO receptors in vivo, e.g.,
 CC to treat blood disorders or thrombocytopaenia associated with bone marrow
 CC transfusions, radiotherapy or chemotherapy. The present sequence
 CC represents a specific example of a peptide chain of a branched peptide
 CC which acts as a TPO agonist
 CC
 SO Sequence 16 AA;
 Query Match 100.0%; Score 73; DB 2; Length 16;
 Best Local Similarity 100.0%; Fried. No. 1.6e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IEGPTLRQMLAARA 14
 |||||||
 Db 2 IEGPTLRQMLAARA 15

RESULT 44
 AAW6716 standard; peptide; 16 AA.
 ID AAW6716;
 AC AAW6716;
 XX
 DT 01-DEC-1998 (first entry)
 DE Peptide chain of compound which binds to the thrombopoietin receptor.
 XX thrombopoietin receptor; haematological disorder; screening; agonist;
 KM assay; megakaryocyte; blood disorder; thrombocytopaenia; TPO.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..14
 FT /note= "thrombopoietin receptor agonist"
 FT Modified-site 1
 FT /note= "optional N-terminal acetyl"
 FT Modified-site 14
 FT /note= "N-methyl-Ala"
 FT Modified-site 15
 FT /label= bAla
 FT Modified-site 16
 FT /note= "Epsilon amino group of Lys, in its amide form, is
 FT attached to another peptide chain identical to the region
 FT (residues 1 to 14) of this peptide"
 XX
 PN WO9825965-A2.
 XX 18-JUN-1998.
 PD 09-DEC-1997; 97WO-EP006850.
 PF 11-DEC-1996; 96US-00764640.
 PR (GLAX) GLAXO GROUP LTD.
 XX
 PA Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;
 PI Balasubramanian P, Wagstrom CR, Hendren RM, Degrince RB, Poddaturi S;
 PI Yin Q;
 XX WPI; 1998-377261/32.
 DR
 XX
 PT New peptide compound(s) which can bind and activate thrombopoietin
 PT receptor - may be used in treating haematological disorders and in
 PT methods for screening for new thrombopoietin receptor agonists.
 XX
 PS Claim 2; Page 60; 78pp; English.
 XX
 PS The invention relates to peptide compounds composed of two peptide chains
 CC attached to each of the amino groups of a single Lys in the amide form.
 CC The compounds are of formula (Pept)K(NH2), where Pept is of
 CC formula: X1-I-E-X2-P-T-L-X3-X4-X5-L-X6-X7-X8-X9-X10'. X1 = H or acyl; X2
 CC = Gly or Sar (sarcosine); X3 = Arg, Ala, Nle (norleucine) or N-
 CC acetyllysine; X4 = Gln or Glu; X5 = Trp, L-1-naphthylalanine or Phe; X6 =
 CC Ala, 5-aminopentanoic acid or 2-aminobutyric acid; X7 = Ala,
 CC diphenylalanine, or is absent; X8 = Arg, p- amino-phenylalanine, N-
 CC acetyl-lysine, or is absent; X9, X9' = Ala, beta Ala, N-methyl-alanine,
 CC Sar, or is absent; X10, X10' = beta Ala or is absent. The new peptides
 CC are capable of binding to, and activating, the thrombopoietin (TPO)
 CC receptor. They may be used in vitro as tools for understanding the
 CC biological role of TPO. They may be used as competitive binders in assays
 CC to screen for new TPO receptor agonists. They may be used as reagents for
 CC detecting TPO receptors in living cells, biological fluids, etc. They may
 CC be used to maintain growth and proliferation of TPO-dependent cells and
 CC for in vitro expansion of megakaryocytes. They may be used to activate
 CC TPO receptors in vivo, e.g., to treat blood disorders or
 CC thrombocytopaenia associated with bone marrow transfusions, radiotherapy
 CC or chemotherapy. The present sequence represents a specific example of

CC	(Pep1) K(NH2)
XX	
SS	Sequence 16 AA;

Query Match	100.0%	Score 73:	DB 2;	Length 16;
Best Local Similarity	100.0%	Pred. No.	1.6e-05;	
Matches 14; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

```
QY 1 IEGPTLRQWLAARA 14
    |||||
Db 1 IEGPTLRQWLAARA 14
```

RESULT 45
AAU26005
ID AAU26005 standard; peptide; 16 AA

AC	AAU26005;
XX	
DT	17-DEC-2001 (first entry)

DE	Human thrombopoietin receptor (TPO-R) activator peptide #191
XX	
KW	Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO;

KM Peptidase, human; thrombospondin receptor; TPO-R; TPO; cytokine;
KM haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;
KM bone marrow transplantation; haematological disorder; platelet disorder;
KM enzyme-linked immunosorbent assay; in situ staining; biological fluid;
KM tissue homogenate; fluorescent-activated cell sorting; Western blotting
KM in vitro expansion; megakaryocyte Headpiece Dimer gene; lact gene.

OS	Homo sapiens
XX	
PN	US6251864-B1

PD 26-JUN-2001

PF 01-MAR-2000; 2000US-00516704

PR 07-JUN-1995; 95US-00478128.

PR 07-JUN-1996; 96WO-US009623.

XX
PA (GLAX) GLAXO GROUP LTD.

PI Dower WJ, Barrett RW, Cwiria SE, Gates CM, Schatz PJ;
PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Poduturi S,
PI Yin Q;

WPI; 2001-564142/63.

PT Activating thrombopoietin receptors in cells, used to treat
PR thrombocytopenia and hematological disorders, comprises contacting cells
PR with peptides and peptide mimetics attached to hydrophilic polymers.
XX
PS Disclosure; Col 147-148; 128pp; English.

Sequences ANU25815-ANU26049 represent peptides and peptide mimetics that bind to and activate the human thrombopoietin receptor (TPO-R). Methods of activating thrombopoietin receptors in cells comprise contacting the cells with effective amounts of peptides and peptide mimetics attached to hydrophilic polymers. The methods are used to treat thrombocytopenia such as that due to chemotherapy, radiation therapy or bone-marrow transplantation and to prevent thrombocytopenia in patients at risk. The sequences are used to treat and prevent haematological disorders including thrombocytopenia and platelet disorders. They are used in vitro as unique tools for understanding the biological role of thrombopoietin (TPO) and to develop other compounds that bind to and activate the TPO receptor. The peptides can be used to detect TPO receptors on living cells and fixed cells, in biological fluids, in tissue homogenates, and in purified or natural biological materials. They may also be used for *in situ* staining, fluorescence-activated cell sorting, Western blotting and enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can

CC be used for in vitro expansion of megakaryocytes and their committed
CC progenitors alone or in conjunction with additional cytokines
XX
50 Sequence 16 AA;

Query Match	100.0%	Score 73;	DB 4;	length 16;
Best Local Similarity	100.0%	Pred. No.	1.6e-05;	
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```
QY      1 IEGPTLRQWLARA 14
        |||||
Db      2 IEGPTLRQWLARA 15
```

Search completed: September 1, 2005, 16:12:15
Job time : 65.3597 secs

Job time : 65.3597 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 1, 2005, 15:57:33 ; Search time 10.6763 Seconds
(without alignments)
126.171 Million cell updates/sec

Title: US-10-083-768-13

Perfect score: 73

Sequence: 1 IEGPTRQWLARA 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79: *
1: pirl: *
2: pirl: *
3: pirl: *
4: pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	49.5	67.8	333	2	A36925	transcription acti
2	47	64.4	296	2	AG0147	probable membrane
3	46	63.0	306	2	D70601	UTP-glucose-1-phos
4	44	60.3	200	2	T23485	hypothetical prote
5	44	60.3	207	2	T37464	probable glutathio
6	44	60.3	536	1	SYECB	2,3-dihydroxybenzo
7	44	60.3	536	2	E85558	2,3-dihydroxybenzo
8	44	60.3	536	2	A99708	probable dimethyla
9	43	58.9	285	2	G71337	conserved hypochet
10	43	58.9	683	2	B71325	hypothetical prote
11	42	57.5	473	2	E84853	pol polyprotein -
12	42	57.5	1019	2	T11560	probable phosphopa
13	41	56.2	195	2	F91171	hypothetical 21.8k
14	41	56.2	195	2	F86017	hypothetical phospho
15	41	56.2	195	2	S47694	hypothetical 21.8k
16	41	56.2	249	2	E87575	ABC transporter, A
17	41	56.2	306	2	T45453	UTP-glucose-1-phos
18	41	56.2	326	2	C24430	glyceraldehyde-3-p
19	41	56.2	336	1	DEPZG	glyceraldehyde-3-p
20	41	56.2	337	2	A35080	glyceraldehyde-3-p
21	41	56.2	338	1	DEIS3C	glyceraldehyde-3-p
22	41	56.2	338	2	J01287	glyceraldehyde-3-p
23	41	56.2	719	2	B95325	conserved hypochet
24	41	56.2	750	2	A97501	topoisomerase IV c
25	41	56.2	750	2	A97501	topoisomerase IV c
26	40	54.8	239	2	S25204	strm protein - Str
27	40	54.8	463	2	S27491	hypothetical prote
28	40	54.8	530	2	A81958	probable permease
29	40	54.8	531	2	E81015	ABC transporter, p

30	40	54.8	656	2	S30484	pol polyprotein -
31	40	54.8	656	2	S30483	pol polyprotein -
32	40	54.8	721	2	A39707	erythrocyte membra
33	40	54.8	1123	2	T51517	telomerase reverse
34	40	54.8	1712	1	CGH02B	collagen alpha 2(I
35	39.5	54.1	325	2	A84326	hypothetical prote
36	39	53.4	131	2	S74539	hypothetical prote
37	39	53.4	217	2	S46354	pol polyprotein -
38	39	53.4	267	2	I40327	baf protein - Bord
39	39	53.4	331	2	B48445	glyceraldhyde-3-p
40	39	53.4	331	2	A72514	hypothetical prote
41	39	53.4	400	2	C87021	serine-threonine p
42	39	53.4	600	2	C83221	transport protein
43	39	53.4	791	2	A82291	c-di-GMP phosphodi
44	39	53.4	1034	1	GNLJCA	HIV-1 retropepsin
45	39	53.4	1035	1	GNLJGG	HIV-1 retropepsin
46	39	53.4	1036	1	GNLJGT	HIV-1 retropepsin
47	39	53.4	1055	1	GNLJST	HIV-1 retropepsin
48	39	53.4	1055	2	S53092	pol polyprotein -
49	39	53.4	1058	2	S08436	pol polyprotein -
50	39	53.4	3345	2	T13423	hypothetical prote
51	38	52.1	134	2	B73468	hypothetical prote
52	38	52.1	197	2	G82973	transcription regu
53	38	52.1	246	2	AH0190	probable oxidoredu
54	38	52.1	247	2	PQ0178	glyceraldhyde-3-p
55	38	52.1	295	2	T07730	glyceraldhyde-3-p
56	38	52.1	297	2	B87109	integrane/recombin
57	38	52.1	311	1	RGECK	regulatory protein
58	38	52.1	311	2	AH0867	transcription acti
59	38	52.1	311	2	C85936	positive regulator
60	38	52.1	311	2	H91090	positive regulator
61	38	52.1	314	2	H70723	hypothetical prote
62	38	52.1	337	1	DEPRG	glyceraldhyde-3-p
63	38	52.1	337	1	DESKG	glyceraldhyde-3-p
64	38	52.1	337	1	DEUSGM	glyceraldhyde-3-p
65	38	52.1	337	1	DEZMGC	hypothetical prote
66	38	52.1	339	2	A83358	A/G-specific adeni
67	38	52.1	350	2	B38535	adenine glycosylas
68	38	52.1	350	2	H85953	adenine glycosylas
69	38	52.1	350	2	B91108	adenine glycosylas
70	38	52.1	360	2	S38570	hypothetical prote
71	38	52.1	469	2	AD1926	sensor histidine k
72	38	52.1	589	2	F87626	hypothetical prote
73	38	52.1	635	2	A87433	hypothetical prote
74	38	52.1	816	2	A71006	probable polA prot
75	38	52.1	904	2	C70559	adenylate cyclase
76	38	52.1	1155	2	AC2426	transposase - Cory
77	37.5	51.4	436	2	JC4742	HIV-1 retropepsin
78	37	50.7	151	2	S63748	hypothetical prote
79	37	50.7	155	2	F87542	hypothetical prote
80	37	50.7	224	2	PQ0179	glyceraldhyde-3-p
81	37	50.7	305	2	A24159	glyceraldhyde-3-p
82	37	50.7	335	2	S29813	glyceraldhyde-3-p
83	37	50.7	337	1	DEBHG	glyceraldhyde-3-p
84	37	50.7	337	2	S42479	glyceraldhyde-3-p
85	37	50.7	337	2	T02723	glyceraldhyde-3-p
86	37	50.7	337	2	T02722	glyceraldhyde-3-p
87	37	50.7	338	1	DENDG	glyceraldhyde-3-p
88	37	50.7	338	2	T06781	glyceraldhyde-3-p
89	37	50.7	341	1	DEJMG	glyceraldhyde-3-p
90	37	50.7	341	2	T08147	glyceraldhyde-3-p
91	37	50.7	341	2	AG0195	probable exported
92	37	50.7	352	2	G83636	conserved hypochet
93	37	50.7	391	2	T36739	hypothetical prote
94	37	50.7	407	2	A86298	hypothetical prote
95	37	50.7	422	2	F96826	hypothetical prote
96	37	50.7	433	2	S51837	glyceraldhyde-3-p
97	37	50.7	433	2	S51836	glyceraldhyde-3-p
98	37	50.7	438	2	G87337	membrane protein, d
99	37	50.7	480	2	H84747	probable steroid, d
100	37	50.7	486	2	B86411	protein F3M18.4 [1

ALIGNMENTS

RESULT 1

A36925 transcription activator *lysr*-type Cbdr - *Xanthobacter flavus*

C:Species: *Xanthobacter flavus*
 C:Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A36925; S13578; S35408
 R:van den Bergh, E.R.E.; Dijkhuizen, L.; Meijer, W.G.

A:Title: Cbdr, a *lysr*-type transcriptional activator, is required for expression of the
 A:Reference number: A36925; MUID:94012468; PMID:8407781

A:Accession: A36925

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333 <VAN>

A:Cross-references: UNIPROT:P25545; EMBL:Z22705; NID:G297851; PIDN:CA80406.1; PID:G5818
 R:Meijer, W.G.; Arndberg, A.C.; Enequist, H.G.; Terpstra, P.; Lidstrom, M.E.; Dijkhuizen,
 M.O. Gen. Genet. 225, 320-330, 1991

A:Title: Identification and organization of carbon dioxide fixation genes in *Xanthobacte*
 A:Reference number: S13573; MUID:91172133; PMID:1900916

A:Accession: S13578

A:Molecule type: DNA

A:Residues: 1-150 <MEI>

A:Cross-references: EMBL:X17252

A:Gene: cbbR

A:Gene: cbbR

A:Start codon: GNG

A:Superfamily: transcription activator *lysr*-type

C:Keywords: DNA binding; transcription regulation

Query Match 67.8%; Score 49.5; DB 2; Length 333;
 Best Local Similarity 66.7%; Pred. No. 0.98;
 Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 IEG-PTLRQWLARA 14
 :|||:|||||
 DB 264 VEGLPVRLQWLARA 278

RESULT 2

AG0147 Probable membrane protein YPO1203 [imported] - *Yersinia pestis* (strain CO92)C:Species: *Yersinia pestis*

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C:Accession: AG0147

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.
 demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
 11; M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,

Nature 413, 523-527, 2001

A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AG0147

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-296 <RUR>

A:Cross-references: UNIPROT:Q8ZGS7; GB:AL590842; PIDN:CAC90042.1; PID:G15979263; GSPDB:G

C:Genetics:

A:Gene: YPO1203

Query Match 64.4%; Score 47; DB 2; Length 296;
 Best Local Similarity 81.8%; Pred. No. 2.3;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PTLRQWLARA 14
 |||||
 DB 66 PTLRQWLARA 76

RESULT 3

D70601 UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) *galU* [similarity] - *Mycobacteri*C:Species: *Mycobacterium tuberculosis*

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: D70601

R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
 ; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S
 ; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulton, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
 A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: D70601

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-306 <COI>

A:Cross-references: UNIPROT:O05576; GB:Z94752; GB:AL123456; NID:G3261731; PIDN:CA808153
 A:Experimental source: strain H37Rv

C:Genetics:

A:Gene: *galU*C:Superfamily: *Escherichia coli* UTP-glucose-1-phosphate uridylyltransferase

C:Keywords: nucleotidyltransferase

Query Match 63.0%; Score 46; DB 2; Length 306;
 Best Local Similarity 72.7%; Pred. No. 3.5;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GPTLRQWLAR 13
 |||||
 DB 290 GPTLRQWLAR 300

RESULT 4

T23485 Hypothetical protein K08F4.11 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T23485

R:Hemby, C.

Submitted to the EMBL Data Library, January 1996

A:Reference number: Z19746

A:Accession: T23485

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-200 <WIL>

A:Cross-references: EMBL:Z68879; PIDN:CA93088.1; GSPDB:GN00022; CESP:K08F4.11

A:Experimental source: clone K08F4

C:Genetics:

A:Gene: CESP:K08F4.11

A:Map position: 4

A:Introns: 45/1; 76/1; 111/3

C:Superfamily: glutathione transferase

Query Match 60.3%; Score 44; DB 2; Length 200;
 Best Local Similarity 61.5%; Pred. No. 4.9;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAR 13
 |||||
 DB 183 IEGPTLRQWLAR 195

RESULT 5

T37464 Probable glutathione transferase (EC 2.5.1.18) GS73 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T37464

R:Tawe, W.N.; Eschbach, M.L.; Walzer, R.D.; Henkle-Duehnssen, K.
 Submitted to the EMBL Data Library, June 1997

A:Description: Paraquat mediates differential gene expression in *C. elegans*.
 A:Reference number: Z21702

A:Accession: T37464

A:Status: preliminary

A:Molecule type: mRNA

A:Gene: *galU*

A:Residues: 1-207 <TRAM>
 A:Cross-references: UNIPROT:O16116; EMBL:AF010241; PDB:AA85419.1
 A:Experimental source: strain Bristol N2
 C:Genetic:
 A:Gene: GST3
 C:Superfamily: glutathione transferase
 C:Keywords: transferase

Query Match 60.3%; Score 44; DB 2; Length 207;
 Best Local Similarity 61.5%; Pred. No. 5.1;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAAR 13
 DB 190 IETPKLEWLAKR 202

RESULT 6
 SYCEB
 2,3-dihydroxybenzoate-[carrier protein] ligase (EC 6.2.1.-) ente - Escherichia coli (str N1/Alternate names: 2,3-dihydroxybenzoate-AMP ligase [mismomer]; dihydroxybenzoic acid-ac C/Species: Escherichia coli
 C/Date: 31-Dec-1989 #sequence_revision 21-Nov-1997 #text_change 09-Jul-2004
 C/Accession: H64792; A48308; A32047; I41058; S08076
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: H64792
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-536 <BIAT>
 A:Cross-references: UNIPROT:P10378; GB:AE000165; GB:U00096; NID:G1786808; PDB:AACT3695.
 A:Experimental source: strain K-12, substrain MG1655
 R:Staab, J.F.; Elkins, M.F.; Barthart, C.F.
 FEMS Microbiol. Lett. 59, 15-19, 1989
 A:Title: Nucleotide sequence of the Escherichia coli ente gene.
 A:Reference number: A48308; MUID:89230355; PMID:2525505
 A:Note: In Medline 89290355 this citation is erroneously given as volume 50 rather than 59.
 A:Accession: A48308
 A:Molecule type: DNA
 A:Residues: 1366, 'ECRKSSTAAR', 379-536 <STA>
 A:Cross-references: GB:M27490; EMBL:X15058; NID:G41345; PDB:CAA33158.1; PID:G41346
 R:Li, J.; Duncan, K.; Walsh, C.T.
 J. Bacteriol. 171, 791-798, 1989
 A:Title: Nucleotide sequence of a cluster of Escherichia coli enterobactin biosynthesis A:Reference number: A91904; MUID:89123155; PMID:2521622
 A:Accession: A32047
 A:Molecule type: DNA
 A:Residues: 393-536 <LIU>
 A:Cross-references: GB:M24148; NID:G304949; PDB:AAA16101.1; PID:G450380
 C/Comment: The enzymatic steps in the condensation of L-serine and 2,3-dihydroxybenzoic ty is based on the recognized homology with 4-coumarate-CoA ligase and by analogy with C/Comment: The formation of 2,3-dihydroxybenzoyl-AMP has been observed. The rapid reaction carrier protein) to release AMP, has also been observed.
 C:Genetic:
 A:Gene: ente
 A:Map position: 14 min
 C:Function:
 A:Description: catalyzes the formation of 2,3-dihydroxybenzoyl-[carrier protein], AMP and A:Pathway: enterobactin biosynthesis
 A:Note: this is one component of a membrane-bound multienzyme complex that catalyzes the for transport into the cell
 C:Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
 C:Keywords: acid-thiol ligase; enterobactin biosynthesis; membrane-associated complex
 P:69-526/Domain: acetate-CoA ligase homology <ACL>

Query Match 60.3%; Score 44; DB 1; Length 536;
 Best Local Similarity 57.1%; Pred. No. 13;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 IEGPTLRQWLAAAR 14

DB 521 VDKKQLRWLASRA 534

RESULT 7
 E85558
 2,3-dihydroxybenzoate-AMP ligase [imported] - Escherichia coli (strain O157:H7, substra C/Species: Escherichia coli
 C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 01-Mar-2002
 C/Accession: E85558
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: E85558
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-536 <STO>
 A:Cross-references: GB:AE005174; NID:G12513487; PDB:AA654929.1; GSPDB:GN00145; UMGDB:20 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetic:
 A:Gene: ente
 C:Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology

Query Match 60.3%; Score 44; DB 2; Length 536;
 Best Local Similarity 57.1%; Pred. No. 13;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAAR 14
 DB 521 VDKKQLRWLASRA 534

RESULT 8
 A99708
 2,3-dihydroxybenzoate-AMP ligase [imported] - Escherichia coli (strain O157:H7, substra C/Species: Escherichia coli
 C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C/Accession: A99708
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: A99708
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-536 <HAY>
 A:Cross-references: UNIPROT:Q8XEV3; GB:BA000007; PDB:BAR34056.1; PID:G13360091; GSPDB: A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetic:
 A:Gene: ECG0633
 C:Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology

Query Match 60.3%; Score 44; DB 2; Length 536;
 Best Local Similarity 57.1%; Pred. No. 13;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAAAR 14
 DB 521 VDKKQLRWLASRA 534

RESULT 9
 G71337
 probable dimethyladenosine transferase (KsgA) - syphilis spirochete C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C/Accession: G71337
 R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi rson, J.; Khailak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998
A>Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: G71337
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-285 <COL>
A:Cross-references: UNIPROT:O83357; GB:AE001213; GB:AE000520; NID:G3322606; PIDN:AAC6532
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0337
C:Superfamily: rRNA (adenine-N6-)-methyltransferase

Query Match 58.9%; Score 43; DB 2; Length 285;
Best Local Similarity 64.3%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EGPTRLQWLARA 14
||| ||| ||| |||
Db 98 IEGDVLQGMHAA 111

RESULT 10
B71325
conserved hypothetical protein TP0421 - syphilis spirochete
C:Species: *Treponema pallidum* subsp. *pallidum* (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: B71325
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
iron, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A>Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: B71325
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-683 <COL>
A:Cross-references: UNIPROT:O83436; GB:AE001220; GB:AE000520; NID:G3322705; PIDN:AAC6540
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0421

Query Match 58.9%; Score 43; DB 2; Length 683;
Best Local Similarity 69.2%; Pred. No. 25;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EGPTRLQWLARA 13
||| ||| ||| |||
Db 89 IEGALHONGAAR 101

RESULT 11
E84853
hypothetical protein At2g42400 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84853
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.B.; Umayam, L.; Tallon, L.
eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84853
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-473 <STO>
A:Cross-references: UNIPROT:Q9SLB9; GB:AE002093; NID:G4567312; PIDN:AAD23723.1; GSPDB:GN
C:Genetics:
A:Gene: At2g42400
A:Map position: 2

Query Match 57.5%; Score 42; DB 2; Length 473;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EGPTRLQWL 10
||| ||| ||| |||
Db 343 VEGTIREWL 352

RESULT 12
T11560
pol polyprotein - simian immunodeficiency virus SIVsm (strain ES43) (fragment)
C:Species: simian immunodeficiency virus SIVsm
A:Variety: strain ES43
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T11560
R:Hirsch, V.M.; Adger-Johnson, D.; Campbell, B.; Goldstein, S.; Brown, C.; Elkins, W.R.;
J. Virol. 71, 1608-1620, 1997
A>Title: A molecularly cloned, pathogenic, neutralization-resistant simian immunodeficie
A:Reference number: Z17285; MUID:97151152; PMID:8995688
A:Accession: T11560
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1019 <HIR>
A:Cross-references: UNIPROT:P89154; EMBL:U72748; NID:G1695908; PIDN:AAC56559.1; PID:G165
C:Genetics:
A:Gene: pol
C:Superfamily: pol polyprotein
C:Keywords: AIDS; immunodeficiency

Query Match 57.5%; Score 42; DB 2; Length 1019;
Best Local Similarity 87.5%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EGPTRLQW 9
||| ||| ||| |||
Db 184 BGPXLQW 191

RESULT 13
F91171
probable phosphopantetheinyltransferase [imported] - *Escherichia coli* (strain O157:H7, #
C:Species: *Escherichia coli*
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: F91171
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91171
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195 <HAY>
A:Cross-references: UNIPROT:O8X5U4; GB:BA000007; PIDN:BA837765.1; PID:G13363816; GSPDB:(
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECS4342

Query Match 56.2%; Score 41; DB 2; Length 195;
Best Local Similarity 53.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 EGPTRLQWLARA 14
||| ||| ||| |||
Db 27 QGPRRRRWLAGRA 39

RESULT 14
F86017
probable phosphopantetheinyltransferase [imported] - *Escherichia coli* (strain O157:H7, #
C:Species: *Escherichia coli*
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C/Accession: F86017
 R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoulis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A/Reference number: A85480; MUID:21074935; PMID:11206551
 A/Accession: F86017
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-195 <STO>
 A/Cross-references: UNIPROT:Q8X5U4; GB:AE005174; NID:g12518155; PIDN:ANG58602.1; GSPDB:C
 A/Experimental source: strain O157:H7, Substrain EDL933
 C/Genetics:
 A/Gene: Z4867

Query Match 56.2%; Score 41; DB 2; Length 195;
 Best Local Similarity 53.8%; Pred. No. 15;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 EGPTLRQWLARA 14
 :|||:|||||
 Db 27 QGPRRRRWLAGRA 39

RESULT 15
 S47694
 hypothetical 21.8K protein (feyr-nika intergenic region) - *Escherichia coli* (strain K-12
 N/Alternate names: hypothetical protein o195
 C/Species: *Escherichia coli*
 C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
 C/Accession: S47694; F65144
 R/Plunkett, G.
 submitted to the EMBL Data Library, March 1994
 A/Accession number: S47666
 A/Accession: S47694
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-195 <PLU>
 A/Cross-references: UNIPROT:P37623; EMBL:U00039; NID:g466582; PIDN:AAB18450.1; PID:g4666
 R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Snao, Y.
 Science 277, 1453-1462, 1997
 A/Title: The complete genome sequence of *Escherichia coli* K-12.
 A/Reference number: A64720; MUID:97426617; PMID:9278503
 A/Accession: F65144
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-195 <BLAT>
 A/Cross-references: GB:AE000423; GB:U00096; NID:g1789880; PIDN:AAC76500.1; PID:g1789886;
 A/Experimental source: strain K-12, Substrain MG1655
 C/Genetics:
 A/Gene: ynhu

Query Match 56.2%; Score 41; DB 2; Length 195;
 Best Local Similarity 53.8%; Pred. No. 15;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 EGPTLRQWLARA 14
 :|||:|||||
 Db 27 QGPRRRRWLAGRA 39

RESULT 16
 E87575
 ABC transporter, ATP-binding protein CC2634 [imported] - *Caulobacter crescentus*
 C/Species: *Caulobacter crescentus*
 C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C/Accession: E87575
 R/Nierman, W.C.; Felblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eissen, J.; Heidelberg, J.
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 R.; J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4135-4141, 2001
 A/Title: Complete Genome Sequence of *Caulobacter crescentus*.

A/Reference number: A87249; MUID:21173698; PMID:11259647
 A/Accession: E87575
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-249 <STO>
 A/Cross-references: UNIPROT:Q9A535; GB:AE005673; NID:g13424211; PIDN:AAK24601.1; GSPDB:
 C/Genetics:
 A/Gene: CC2634

Query Match 56.2%; Score 41; DB 2; Length 249;
 Best Local Similarity 58.3%; Pred. No. 20;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 EGPTLRQWLAR 13
 :|||:|||||
 Db 76 QAPTLAPWLSAR 87

RESULT 17
 T45453
 UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) galu [similarity] - *Mycobacter*
 C/Species: *Mycobacterium lepre*
 C/Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T45453
 R/James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, February 1998
 A/Reference number: Z22967
 A/Accession: T45453
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-306 <JMB>
 A/Cross-references: UNIPROT:Q9Z5G1; EMBL:AL035500; PIDN:CAB36696.1
 A/Experimental source: cosmid U373
 C/Genetics:
 A/Note: galu
 C/Superfamily: *Escherichia coli* UTP-glucose-1-phosphate uridylyltransferase
 C/Keywords: nucleotidyltransferase

Query Match 56.2%; Score 41; DB 2; Length 306;
 Best Local Similarity 63.6%; Pred. No. 24;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 GPTLRQWLAR 13
 :|||:|||||
 Db 290 GPDLRWLVER 300

RESULT 18
 C24430
 glyceraldehyde-3-phosphate dehydrogenase (NADP) (phosphorylating) (EC 1.2.1.13) C, cyto
 C/Species: *Nicotiana tabacum* (common tobacco)
 C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
 C/Accession: C24430
 R/Shih, M.C.; Lazar, G.; Goodman, H.M.
 Cell 47, 73-80, 1986
 A/Title: Evidence in favor of the symbiotic origin of chloroplasts: primary structure a
 A/Reference number: A90888; MUID:87002494; PMID:3757034
 A/Accession: C24430
 A/Molecule type: mRNA
 A/Residues: 1-326 <SHI>
 A/Cross-references: UNIPROT:P09094; GB:M14419; NID:g170240; PIDN:AAA34077.1; PID:g17024
 C/Genetics:
 A/Gene: gapC
 C/Superfamily: glyceraldehyde-3-phosphate dehydrogenase
 C/Keywords: cytosol; NADP; oxidative phosphorylation; oxidoreductase

Query Match 56.2%; Score 41; DB 2; Length 326;
 Best Local Similarity 35.7%; Pred. No. 26;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 1 IEPTLRQWLARA 14
 :|||:|||||
 Db 179 VDGSMDWAGRA 192

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RESULT 19
DEPZG
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - parsley
C:Species: Petroselinum crispum (parsley)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: S18484
R:Martin, W.; Gierl, A.; Saedler, H.
Nature 339, 46-48, 1989
A:Title: Molecular evidence for pre-Cretaceous angiosperm origins.
A:Reference number: S17991
A:Accession: S18484
A:Status: nucleic acid sequence not shown; translation not shown
A:Residues: 1-336 <MRA>
A:Molecule type: mRNA
C:Cross-references: UNIPROT:P26519; EMBL:X60344; NID:G20548; PIDN:CAA42902.1; PID:G20549
C:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1991
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; oxidoreductase
F:4-34/Region: beta-alpha-beta NAD nucleotide-binding fold
F:153/180/Active site: Cys, His #status predicted

Query Match      56.2%; Score 41; DB 1; Length 336;
Best Local Similarity 35.7%; Pred. No. 27;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 IEGPLRLQWLARA 14
      ::|::|::|::|
Db      189 VDGPMSKMDWRGGR 202

RESULT 20
A35080
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - common ice plant
C:Species: Mesembryanthemum crystallinum (common ice plant)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 09-Jul-2004
C:Accession: A35080
R:Ostrem, J.A.; Vernon, D.M.; Bohmert, H.J.
J. Biol. Chem. 265, 3497-3502, 1990
A:Title: Increased expression of a gene coding for NAD:glyceraldehyde-3-phosphate dehydrogenase.
A:Reference number: A35080; MUID:90154012; PMID:2303458
A:Accession: A35080
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-337 <OST>
A:Cross-references: UNIPROT:P17878; GB:J05223; NID:G167263; PIDN:AAA33033.1; PID:G167264
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: oxidoreductase

Query Match      56.2%; Score 41; DB 2; Length 337;
Best Local Similarity 35.7%; Pred. No. 27;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 IEGPLRLQWLARA 14
      ::|::|::|::|
Db      190 VDGPMSKMDWRGGR 203

RESULT 21
DEIS3C
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12), cytosolic - white clover
N:Alternat names: triosephosphate dehydrogenase
C:Species: Sinapis alba (white mustard)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: A24796
R:Martin, W.; Cerff, R.
Eur. J. Biochem. 159, 323-331, 1986
A:Title: Prokaryotic features of a nucleus-encoded enzyme. cDNA sequences for chloroplast
A:Reference number: A24796; MUID:87004643; PMID:3530755
A:Accession: A24796
A:Molecule type: mRNA

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A:Residues: 1-338 <NM>
A:Cross-references: UNIPROT:P04796; GB:X04301; NID:g21142; PIDN:CAA27844.1; PID:g21143
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: glucosyltransferase; glycolysis; homotrimer; NAD; oxidoreductase
F/2-338/Product: glyceraldehyde-3-phosphate dehydrogenase #status experimental <MAT>
F/7-37/Region: beta-alpha-beta NAD nucleotide-binding fold
F/156/183/Active site: Cys, His #status predicted

Query Match          56.2%; Score 41; DB 1; Length 338;
Best Local Similarity 35.7%; Pred. No. 27;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 IEGETLRQWLAARA 14
Db      192 VDGSPMKDWRGGR 205

RESULT 22
QJ01287
glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12), cytosolic - A
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 31-Mar-1992 #sequence_reviseion 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: J01287; J50614
R:Smith, M.C.; Heinrich, P.; Goodman, H.M.
Gene 104, 133-138, 1991
A:Title: Cloning and chromosomal mapping of nuclear genes encoding chloroplast and cyto-
A:Reference number: J01285; MUID:92009205; PMID:1916285
A:Accession: J01287
A:Molecule type: DNA
A:Residues: 1-338 <SH1>
A:Cross-references: UNIPROT:P25856; GB:M64119; NID:g166709; PIDN:AAA32796.1; PID:g166710
A:Accession: J50614
A:Molecule type: mRNA
A:Residues: 1-338 <SH11>
A:Cross-references: GB:M64116; NID:g166705; PIDN:AAA32794.1; PID:g166706
A:Experimental source: leaf
C:Genetics:
A:Gene: gapC
A:Map position: 3 0.0cM
A:introns: 2/1; 12/1; 45/3; 84/2; 117/3; 167/2; 187/1; 267/2
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: cytosol; oxidoreductase

Query Match          56.2%; Score 41; DB 2; Length 338;
Best Local Similarity 35.7%; Pred. No. 27;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 IEGETLRQWLAARA 14
Db      192 VDGSPMKDWRGGR 205

RESULT 23
B95325
conserved hypothetical protein Sma0937 [imported] - Sinorhizobium meliloti (strain 1021)
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_reviseion 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: B95325
R:Barnett, M.V.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow-
A:Kalmann, S.; Keating, D.H.; Palm, C.; Beck, M.C.; Surzycki, R.; Wells, D.H.; Yen, K.C
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: B95325
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-719 <KUR>
A:Cross-references: UNIPROT:Q92ZM3; GB:AE006469; PIDN:AAK65164.1; PID:g14523607; GSPDB:
R:Gallibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
Bela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001

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A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure, hebulu, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: Sma0937

A:Genome: plasmid

Query Match 56.2%; Score 41; DB 2; Length 719;

Best Local Similarity 46.2%; Pred. No. 58;

Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEPTLRQWLAR 13

DB 71 LDDEVRQWLTRAK 83

RESULT 24

A97501
topoisomerase iv chain a [imported] - *Agrobacterium tumefaciens* (strain C58, Cereon)

C:Species: *Agrobacterium tumefaciens*

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C:Accession: A97501

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*

A:Reference number: A97559; MUID:21608551; PMID:11743194

A:Accession: A97501

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-750 <KUR>

A:Cross-references: UNIPROT:Q8UG82; GB:AB007869; PIDN:AAK86962.1; PID:g15156198; GSPDB:Q

A:Genetics:

A:Gene: AGR_C_2144

A:Map position: circular chromosome

C:Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase

Query Match 56.2%; Score 41; DB 2; Length 750;

Best Local Similarity 66.7%; Pred. No. 60;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GPTLRQWLARA 14

DB 721 GBELREWLADRA 732

RESULT 25

AE2719
topoisomerase IV subunit A parC [imported] - *Agrobacterium tumefaciens* (strain C58, Dupo

C:Species: *Agrobacterium tumefaciens*

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: AE2719

R:Wood, D.W.; Setudal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tso, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AE2719

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-750 <KUR>

A:Cross-references: UNIPROT:Q8UG82; GB:AB008686; PIDN:AA42171.1; PID:g17739560; GSPDB:Q

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: parC

A:Map position: circular chromosome

C:Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase

Query Match 56.2%; Score 41; DB 2; Length 750;

Best Local Similarity 66.7%; Pred. No. 60;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GPTLRQWLARA 14

DB 721 GBELREWLADRA 732

RESULT 26

S25204
srnx protein - *Streptomyces ambofaciens*

C:Species: *Streptomyces ambofaciens*

C:Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 09-Jul-2004

C:Accession: S25204; S21599

R:Geistlich, M.; Losick, R.; Turner, J.R.; Rao, R.N.

Mol. Microbiol. 6, 2019-2029, 1992

A:Title: Characterization of a novel regulatory gene governing the expression of a pol

A:Reference number: S25202; MUID:92374852; PMID:1508047

A:Accession: S25204

A:Molecule type: DNA

A:Residues: 1-239 <GBI>

A:Cross-references: UNIPROT:Q00510; EMBL:X63451; NID:946699; PIDN:CAA45052.1; PID:g46570

C:Genetics:

A:Gene: srnx

F:39-139/Domain: bioc homology <BIOC>

Query Match 54.8%; Score 40; DB 2; Length 239;

Best Local Similarity 50.0%; Pred. No. 28;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 IEPTLRQWLARA 14

DB 63 VSGLESEWMAARA 76

RESULT 27

S27491
hypothetical protein A - *Bacillus firmus*

C:Species: *Bacillus firmus*

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: S27491

R:Quirk, P.G.; Krulwich, T.A.

submitted to the EMBL Data Library, October 1991

A:Reference number: S27490

A:Accession: S27491

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-463 <QHI>

A:Cross-references: UNIPROT:P30267; GB:L02548; EMBL:M74194; NID:g143118; PIDN:AAA22559.

Query Match 54.8%; Score 40; DB 2; Length 463;

Best Local Similarity 61.5%; Pred. No. 54;

Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EGPTLRQWLARA 14

DB 296 EGKTSROWALERA 308

RESULT 28

AB1958
probable permease NMA0414 [imported] - *Neisseria meningitidis* (strain Z2491 serogroup A

C:Species: *Neisseria meningitidis*

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C:Accession: AB1958

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.

A:Reference number: AB1775; MUID:20222556; PMID:10761919

A:Accession: AB1958

A:Status: Preliminary

A:Molecule type: DNA
 A:Residues: 1-530 <PAR>
 A:Cross-references: UNIPROT:Q9JWB3; GB:AL162753; GB:AL157959; NID:G7379120; PIDN:CAH8371
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: NMA0414

Query Match 54.8%; Score 40; DB 2; Length 530;
 Best Local Similarity 72.7%; Pred. No. 62;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEGETLRQWLA 11
 ||| ||| |||
 Db 190 IEMPVLRPWLA 200

RESULT 29

ABC transporter, permease protein NMB2026 [imported] - Neisseria meningitidis (strain MC
 C:Species: Neisseria meningitidis
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: E81015
 R:Retcllin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; MUID:2015755; PMID:10710307
 A:Accession: E81015
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-531 <REF>
 A:Cross-references: UNIPROT:Q9JX19; GB:AE002552; GB:AE002098; NID:G7227279; PIDN:AAF4234
 A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB2026

Query Match 54.8%; Score 40; DB 2; Length 531;
 Best Local Similarity 72.7%; Pred. No. 62;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEGETLRQWLA 11
 ||| ||| |||
 Db 191 IEMPVLRPWLA 201

RESULT 30

S30484
 pol polyprotein - human immunodeficiency virus type 2
 C:Species: human immunodeficiency virus type 2, HIV-2
 C>Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 23-Mar-2001
 C:Accession: S30484
 R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
 submitted to the EMBL Data Library, December 1992
 A:Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa
 A:Reference number: S30460
 A:Accession: S30484
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-656 <GAO>
 A:Cross-references: EMBL:M87114
 C:Superfamily: pol polyprotein

Query Match 54.8%; Score 40; DB 2; Length 656;
 Best Local Similarity 66.7%; Pred. No. 77;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 IEGETLRQW 9
 :||| |||
 Db 29 MDGPKLRQW 37

RESULT 31

S30483
 pol polyprotein - human immunodeficiency virus type 2
 C:Species: human immunodeficiency virus type 2, HIV-2
 C>Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 23-Mar-2001
 C:Accession: S30483
 R:Gao, F.; Yue, L.; White, A.T.; Pappas, P.G.; Barchue, J.; Hanson, A.P.; Greene, B.M.;
 submitted to the EMBL Data Library, December 1992
 A:Description: Human infection by genetically diverse SIVSM-related HIV-2 in west Africa
 A:Reference number: S30460
 A:Accession: S30483
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-656 <GAO>
 A:Cross-references: EMBL:M87111
 C:Superfamily: pol polyprotein

Query Match 54.8%; Score 40; DB 2; Length 656;
 Best Local Similarity 66.7%; Pred. No. 77;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 IEGETLRQW 9
 :||| |||
 Db 29 MDGPKLRQW 37

RESULT 32

A39707
 erythrocyte membrane band 4.2 protein - human
 N:Alternate names: pallidin
 N:Contains: erythrocyte membrane band 4.2 protein, long splice form; erythrocyte membra
 C:Species: Homo sapiens (man)
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: A39707; A34865; B34865; A34883
 R:Korsgren, C.; Cohen, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 88, 4840-4844, 1991
 A:Title: Organization of the gene for human erythrocyte membrane protein 4.2: structura
 A:Reference number: A39707; MUID:91271288; PMID:2052563
 A:Accession: A39707
 A:Molecule type: DNA
 A:Residues: 1-721 <KOR1>
 A:Cross-references: UNIPROT:P16452; GB:L06519; NID:G306738; PIDN:AAA52385.1; PID:G30674
 A:Experimental source: cell type erythrocyte; tissue type peripheral blood; tissue lib
 R:Sun, L.A.; Chien, S.; Chang, L.S.; Lambert, K.; Blise, S.A.; Bouhasstra, E.E.; Nagel
 Proc. Natl. Acad. Sci. U.S.A. 87, 955-959, 1990
 A:Title: Molecular cloning of human protein 4.2: a major component of the erythrocyte m
 A:Reference number: A34865; MUID:90138995; PMID:1689063
 A:Accession: A34865
 A:Molecule type: mRNA
 A:Residues: 1364, 'KRGJPC', 371-379, 'H', 381-405, 'L', 407-721 <SUN1>
 A:Cross-references: GB:M30647; NID:G189433; PIDN:AAA36401.1; PID:G189434
 A:Accession: B34865
 A:Molecule type: mRNA
 A:Residues: 1-33, 34-364, 'KRGJPC', 371-379, 'H', 381-405, 'L', 407-721 <SUN2>
 A:Cross-references: GB:M30646; NID:G189435; PIDN:AAA36402.1; PID:G189436
 A:Experimental source: isolate Sickie cell patient; cell type reticulocyte
 A>Note: parts of this sequence were determined by protein sequencing
 R:Korsgren, C.; Lawler, J.; Lambert, S.; Speichter, D.; Cohen, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 613-617, 1990
 A:Title: Complete amino acid sequence and homologies of human erythrocyte membrane prot
 A:Reference number: A34883; MUID:90138879; PMID:2300550
 A:Accession: A34883
 A:Molecule type: mRNA
 A:Residues: 1-33, 34-721 <KOR2>
 A:Cross-references: GB:M29399; NID:G182083; PIDN:AAA35798.1; PID:G182084
 C:Comment: This protein is a major constituent of the erythrocyte membrane. It apparent
 C:Genetics:
 A:Gene: GDB:EBB42; PA
 A:Cross-references: GDB:127385; OMIM:177070
 A:Map position: 15q15-15q15
 A:Superfamily: protein-glutamine gamma-glutamyltransferase
 C:Keywords: alternative splicing; blocked amino end; glycoprotein; lipoprotein; myristic
 F,2-721/Product: erythrocyte membrane band 4.2 protein, long splice form #status predic

F,2,3,34-721/Product: erythrocyte membrane band 4.2 protein, short splice form #status P
 F,298-316/Domain: transmembrane #status predicted <TRM>
 F,518-520/Region: cell attachment (R-G-D) motif
 F,2/Modified site: myristylated amino end (GIY) (in mature form) #status predicted
 F,103,420,447,529,604,705/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F,278/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted

Query Match 54.8%; Score 40; DB 2; Length 721;
 Best Local Similarity 70.0%; Pred. No. 85;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4 PTLRQMLAAR 13
 Db 280 PTLRQMLTGR 289

RESULT 33

T51517
 telomerase reverse transcriptase - Arabidopsis thaliana

N/Alternate names: protein F5E19_190

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C/Accession: T51517

R/Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Men

submitted to the Protein Sequence Database, August 2000

A/Reference number: 225394

A/Accession: T51517

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1123 <SAT>

A/Cross-references: UNIPROT:Q9SPU7; EMBL:AL391147

A/Experimental source: cultivar Columbia; BAC clone F5E19

C/Genetics:

A/Map position: '5

A/Introns: 100/3; 125/3; 147/3; 185/1; 300/3; 325/1; 369/2; 414/3; 765/3; 942/2; 1033/2

A/Note: F5E19_190

Query Match 54.8%; Score 40; DB 2; Length 1123;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 1 IEPTLRQMLAA 12
 Db 200 VQPTKQWLSS 211

RESULT 34

CGH028
 collagen alpha 2(IV) chain precursor - human

N/Alternate names: procollagen alpha 2(IV) chain

C/Species: Homo sapiens (man)

C/Date: 07-Jun-1990 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004

C/Accession: A32024; S00007; S02624; S00246; S17678; S16911; B32117; S16877; S00165; S39

R/Hoschlika, S.L.; Tryggvason, K.

J. Biol. Chem. 263, 19488-19493, 1988

A/Title: The complete primary structure of the alpha2 chain of human type IV collagen an

A/Reference number: A32024; MUID:8906769; PMID:3198637

A/Accession: A32024

A/Molecule type: mRNA

A/Residues: 1-1712 <HOS1>

A/Cross-references: UNIPROT:P08572; EMBL:J04210; EMBL:X05610; GB:M20753; NID:g29550; PID

R/Hoschlika, S.L.; Kurkinen, M.; Tryggvason, K.

FEBS Lett. 216, 281-286, 1987

A/Title: Nucleotide sequence coding for the human type IV collagen alpha-2 chain cDNA re

ated region.

A/Reference number: S00007; MUID:87219158; PMID:3582677

A/Accession: S00007

A/Molecule type: mRNA

A/Residues: 1254-1398, 'V', 1400-1712 <HOS2>

A/Cross-references: EMBL:J04210; EMBL:X05610; GB:M20753; NID:g29550; PIDN:CAA29098.1; PI

R/Hoschlika, S.L.; Tryggvason, K.

FEBS Lett. 224, 297-305, 1987

A/Title: Extensive structural differences between genes for the alpha(1) and alpha(2) c

A/Reference number: S02624; MUID:88083553; PMID:2826228

A/Accession: S02624

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1347-1350;1377-1383;1426-1432;1465-1471;1529-1535;1625-1630 <HOS3>

A/Note: complete nucleotide sequence not shown

R/Brazel, D.; Pollner, R.; Oberhauser, I.; Kuehn, K.

Eur. J. Biochem. 172, 35-42, 1988

A/Title: Human basement membrane collagen (type IV): the amino acid sequence of the al

A/Reference number: S00246; MUID:88151998; PMID:3345760

A/Accession: S00246

A/Molecule type: mRNA

A/Residues: 1-682, 'G', 684-1043

A/Cross-references: EMBL:X05562; NID:g30075; PIDN:CAA29076.1; PID:g30076

R/Oberhauser, I.

submitted to the EMBL Data Library, June 1987

A/Reference number: S17678

A/Accession: S17678

A/Molecule type: mRNA

A/Residues: 1-470, 'P', 472-682, 'G', 684-1043 <OBE>

A/Cross-references: EMBL:X05562; NID:g30075; PIDN:CAA29076.1; PID:g30076

R/Poeschl, E.; Pollner, R.; Kuehn, K.

EMBO J. 7, 2687-2695, 1988

A/Title: The genes for the alpha1(IV) and alpha2(IV) chains of human basement membrane

A/Reference number: S02738; MUID:89030632; PMID:2846280

A/Accession: S16911

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-33 <POS>

A/Cross-references: EMBL:X12784; GB:M36963; NID:g30072; PIDN:CAA11275.1; PID:g30073

R/Soininen, R.; Hotari, M.; Hoschlika, S.L.; Prockop, D.J.; Tryggvason, K.

J. Biol. Chem. 263, 17217-17220, 1988

A/Title: The structural genes for alpha1 and alpha2 chains of human type IV collagen ar

A/Reference number: A92690; MUID:89034231; PMID:3182844

A/Accession: B32117

A/Molecule type: DNA

A/Residues: 1-33 <SO11>

A/Cross-references: EMBL:J04217; EMBL:J05039; NID:g180759; PIDN:AAA53097.1; PID:g553233

R/Soininen, R.; Hotari, M.; Ganguly, A.; Prockop, D.J.; Tryggvason, K.

J. Biol. Chem. 264, 13565-13571, 1989

A/Title: Structural organization of the gene for the alpha-1 chain of human type IV col

A/Reference number: S16877; MUID:89340433; PMID:2701944

A/Accession: S16877

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-33 <SO12>

A/Cross-references: EMBL:J04217; NID:g180759; PIDN:AAA53097.1; PID:g553233; EMBL:J05039

A/Note: This sequence was submitted to the EMBL Data Library, October 1988

R/Siebold, B.; Qian, R.Q.; Glanville, R.W.; Hofmann, H.; Deutmann, R.; Kuehn, K.

Eur. J. Biochem. 168, 569-575, 1987

A/Title: Construction of a model for the aggregation and cross-linking region (7S domai

is region.

A/Reference number: S00165; MUID:88029476; PMID:3117548

A/Accession: S00165

A/Molecule type: Protein

A/Residues: 37-247 <SE1>

A/Note: the sequence from Fig. 4 is inconsistent with that from Fig. 3 in having 175-Gl

R/Ehle, J.A.; Golbik, R.; Mann, K.; Kuehn, K.

EMBO J. 12, 4795-4802, 1993

A/Title: The alpha-1-beta-1 integrin recognition site of the basement membrane collagen

A/Reference number: S39614; MUID:94038963; PMID:8223488

A/Accession: S39615

A/Molecule type: Protein

A/Residues: 407-570 <EBL>

R/MacWright, R.S.; Benson, V.A.; Lovello, K.T.; van der Rest, M.; Fietzek, P.P.

Biochemistry 22, 4940-4948, 1983

A/Title: Isolation and characterization of pepsin-solubilized human basement membrane (

A/Reference number: S16910; MUID:84053346; PMID:6416291

A/Accession: S16912

A/Molecule type: Protein

A/Residues: 490-492, 'X', 494-496, 675-677, 'G', 679-680, 'G', 682, 684-685, 'P' <MAC>

A/Experimental source: placenta

R:Glanville, R.W.; Rauter, A.
 Hoppe-Seyler's Z. Physiol. Chem. 362, 943-951, 1961
 A:Title: Peptin fragments of human placental basement-membrane collagens showing internal
 A:Reference number: S16908; MUID:82005835; PMID:6792033
 A:Accession: B58517
 A:Molecule type: protein
 A:Residues: 490-492, 'X', 494-501, 'P', 503-507, 952-957, 'X', 959-966, 'X', 968, 984-986, 'X', 988-
 81-1185 <G1A>
 R:Killen, P.D.; Francomano, C.A.; Yamada, Y.; Modi, W.S.; O'Brien, S.J.
 Hum. Genet. 77, 318-324, 1987
 A:Title: Partial structure of the human alpha-2(IV) collagen chain and chromosomal local
 A:Reference number: S01450; MUID:86085168; PMID:3692475
 A:Accession: S01450
 A:Molecule type: mRNA
 A:Residues: 1040, 'L', 1042-1398, 'V', 1400-1418, 'W', 1420-1635, 'V', 1637-1712 <K1L>
 A:Cross-references: EMBL:M4766; NID:G537328; PIDN:AA52043.1; PID:G537329
 R:Siebold, B.; Deutmann, R.; Kuehn, K.
 Eur. J. Biochem. 176, 617-624, 1988
 A:Title: The arrangement of intra- and intermolecular disulfide bonds in the carboxyterm
 A:Reference number: S02550; MUID:89005112; PMID:2844531
 A:Accession: S02550
 A:Molecule type: protein
 A:Residues: 1480-1535, 1545-1614, 1617-1662, 'H', 1664-1700, 'G', 1705-1708, 1710-1712 <SIE2>
 A>Note: the sequence form Fig. 7 is inconsistent with that shown in Fig. 11 in having 17
 R:Myers, J.C.; Howard, P.S.; Jelen, A.M.; Dion, A.S.; Macarak, E.J.
 J. Biol. Chem. 262, 9231-9238, 1987
 A:Title: Duplication of type IV collagen COOH-terminal repeats and species-specific exp
 A:Reference number: A27114; MUID:87250571; PMID:2439508
 A:Accession: B27114
 A:Molecule type: mRNA
 A:Residues: 1486-1574, 'T', 1576-1712 <MYE>
 A:Cross-references: EMBL:J02760; NID:G180425; PIDN:AA58422.1; PID:G180426
 C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
 ed and subsequently O-glycosylated.
 C:Genetics:
 A:Gene: GDB:COL4A2
 A:Cross-references: GDB:119792; OMIM:120090
 A:Map position: 13q34-13q34
 A:Insertions: 15/2; 33/3; 1360/1; 1429/1; 1468/1; 1532/1; 1527/3 #status incomplete
 A>Note: the alpha 1(IV) and alpha 2(IV) chain genes are encoded on opposite strands with
 C:Complex: Type IV collagen is a heterotrimer of two alpha 1(IV) chains (see PIR:CGH4B)
 domains (with disulfide and desmosine cross-links), dimeric associations among trimer ca
 rrupted helical domain (with disulfide and desmosine cross-links).
 C:Function:
 A:Description: structural component of basement membrane
 C:Superfamily: collagen alpha 1(IV) chain
 C:Keywords: basement membrane; cell binding; coiled coil; extracellular matrix; glycopro
 P:1-28/Domain: signal sequence #status predicted <SIG>
 P:29-1112/Product: collagen alpha 2(IV) chain #status predicted <MAT>
 F:29-57/Domain: amino-terminal nonhelical, NHL <NHL>
 F:58-1485/Region: interrupted helical
 F:362-364/Region: cell attachment (R-G-D) motif
 F:784-786/Region: cell attachment (R-G-D) motif
 F:868-870/Region: cell attachment (R-G-D) motif
 F:889-891/Region: cell attachment (R-G-D) motif
 F:970-972/Region: cell attachment (R-G-D) motif
 F:1069-1071/Region: cell attachment (R-G-D) motif
 F:1228-1230/Region: cell attachment (R-G-D) motif
 F:1452-1454/Region: cell attachment (R-G-D) motif
 F:1486-1712/Domain: carboxyl-terminal nonhelical, NCL <NCL>
 F:1495-1593/Domain: collagen IV carboxyl-terminal repeat <CTR>
 F:1603-1708/Domain: collagen IV carboxyl-terminal repeat <CTR>
 F:42, 47, 51, 53, 137, 483, 485/Disulfide bonds: interchain #status predicted
 F:57, 87, 90, 102, 165, 168, 225, 239, 242/Binding site: carbohydrate (lys) (covalent) #status p
 F:57/Modified site: 5-hydroxylysine (lys) #status atypical
 F:63, 75, 96, 114, 120, 123, 150, 159, 166, 189, 198, 201, 213, 216, 219, 496, 499, 955, 964, 1103, 1115
 F:87, 90, 102, 165, 168, 225, 239, 242/Modified site: 5-hydroxylysine (lys) #status experimenta
 F:138/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:209/Modified site: 4-hydroxyproline (Pro) #status atypical
 F:661-681/Disulfide bonds: #status predicted
 F:1275/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:1504-1590, 1537-1593/Disulfide bonds: (or 1504-1593, 1537-1590) #status experimental
 F:1549-1555, 1658-1665/Disulfide bonds: #status experimental

F:1612-1705, 1646-1708/Disulfide bonds: (or 1612-1708, 1646-1705) #status experimental
 Query Match 54.8%; Score 40; DB 1; Length 1712;
 Best Local Similarity 60.0%; Pred. No. 26+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 IEGPTLROWL 10
 : |||||
 Db 8 VAGPALRWL 17
 RESULT 35
 A84326
 hypothetical protein Vng1740C [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: A84326
 R:Ng, W.V.; Kennedy, S.P.; Malaitas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Jaeky, i
 ; Leichter, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabil
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; L
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: A84326
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-325 <STO>
 A:Cross-references: UNIPROT:Q9HP97; GB:AE004437; NID:G10581200; PIDN:AA619973.1; GSPDB:
 C:Genetics:
 A:Gene: VNG1740C
 Query Match 54.1%; Score 39.5; DB 2; Length 325;
 Best Local Similarity 64.3%; Pred. No. 46;
 Matches 9; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
 QY 1 IEGPTLROWLAARA 14
 : |||||
 Db 14 LRGPA-AAWLAARA 26

RESULT 36
 S74539
 hypothetical protein slr0740 - Synechocystis sp. (strain PCC 6803)
 C:Species: Synechocystis sp.
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C:Accession: S74539
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
 O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
 S.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S74539
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-131 <UNP>
 A:Cross-references: UNIPROT:P72684; EMBL:D90899; GB:AB001339; NID:G1651650; PIDN:BA1166
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C:Superfamily: Synechocystis hypothetical protein slr0740
 Query Match 53.4%; Score 39; DB 2; Length 131;
 Best Local Similarity 87.5%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 PTLROWLA 11
 : |||||
 Db 29 POLROWLA 36
 RESULT 37
 S46354

Query Match 53.4%; Score 39; DB 2; Length 400;
 Best Local Similarity 69.2%; Pred. No. 69;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEGETLRQWIAAR 13
 |||||
 Db 86 IEGETLRQWIAAR 98

RESULT 42

Transport protein Hasd PA3406 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 16-Aug-2004
 C/Accession: C83221
 C/Owner: C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.U.; Badian, S.; Yan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam, J.; Lory, S.; Olson, M.V.
 A/Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A/Reference number: A82950; PMID:20437337; PMID:10984043
 A/Accession: C83221
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-600 <STO>
 A/Cross-references: UNIPROT:Q9HYH9; GB:AE004761; GB:AE004091; NID:G949533; PIDN:AMG0679
 A/Experimental source: strain PA01
 C/Genetics:
 A/Gene: hasd
 C/Superfamily: ATP-binding cassette homology

Query Match 53.4%; Score 39; DB 2; Length 600;
 Best Local Similarity 58.3%; Pred. No. 1e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEGETLRQWIAA 12
 |||||
 Db 392 LDGADLRQMSAA 403

RESULT 43

c-di-GMP phosphodiesterase A-related protein VC0703 [imported] - Vibrio cholerae (strain C/Species: Vibrio cholerae

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C/Accession: A82291
 R/Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gilm, M.L.; Dodson, R.J.; Chaudson, D.; Ernolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.I.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 A/Nature 406, 477-483, 2000
 A/Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A/Reference number: A82035; MUID:20406833; PMID:10952301
 A/Accession: A82291
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-791 <HR1>
 A/Cross-references: UNIPROT:Q9KJ26; GB:AE004157; GB:AE003852; NID:G9655148; PIDN:AAF3366
 A/Experimental source: serogroup O1, strain N16961, biotype El Tor
 C/Genetics:
 A/Gene: VC0703
 A/Map position: 1

Query Match 53.4%; Score 39; DB 2; Length 791;
 Best Local Similarity 63.6%; Pred. No. 1.4e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEGETLRQWIAA 11
 |||||
 Db 730 IESETWQWIAA 740

RESULT 44

GNLJCA

HIV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 2 (isolate CAM2/GuN/Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA poly C/Species: human immunodeficiency virus type 2, HIV-2
 A/Note: host Homo sapiens (man)
 C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C/Accession: B38475; J00974
 R/Tritem, M.; Hill, F.; Karpas, A.
 U. Gen. Virol. 72, 721-724, 1991
 A/Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus cy A/Reference number: A38475; MUID:91170959; PMID:2005437
 A/Accession: B38475
 A/Molecule type: DNA
 A/Residues: 1-1034 <TRI>
 A/Cross-references: UNIPROT:P24107
 A/Note: readthrough of the terminator TGA may occur between codons ATT for 564-Ile and C C/Comment: The cleavage sites of this polypeptide have not been determined.

C/Superfamily: pol polypeptide
 C/Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucle F/95-183/Product: retropepsin #status predicted <RTP>
 F/109/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 53.4%; Score 39; DB 1; Length 1034;
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGPTLRQW 9
 |||||
 Db 200 DGPRLRQW 207

RESULT 45

GNLJCG

HIV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 2 (isolate GH-1) N/Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA pol C/Species: human immunodeficiency virus type 2, HIV-2
 A/Note: host Homo sapiens (man)
 C/Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
 C/Accession: J50328
 R/Hasegawa, A.; Tsujimoto, H.; Maki, N.; Ishikawa, K.; Miura, T.; Fukasawa, M.; Miki, K A/ISRS Res. Hum. Retroviruses 5, 593-604, 1989

A/Title: Sequence of a distinct HIV-2 isolate from Ghana showing significant divergence A/Reference number: J50327; MUID:90122350; PMID:2611042
 A/Accession: J50328
 A/Molecule type: DNA
 A/Residues: 1-1035 <HAS>
 A/Cross-references: UNIPROT:P18042
 A/Note: this sequence was submitted to JIPRD, October 1989
 C/Comment: Cleavage sites that yield the mature proteins remain to be determined.
 C/Genetics:
 A/Gene: pol
 A/Start codon: ACA
 C/Superfamily: pol polypeptide
 C/Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; nucleotidyltransferase; F/85-183/Product: retropepsin #status predicted <RTP>
 F/109/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 53.4%; Score 39; DB 1; Length 1035;
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGPTLRQW 9
 |||||
 Db 200 DGPRLRQW 207

Search completed: September 1, 2005, 16:23:02
 Job time : 12.6763 secs


```

RESULT 1
Q742B3 PRELIMINARY; PRT; 302 AA.
AC 0742B3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Calu.
GN Name=gali; OrderedLocNames=MAP0924;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=k10;
RL Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017230; AA03241.1;
DR GO; GO:0016779; F:nucleotidyltransferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR005835; NTP transferase.
DR Pfam; PF00483; NTP_transferase; 1.
DR Complete proteome.
KW SEQUENCE 302 AA; 32149 MW; 4E5D2B1AB572BAE7 CRC64;
SQ

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Query Match 68.5%; Score 50; DB 2; Length 302;
Best Local Similarity 81.8%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 3 GPTLRQWLAR 13
Db 286 GPDLRQWLAR 296

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```

RESULT 2
CBBR_XANFL STANDARD; PRT; 333 AA.
AC P2545;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE HTH-type transcriptional regulator cbbR (Rubisco operon
DE transcriptional regulator)
GN Name=cbbR; Synonyms=cfko;
OS Xanthobacter flavus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Xanthobacter.
OX NCBI_TaxID=281;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4-14;
RX MEDLINE=94012468; PubMed=8407781;
RA van den Berg E., Dijkhuizen L., Meijer W.G.;
RA "CbbR, a LysR-type transcriptional activator, is required for
RT expression of the autotrophic CO2 fixation enzymes of Xanthobacter
RT flavus."
RT J. Bacteriol. 175:6097-6104(1993).
RN [2]
RP SEQUENCE OF 1-150 FROM N.A.
RC STRAIN=H4-14;
RX MEDLINE=91172133; PubMed=1900916;
RA Meijer W.G., Arberg A.C., Enequist H.G., Terpstra P., Lidstrom M.E.,
RA Dijkhuizen L.;
RT "Identification and organization of carbon dioxide fixation genes in
RT Xanthobacter flavus H4-14."
RL Mol. Gen. Genet. 225:320-330(1991).
CC -1- FUNCTION: Transcriptional activator for the cbb operon (cbbLXFP)
CC for Rubisco and other Calvin cycle genes. Binds specifically to
CC two binding sites in the cbbR-cbbL intergenic region.
CC -1- SIMILARITY: Contains 1 HTH LysR-type DNA-binding domain.
CC

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z22705; CAAB0406.1;
DR EMBL; X17252; -; NOT_ANNOTATED_CDS.
DR PIR; A36925; A36925.
DR InterPro; IPR000847; HTH_LYER.
DR InterPro; IPR005119; LysR_subst.
DR InterPro; IPR009058; Wng_hlx_DNA_bnd.
DR Pfam; PF00126; HTH_1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS50931; HTH_LYER; 1.
KW Activator; DNA-binding; Transcription regulation.
FT DOMAIN 5 62
FT DNA BIND 22 41
FT H-T-H motif (By similarity).
SQ SEQUENCE 333 AA; 36003 MW; 9B375B4FB2D1E873 CRC64;

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Query Match 67.8%; Score 49.5; DB 1; Length 333;
Best Local Similarity 66.7%; Pred. No. 3.4;
Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

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QY 1 IEG-PTLRQWLARA 14
Db 264 VEGLPVVRQWLAVRA 278

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RESULT 3
Q9RKM5 PRELIMINARY; PRT; 319 AA.
AC Q9RKM5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative MerR family transcriptional regulator.
GN ORFNames=SCD17.06c;
OS Streptomyces coelicolor.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/41741a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Baleman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsbey T., Howarth S.,
RA Hwang C.-H., Kleser A., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Ruter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)."
RL Nature 417:141-147(2002).
CC -1- SIMILARITY: Contains 1 HTH merR-type DNA-binding domain.
CC EMBL; AL939118; CAB56383.1;
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000551; HTH_MerR.
DR InterPro; IPR009061; Putativ_DNA_bind.
DR Pfam; PF00376; MerR; 1.
DR PRINTS; PR00040; HTHMERR.
DR SMART; SM00422; HTH_MER_R; 1.
DR PROSITE; PS50937; HTH_MER_R; 1.
KW Complete proteome; DNA-binding.

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SEQUENCE 319 AA; 34841 MW; 1F51905A8BA5365E CRC64;

Query Match 67.1%; Score 49; DB 2; Length 319;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EGPTLRQWLAAR 13
DB 258 DGPALVYRMIAAR 108

RESULT 4

ID Q9L8D4 PRELIMINARY; PRT; 607 AA.
AC Q9L8D4
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein (fragment).
OS Polyangium cellulorum (Sorangium cellulorum).
OC Sorangium; Proteobacteria; Delaproteobacteria; Myxococcales;
OC NCB1_TaxID=56;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=So ce90;
RX MEDLINE=20130945; PubMed=10662695; DOI=10.1016/S1074-5521(00)00075-2;
RA Mojar I., Schupp T., Ono M., Zirkle R.E., Milnamow M.,
RA Novak-Thompson B., Engel N., Toupet C., Strattmann A., Cyr D.D.,
RA Gorchach J., Mayo J.M., Hu A., Goff S., Schmidt J., Liong J.M.;
RT "The biosynthetic gene cluster for the microtubule-stabilizing agents
RT epothilones A and B from Sorangium cellulorum So ce90.";
RL Chem. Biol. 7:97-109 (2000).
DR EMBL; AF210843; AAF6904.1; -.
KW Hypothetical protein.
FT NOK TRR 1
SQ SEQUENCE 607 AA; 66326 MW; F113CA299B25048E CRC64;

Query Match 65.8%; Score 48; DB 2; Length 607;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 IEPTLRQWLAAR 13
DB 96 VDGPAVYRMIAAR 108

RESULT 5

ID Q8QUU6 PRELIMINARY; PRT; 941 AA.
AC Q8QUU6
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ORF14.
OS Infectious spleen and kidney necrosis virus.
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae;
OC NCB1_TaxID=180170;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21874810; PubMed=11878882; DOI=10.1006/viro.2001.1208;
RA He J.G., Deng M., Weng S.P., Li Z., Zhou S.Y., Long Q.X., Wang X.Z.,
RA Chan S.M.;
RT "Complete genome analysis of the mandarin fish infectious spleen and
RT kidney necrosis iridovirus";
RL Virology 291:126-139 (2001).
DR EMBL; AF371960; AAL98838.1; -.
SQ SEQUENCE 941 AA; 106703 MW; EB663998C7F6CE83 CRC64;

Query Match 65.8%; Score 48; DB 2; Length 941;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEPTLRQWLAAR 14
DB 581 VQPTLRQWLAAR 594

RESULT 6

ID Q66D06 PRELIMINARY; PRT; 296 AA.
AC Q66D06
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Putative drug/metabolite (DME family) efflux pump precursor.
GN ORFNames=YPN1243;
OS Yersinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCB1_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala M.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinebusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francois V., Souza B., Dacheux D., Elliott J.M.,
RA Derblat A., Hauser L.J., Garcia B.;
RT "Insights into the genome evolution of Yersinia pestis through whole
RT genome comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831 (2004).
DR EMBL; BX96398; CAH20483.1; -.
DR InterPro; IPR00620; DUF6.
DR Pfam; PF00892; DUF6; 2.
KW Signal.
FT SIGNAL 1
SQ SEQUENCE 296 AA; 31407 MW; 4D3E486D32DBAC11 CRC64;

Query Match 64.4%; Score 47; DB 2; Length 296;
Best Local Similarity 61.8%; Pred. No. 8.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PTLRQWLAAR 14
DB 66 PTLRQWLAAR 76

RESULT 7

ID Q8ZGS7 PRELIMINARY; PRT; 296 AA.
AC Q8ZGS7
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Putative membrane protein (Putative transmembrane protein).
GN Yersinia pestis.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCB1_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Bover Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titchell R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holtroyd S., Jagsels K., Kariyeh A.V.,
RA Leather S., Moulton S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527 (2001).

```

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1126/JCB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G., III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=91001 / Biovar Mediaevalis;
RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
RA Yang R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ414147; CAC90042.1; -.
DR EMBL: AE013900; AAM86536.1; -.
DR EMBL: AE017130; AAS61189.1; -.
DR PIR: AG0147; AG0147.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR Pfam: PF00892; DUF6; 2.
DR Complete proteome; Transmembrane.
SQ SEQUENCE 296 AA; 31378 MW; 45947413DCD54CF6 CRC64;

Query Match 64.4%; Score 47; DB 2; Length 296;
Best Local Similarity 81.8%; Pred. No. 8.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PTLRQWLARA 14
Db 66 PTLRQWLARA 76

RESULT 8
Q7D906 PRELIMINARY; PRT; 306 AA.
AC Q7D906;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DR UTP-glucose-1-phosphate uridylyltransferase (EC 2.7.7.9).
GN Name-gall; OrderedLocNames=MT1022;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RX DOI=10.1126/JCB.184.19.5479-5490.2002;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J.D., Deboy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
RA Salzberg S.L., Delcher A., Uterback T.R., Weidman J.F., Khouri H.M.,
RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
RA Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).
DR EMBL: AE000516; AAK45263.1; -.
DR TIGR: MT1022; -.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0003983; F:UTP-glucose-1-phosphate uridylyltransferase. . .; IEA.
DR GO: GO:0009058; P:bioynthesis; IEA.
DR InterPro: IPR005835; NTP transferase.
DR Pfam: PF00483; NTP_transferase; 1.
DR Nucleotidyltransferase; Transferase.

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SQ SEQUENCE 306 AA; 32406 MW; 880D3BB86CBA3EA CRC64;

Query Match 63.0%; Score 46; DB 2; Length 306;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GPTLRQWLAR 13
Db 290 GPTLRQWLAR 300

RESULT 9
Q05576 PRELIMINARY; PRT; 306 AA.
AC Q05576;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DR PROBABLE UTP-glucose-1-phosphate uridylyltransferase GALU (UDP-
DE GLUCOSE PYROPHOSPHORYLASE) (UDPGP) (ALPHA-D-GLUCOSYL-1-PHOSPHATE
DE URIDYLTYLTRANSFERASE) (URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE) (EC
DE 2.7.7.9).
DR Name=gall; OrderedLocNames=Rv0933;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/311159;
RX Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
RX Harris D.E., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III,
RX Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
RX Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
RX Holtroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
RX Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
RX Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RX Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
DR EMBL: BX842575; CAB08153.1; -.
DR PIR: D70601; D70601.
DR Tuberculosis; Rv0933; -.
DR GO: GO:0016779; F:nucleotidyltransferase activity; IEA.
DR GO: GO:0009058; P:bioynthesis; IEA.
DR InterPro: IPR005835; NTP transferase.
DR Pfam: PF00483; NTP_transferase; 1.
DR Complete proteome.
SQ SEQUENCE 306 AA; 32378 MW; 24C2387443B0A3E8 CRC64;

Query Match 63.0%; Score 46; DB 2; Length 306;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GPTLRQWLAR 13
Db 290 GPTLRQWLAR 300

RESULT 10
Q7U0W3 PRELIMINARY; PRT; 306 AA.
AC Q7U0W3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DR PROBABLE UTP-glucose-1-phosphate uridylyltransferase GALU (UDP-
DE GLUCOSE PYROPHOSPHORYLASE) (UDPGP) (ALPHA-D-GLUCOSYL-1-PHOSPHATE
DE URIDYLTYLTRANSFERASE) (URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE) (EC
DE 2.7.7.9).
GN Name=gall; OrderedLocNames=Mb1020;

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OS Mycobacterium bovis
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA MEDLINE=22709107;
RA Garnier T., Eigimeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duchoy S., Grondin S., Lacroix C., Monsempé C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hwison R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248337; CAD93881.1;
DR GO; GO:0016779; F:nucleosidyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR005835; NTP transferase.
DR Pfam; PF00483; NTP transferase; 1.
KM Complete proteome; Nucleosidyltransferase; Transferase.
SQ SEQUENCE 306 AA; 32406 MW; 880D3BB88CB0A3EA CRC64;

Query Match 63.0%; Score 46; DB 2; Length 306;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 GPTLRQWLAR 13
Db 290 GPTLRQWLVAR 300

RESULT 11
O89RH2 PRELIMINARY; PRT; 580 AA.
ID O89RH2
AC O89RH2;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE B11800 protein.
GN OrderedLocustNames=b11800;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobiium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RA MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamiasawa K., Uchiyama T.,
RA Sasamoto S., Watanabe A., Idegawa K., Itiguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Tsuruta H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005945; BAC48065.1;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR001932; P2C-like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00481; P2C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00332; P2C; 1.
DR SMART; SM00331; P2C; 1.
DR PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 580 AA; 64916 MW; 6AD3A06B6FAE143B CRC64;

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Query Match 63.0%; Score 46; DB 2; Length 580;
Best Local Similarity 80.0%; Pred. No. 24;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IEQPTLRQWL 10
Db 355 IEQPTLRQWL 364

RESULT 12
O66272 PRELIMINARY; PRT; 245 AA.
ID O66272
AC O66272;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Photosynthetic reaction center L subunit (Fragment).
GN Name=pufl;
OS Erythrobacter litoralis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=39960;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMM14332; PubMed=11832943; DOI=10.1038/415630a;
RA MEDLINE=21822632;
RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
RA Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;
RT "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633(2002).
DR EMBL; AB010981; BAA25791.1;
DR HSSP; P02954; 10OV.
DR GO; GO:0030077; C:light-harvesting complex (sensu Proteobact. . .; IEA.
DR GO; GO:0045156; F:electron transporter, transferring electron. . .; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019684; P:photosynthesis, light reaction; IEA.
DR InterPro; IPR005871; Photo_L.
DR InterPro; IPR000484; Photo_RC.
DR Pfam; PF00124; Photo_RC; 1.
DR PRINTS; PR00256; REACTCENTRE.
DR TIGRFAMs; TIGR01157; pufl; 1.
DR PROSITE; PS00244; REACTION_CENTER; 1.
FT NON TER 1
SQ SEQUENCE 245 AA; 27214 MW; 52B268713E199ABD CRC64;

Query Match 61.6%; Score 45; DB 2; Length 245;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 IEQPTLRQWL 10
Db 26 IEQPTLRQWL 35

RESULT 13
O82989 PRELIMINARY; PRT; 249 AA.
ID O82989
AC O82989;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Photosynthetic reaction center L subunit (Fragment).
GN Name=pufl;
OS Erythrobacter sp.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_TaxID=1042;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MBIC3019; PubMed=11832943; DOI=10.1038/415630a;
RA MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,

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RA Hamada T., Eisen J.A., Fraser C.M., DeJong E.F.;
RT "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633(2002).
DR EMBL; AB015708; BAA32995.1; -.
DR HSSP; P02954; 1YST.
DR GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte. . .; IEA.
DR GO; GO:0045156; F:electron transporter, transferring electron. . .; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019684; P:photosynthesis, light reaction; IEA.
DR InterPro; IPR005871; Photo_L.
DR InterPro; IPR000484; Photo_RC.
DR Pfam; PF00124; Photo_RC.1.
DR PRINTS; PR00256; REACTCENTRE.
DR TIGRFAMs; TIGR01157; pufL.1.
DR PROSITE; PS00244; REACTION_CENTER.1.
FT NON TER 1
SQ SEQUENCE 249 AA; 27702 MW; 4D68BDC82B7166AD CRC64;

Query Match 61.6%; Score 45; DB 2; Length 249;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 IEQPTLRQWL 10
Db 26 IEQPTLRQWL 35

RESULT 14
OQXDV0 PRELIMINARY; PRT; 278 AA.
AC OQXDV0;
ID 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Photosynthetic reaction center L subunit.
GN Name=pufL;
OS Erythrobacter sp. MBIC3960.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Erythrobacter.
OX NCBI_Taxid=94771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MEIC3960;
RX MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
RA Hamada T., Eisen J.A., Fraser C.M., DeJong E.F.;
RT "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633(2002).
DR EMBL; AB027515; BAA78672.1; -.
DR HSSP; P02954; 1YST.
DR GO; GO:0030077; C:light-harvesting complex (sensu Proteobacte. . .; IEA.
DR GO; GO:0045156; F:electron transporter, transferring electron. . .; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0019684; P:photosynthesis, light reaction; IEA.
DR InterPro; IPR005871; Photo_L.
DR InterPro; IPR000484; Photo_RC.
DR Pfam; PF00124; Photo_RC.1.
DR PRINTS; PR00256; REACTCENTRE.
DR TIGRFAMs; TIGR01157; pufL.1.
DR PROSITE; PS00244; REACTION_CENTER.1.
SQ SEQUENCE 278 AA; 30735 MW; 0BB618844B3C54FB CRC64;

Query Match 61.6%; Score 45; DB 2; Length 278;
Best Local Similarity 80.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 IEQPTLRQWL 10
Db 55 IEQPTLRQWL 64

RESULT 15
O7WIX1

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ID O7WIX1 PRELIMINARY; PRT; 421 AA.
AC O7WIX1;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative phenylacetate-CoA ligase.
GN OrderedlocusNames=BP0223;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_Taxid=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leather S., Moule S., Norbertczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640423; CAE39964.1; -.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 2.
KW Complete proteome; Ligase.
SQ SEQUENCE 421 AA; 45579 MW; 13D6606AF1FDEC21 CRC64;

Query Match 61.6%; Score 45; DB 2; Length 421;
Best Local Similarity 80.0%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 4 PTLRQWLAR 13
Db 221 PSLRQWLAR 230

RESULT 16
O7WQUB PRELIMINARY; PRT; 421 AA.
ID O7WQUB;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative phenylacetate-CoA ligase.
GN OrderedlocusNames=BB0227;
OS Bordetella bronchiseptica.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_Taxid=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leather S., Moule S., Norbertczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,

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RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Mac. Gene. 35:32-40(2003).
DR EMBL; BX640437; CAE30725.1; -.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 2.
KW Complete proteome; Ligase.
SQ SEQUENCE 421 AA; 45558 MW; A6CDBC9C731A49C CRC64;

Query Match 61.6%; Score 45; DB 2; Length 421;
Best Local Similarity 80.0%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PTLROWLAAR 13
DB 221 PSLRDWLAAR 230

RESULT 17
Q885P2 PRELIMINARY; PRT; 756 AA.
ID Q885P2:
AC Q885P2:
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Dimeitylsulfoxide reductase.
GN OrderedLocusNames=PSPT01789;
OS Pseudomonas syringae (pv. tomat).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RM SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buehl C.R., Joarist V., Lindeberg M., Selengut U., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Davsberry S.C., Birkac L.M., Beaman M.J., Haft D.H.,
RA Ruppel W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Pedorova N.B., Tran B., Russell D., Berry K.J.,
RA Uteerbeck T.R., Van Aken S.E., Feldblyum T.V., D'Ancenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartimour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomat DC3000 ";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
DR EMBL; AE016862; AAO55309.1; -.
DR HSSP; Q57366; 1E01.
DR TIGR; PSP01789; -.
DR GO; GO:0030151; F:molybdenum ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR009010; Asp-decarb fold.
DR InterPro; IPR006557; Mol_dinuc_bind.
DR Pfam; PF01568; Molydop_binding; 1.
KW Complete proteome.
SQ SEQUENCE 756 AA; 83189 MW; 31E9614DE2B2B2C CRC64;

Query Match 61.6%; Score 45; DB 2; Length 756;
Best Local Similarity 61.5%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 IEGPLROWLAAR 13
DB 222 LAGPTHOWLAAR 234

RESULT 18
GTS3_CABEL STANDARD; PRT; 207 AA.
ID GTS3_CABEL:
AC O16116; Q21357;
DT 10-OCT-2003 (Rel. 42, Created)

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DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Glutathione S-transferase 3 (EC 2.5.1.18) (GST class-sigma) (ceGSTR3).
GN Name=gst-3; ORFNames=K08F4.11;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RM SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Tawe W.N., Bachrach M.-L., Walter R.D., Henkle-Duehn K.;
RT "Paracat mediates differential gene expression in C. elegans.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RM SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [3]
RM REVISIONS.
RA Durbin R.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Conjugation of reduced glutathione to a wide number of
CC exogenous and endogenous hydrophobic electrophiles (by
CC similarity).
CC -1- SIMILARITY: Belongs to the GST superfamily. Sigma family.
CC -----
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CC -----
DR EMBL; AF010241; AAB65419.1; -.
DR EMBL; Z68879; CAA93088.2; -.
DR PIR; T37464; T37464.
DR HSSP; P24472; 1GUK.
DR WormBase; WBGene00001751; gst-3.
DR WormPep; K08F4.11; CE25050.
DR GO; GO:0004364; F:glutathione transferase activity; ISS.
DR InterPro; IPR010987; GST_C-like.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Transferase.
SQ SEQUENCE 207 AA; 23735 MW; 72545319FCFCEBDA CRC64;

Query Match 60.3%; Score 44; DB 1; Length 207;
Best Local Similarity 61.5%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 IEGPLROWLAAR 13
DB 190 IETPLKWLAKR 202

RESULT 19
ENTE_ECO57 STANDARD; PRT; 536 AA.
ID ENTE_ECO57:
AC Q8XBV3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Enterobactin synthetase component B (Enterobactin synthase B)
DE [Includes: 2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58)]

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CC      adenosine 5'-monophosphate + acyl-holo-entB.
CC      -1- PATHWAY: Siderophore biosynthesis; enterobactin biosynthesis.
CC      -1- SUBUNIT: Proteins entB, entD, entE, and entF form a multienzyme
CC      complex called enterobactin synthetase.
CC      -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC      family. EntB subfamily.
-----
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-----
DR      EMBL; U00096; AAC73695.1; -
DR      EMBL; U82598; AAB40794.1; -
DR      EMBL; X15058; CA33158.1; -
DR      EMBL; M24148; AAA16101.1; -
DR      EMBL; M36700; AAA18492.1; -
DR      PIR; H64792; SYCEB.
DR      HSSP; P40871; IMD9.
DR      ECHOBASE; EB0259; -.
DR      EcoGene; EG10263; entE.
DR      InterPro; IPR000873; AMP-bind.
DR      Pfam; PF00501; AMP-binding; 1.
DR      PRINTS; PR00154; AMPBINDING.
DR      TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
DR      TIGRFAMs; TIGR01923; menB; 1.
DR      PROSITE; PS00455; AMP BINDING; 1.
KW      Acyltransferase; Complete proteome; Enterobactin biosynthesis;
KW      Iron transport; Ligase; Multifunctional enzyme; Transferase;
KW      Transport.
SQ      SEQUENCE 536 AA; 378 DAEQNPLPQG -> ECRRKSTAPR (in Ref. 1).
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Query Match 60.3%; Score 44; DB 1; Length 536;
Best Local Similarity 57.1%; Pred. No. 50;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
-----
QY      1 IEGBTLROWLAARA 14
DB      521 VDKKQLROWLAASRA 534
-----
RESULT 21
O83M10 PRELIMINARY; PRT; 536 AA.
AC      O83M10; Q7C2S3;
DT      01-JUN-2003 (TREMBlrel. 24, Created)
DT      01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT      25-OCT-2004 (TREMBlrel. 26, Last annotation update)
DE      2,3-dihydroxybenzoate-AMP ligase.
GN      Name=entB; OrderedLocNames=S0514, SFO508;
OS      Shigella flexneri.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Shigella.
OX      NCBI_TaxID=623;
ON      [1]
RA      Yu J.;
RA      "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RA      through comparison with genomes of Escherichia coli K12 and O157.",
RA      Nucleic Acids Res. 30:4432-4441 (2002).
[2]
RA      SEQUENCE FROM N.A.
RA      STRAIN=2457T;

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RX      MEDLINE=22590274; PubMed=12704152;
RX      DOI=10.1128/IAI.71.5.2775-2786.2003;
RA      Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA      Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA      Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA      Schwartz D.C., Blattner F.R.;
RT      "Complete genome sequence and comparative genomics of Shigella
RT      flexneri serotype 2a strain 2457T.",
RL      Infect. Immun. 71:2775-2786 (2003).
CC      -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC      family.
-----
DR      EMBL; AE015082; AAN42156.1; -
DR      EMBL; AE016979; AAP16028.1; -
DR      HSSP; P40871; IMD9.
DR      GO; GO:0016874; F:ligase activity; IEA.
DR      GO; GO:0008152; P:metabolism; IEA.
DR      InterPro; IPR000873; AMP-bind.
DR      Pfam; PF00501; AMP-binding; 1.
DR      PRINTS; PR00154; AMPBINDING.
DR      PROSITE; PS00455; AMP BINDING; UNKNOWN_1.
KW      Ligase; Complete proteome.
SQ      SEQUENCE 536 AA; 58851 MW; ABABD6B8692A8D2 CRC64;
-----
Query Match 60.3%; Score 44; DB 2; Length 536;
Best Local Similarity 57.1%; Pred. No. 50;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
-----
QY      1 IEGBTLROWLAARA 14
DB      521 VDKKQLROWLAASRA 534
-----
RESULT 22
O8LMK9 PRELIMINARY; PRT; 760 AA.
AC      O8LMK9;
DT      01-OCT-2002 (TREMBlrel. 22, Created)
DT      01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT      05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE      Putative gag/pol polyprotein (Putative gag-pol polypeptide).
GN      ORFNames=OSJNB003812.4;
OS      Oryza sativa (japonica cultivar-group).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzaceae; Oryza.
OX      NCBI_TaxID=39947;
ON      [1]
RA      Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA      Overton II L.L., Teltin T., Kim M.M., Beta J.J., Jin S.S.,
RA      Padrosh D.W., Talion L.J., Koo H., Zismann V., Heiao J., Blunt S.,
RA      Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblum T.V.,
RA      Yang O.O., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA      White O., Salzberg S.L., Fraser C.M.;
RL      Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[2]
RA      Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[3]
RA      The Rice Chromosome 10 Sequencing Consortium;
RA      "In-depth view of structure, activity, and evolution of rice
RA      chromosome 10.",
RA      Science 300:1566-1569 (2003).
[4]
RA      SEQUENCE FROM N.A.
RA      Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RA      Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AC105932; AAN04966.1; -
DR      EMBL; AE017067; AAP52546.1; -
DR      Gramene; O8LMK9; -.
DR      InterPro; IPR005162; Retrotrans_gag.

```

DR Pfam; PF03732; Retrotrans_gag; 1.
 KM Polypotein.
 SQ SEQUENCE 760 AA; 82020 MW; C51F91AA2EB32A28 CRC64;

Query Match 60.3%; Score 44; DB 2; Length 760;
 Best Local Similarity 46.2%; Pred. No. 71;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IEPTLRQWLAR 13
 : ||||| :
 Db 661 LHGTLQHMMAVK 673

RESULT 23
 KSGA TREPA STANDARD; PRT; 285 AA.

AC 083357;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Dimethyladenosine transferase (EC 2.1.1.-) (S'-adenosylmethionine-6-N',
 DE N'-adenosyl(rRNA) dimethyltransferase) (16S rRNA dimethylase) (High
 DE level kasugamycin resistance protein ksgA) (Kasugamycin
 DE dimethyltransferase).
 GN Name=ksgA; OrderedLocNames=TP0337;
 OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 NCBI_TaxId=160;
 RX STRAIN=160;
 RP SEQUENCE FROM N.A.
 RC MEDLINE=9665876; PubMed=9665876; DOI=10.1126/science.281.5375.375;
 RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
 RA Dodson R.J., Gwinn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
 RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
 RA Uterback T.R., McDonald L.A., Atlich P., Bowman C., Cotton M.D.,
 RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
 RA Weidman J.F., Smith H.O., Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete";
 RL Science 281:375-386(1998).

CC -1- FUNCTION: Specifically, dimethylates two adjacent adenosines in the
 CC loop of a conserved hairpin near the 3' end of 16S rRNA in the 30S
 CC particle. Its inactivation leads to kasugamycin resistance (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the rRNA adenine N-6-methyltransferase
 CC family. KsgA subfamily.
 CC -----

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DR EMBL; AE001213; AAC65323.1; -
 DR PIR; G71337; G71337.

DR TIGR; TP0337; -
 DR HAMAP; MF_00607; -, 1.
 DR InterPro; IPR001737; RNA_A_dimeth.

DR InterPro; IPR000051; SAM_Bind.

DR Pfam; PF00398; RnmaD; 1.

DR SMART; SMO0650; RADC; 1.

DR TIGRfams; TIGR00755; ksgA; 1.

DR PROSITE; PS01131; RNA_A_DIMETH; FALSE_NEG.

KM Antibiotic resistance; Complete proteome; Methyltransferase;
 KM RNA processing; Transferase.

SQ SEQUENCE 285 AA; 32275 MW; 3AF0BCBE16B5D4F CRC64;

Query Match 58.9%; Score 43; DB 1; Length 285;
 Best Local Similarity 64.3%; Pred. No. 39;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IEPTLRQWLARA 14
 : ||||| :
 Db 98 IEQDVLQWMAAAA 111

RESULT 24
 Q7UOE4 PRELIMINARY; PRT; 297 AA.

AC Q7UOE4;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocNames=RB6375;
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 NCBI_TaxId=117;
 RX STRAIN=1;
 RP SEQUENCE FROM N.A.

RC MEDLINE=2725913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
 RA Schlessner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 RT strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; BX294144; CAD74759.1; -
 DR InterPro; IPR000194; ATPase_a/bcentre.

DR InterPro; IPR003169; GYF.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
 DR PROSITE; PS50829; GYF; 1.
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 297 AA; 31805 MW; 475F670F02C78E9B CRC64;

Query Match 58.9%; Score 43; DB 2; Length 297;
 Best Local Similarity 50.0%; Pred. No. 41;
 Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EGPTRQWL 11
 : ||||| :
 Db 176 DGPTKQWIS 185

RESULT 25
 Q8EJ00 PRELIMINARY; PRT; 306 AA.

AC Q8EJ00;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Prophage MuSol, major head subunit, putative.
 GN OrderedLocNames=SO0675;
 OS Shewanella oneidensis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Shewanellaceae; Shewanella.
 NCBI_TaxId=70863;
 RX STRAIN=1;

RP SEQUENCE FROM N.A.

RC MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;

RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos B.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Sehadri R., Ward N.L., Methe B.A.,
 RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M.J.,

RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
 RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,

RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
 RA Lee K., Berry K.J., Lee C., Mueller J., Kouri H.M., Gill J.,

RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
 RA Venter J.C., Neilson K.H., Fraser C.M.;

SQ SEQUENCE 306 AA; 32275 MW; 3AF0BCBE16B5D4F CRC64;


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RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015513; AAN53753.1; -.
DR TIGR; SC0675; -.
KM Complete proteome.
SQ SEQUENCE 306 AA; 34370 MW; F54CCA118AA288CB CRC64;

Query Match 58.9%; Score 43; DB 2; Length 306;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PTLRQWLAAR 13
|:|:|:|
Db 54 PFMKEMWIGAR 63

RESULT 26
ID 082YTS PRELIMINARY; PRT; 354 AA.
AC 082YTS;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein PAE0634.
GN OrderedLocustNames=PAE0634;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IN2 / ATCC 51768 / DSM 7523;
RA MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stettler K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
RW EMBL; AE009776; ALU62908.1; -.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 354 AA; 38642 MW; C5799975B972941 CRC64;

Query Match 58.9%; Score 43; DB 2; Length 354;
Best Local Similarity 61.5%; Pred. No. 49;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IEQPTLRQWLAAR 13
|:|:|:|
Db 84 IDRGLEQWLAAR 96

RESULT 27
ID 082PK5 PRELIMINARY; PRT; 377 AA.
AC 082PK5;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=SAV747;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RA MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kituchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces

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RT avermitilis: deducing the ability of producing secondary
RT metabolites."
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis."
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005023; BAC68457.1; -.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 377 AA; 41307 MW; 0253176AAAB6293 CRC64;

Query Match 58.9%; Score 43; DB 2; Length 377;
Best Local Similarity 61.5%; Pred. No. 52;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IEQPTLRQWLAAR 13
|:|:|:|
Db 168 MEGPDLRAWLPNR 180

RESULT 28
ID 083436 PRELIMINARY; PRT; 683 AA.
AC 083436;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein TP0421.
GN OrderedLocustNames=TP0421;
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=9833770; PubMed=965876; DOI=10.1126/science.281.5375.375;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R.J., Gwin M.L., Hickey B.K., Clayton R.A., Ketchum K.A.,
RA Dosegaren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
RA Utechtack T.R., McDonald L.A., Artlich P., Bowman C., Cotton M.D.,
RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
RA Weidman J.F., Smith H.O., Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RL Science 281:375-388(1998).
DR EMBL; AE001220; AAC65409.1; -.
DR PIR; B71325; B71325.
DR TIGR; TP0421; -.
DR InterPro; IPR011044; Amine_DH_B_like.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001258; NHL.
DR InterPro; IPR001440; TPR.
DR Pfam; PF01436; NHL; 5.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50005; TPR; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
KM Complete proteome.
SQ SEQUENCE 683 AA; 74518 MW; F91407FA7094AADI CRC64;

Query Match 58.9%; Score 43; DB 2; Length 683;
Best Local Similarity 69.2%; Pred. No. 95;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IEQPTLRQWLAAR 13
|:|:|:|
Db 89 IEQAALHMGGAAR 101

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RESULT 29

Q85Y82 PRELIMINARY; PRT; 754 AA.

AC Q85Y82; 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein Y119C1B.5.

GN Name=Y119C1B.5; ORFNames=Y119C1B.5;

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditicoidea;

OC Rhabditidae; Pelodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RX MEDLINE=9069613; PubMed=9851916;

RG WormBase Consortium;

RT "Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium.";

RL Science 282:2012-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Jones K., Murray J., Graves T.;

RT "The sequence of *C. elegans* cosmid Y119C1B.";

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Waterston R.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Waterston R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Waterston R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Waterston R.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

RN [7]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Waterston R.;

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

RN [8]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Waterston R.;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

RN [9]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RA Wilson R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

RN [10]

RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;

RG WormBase Consortium;

RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

CC -1. SIMILARITY: Contains 1 RING-type zinc finger.

DR EMBL; AC006712; AAK9324.1; -

DR WormBase; WBGen00022471; Y119C1B.5.

DR Wormpep; Y119C1B.5; CE27234.

DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.

DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR GO; GO:0016567; P:protein ubiquitination; IEA.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00097; zf-C3HC4; 1.

DR SMART; SM00184; RING; 1.

DR PROSITE; PS50089; ZF_RING_2; 1.

KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 754 AA; 85323 MW; 41BA9297FA3BF05 CRC64;

Query Match 58.9%; Score 43; DB 2; Length 754;

Best Local Similarity 63.6%; Pred. No. 1.1e+02;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 GPTLRQWLAR 13

Db 626 GPCLRKWLAVK 636

RESULT 30

Q8Y015 PRELIMINARY; PRT; 91 AA.

AC Q8Y015; 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Hypothetical protein RSC1059.

GN Name=RS04149; Ordered locus Names=RS041059;

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Ralstonia.

OX NCBI_TaxID=305;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GM11000;

RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;

RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Ariat M., Billault A., Brotier P., Camus J.C., Catolico L., Chandler M., Cholene N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T., Siguler P., Thebaud P., Whalen M., Wincker P., Levy M., Weissbach J., Boucher C.A.;

RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*.";

RL Nature 415:497-502(2002).

DR EMBL; AL646062; CAD14761.1; -

KW Complete proteome.

SQ SEQUENCE 91 AA; 10321 MW; 2B4DFEB37A528AD CRC64;

Query Match 57.5%; Score 42; DB 2; Length 91;

Best Local Similarity 46.2%; Pred. NO. 18;

Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAR 13

Db 75 LDGPVQAWMLAQ 87

RESULT 31

Q8N9N4 PRELIMINARY; PRT; 126 AA.

AC Q8N9N4; 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical protein FLJ36840.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=14702039; DOI=10.1038/ng1285;

DR Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Makamatsu A., Hayaishi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuna M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Nishimura K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Masehino K., Yuki H., Oshima A., Sasaki N., Aochika S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T., Sano S.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
cDNAs";
RL Nat. Genet. 36:40-45 (2004).
DR EMBL; AK094159; BAC04297.1; -
SQ SEQUENCE 126 AA; 14003 MW; AFI0E9375A3D9C7E CRC64;

Query March 57.5%; Score 42; DB 2; Length 126;
Best Local Similarity 58.3%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GPTLRQWLARA 14
|||:|:|
Db 108 GPDLRWAGSRA 119

RESULT 32
Q8XP09 PRELIMINARY; PRT; 252 AA.
AC Q8XP09;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.
GN Name=RS02135; OrderedlocusNames=RS02135;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Broctier P., Camus J.C., Cattolico L.,
RA Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Sigler P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RL Nature 415:497-502 (2002).
CC -1- SIMILARITY: Contains 1 HTH LuxR-type DNA-binding domain.
DR EMBL; AL646085; CAD18730.1; -
DR HSRP; P11470; 1FSE.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR Pfam; PF00196; GerB_1
DR PRINTS; PR01590; HTHPIS.
DR PRINTS; PR00038; HTHLDR.
DR ProDom; PD000307; HTH LuxR; 1.
DR SMART; SM00421; HTH LuxR; 1.
KW Complete proteome; DNA-binding; Plasmid; Transcription;
KW Transcription regulation.
SQ SEQUENCE 252 AA; 27666 MW; 483403EE326F7C2E CRC64;

Query March 57.5%; Score 42; DB 2; Length 252;
Best Local Similarity 53.8%; Pred. No. 52;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IEPTLRQWLAR 13
|||:|:|
Db 76 IDPTLRQWLAR 88

RESULT 33
P90433 PRELIMINARY; PRT; 313 AA.
ID P90433;
AC P90433;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Truncated reverse transcriptase (Fragment).
GN Name=pol;
OS Chimpanzee immunodeficiency virus (SIV/cpz) (CIV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith J.M., Krauselburd E.N., Torres J.V.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family A2.
DR EMBL; U83413; AAB41428.1; -
DR HSRP; Q07387; ITCW.
DR MEROPS; A02.002; -.
DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR001995; Peptidase A2.
DR InterPro; IPR009007; Peptidase A2.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR000477; RVTse.
DR Pfam; PF00077; RVP; 1.
DR Pfam; PF00078; RVT_1; 1.
DR PROSITE; PS00141; ASP_PROT_RETROV; 1.
DR PROSITE; PS01175; ASP_PROT_RETROV; 1.
KW Aspartyl protease; Hydrolase; Protease; RNA-directed DNA polymerase;
KW Transferrase.
FT NON TER
SQ SEQUENCE 313 AA; 34674 MW; 5A0BB016783FC8A6 CRC64;

Query March 57.5%; Score 42; DB 2; Length 313;
Best Local Similarity 87.5%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EGPTLRQW 9
|||:|:|
Db 184 EGPTLRQW 191

RESULT 34
O855N9 PRELIMINARY; PRT; 325 AA.
ID O855N9;
AC O855N9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
 DE Gp74.
 OS Mycobacteriophage Cheqd.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 NC NCB1_TaxID=205876;
 RX SEQUENCE FROM N.A.
 RX MEDLINE=2259260; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
 RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Madeworth C.,
 RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
 RA Brucker W., Kumar V., Kandassamy J., Keenan L., Bardarov S.,
 RA Krizhov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
 RA Hatfull G.F.;
 RT "Origins of highly mosaic mycobacteriophage genomes.";
 RL Cell 113:171-182(2003).
 DR EMBL: AY129336; AAM07992.1; -
 SQ SEQUENCE 325 AA; 35999 MW; 04265796D0B4FC1D CRC64;

Query Match 57.5%; Score 42; DB 2; Length 325;
 Best Local Similarity 61.5%; Pred. No. 67;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGPTLRQWLAR 14
 :|||:|||||
 Db 302 DGPTVQELAR 314

RESULT 35
 P95613 PRELIMINARY; PRT; 326 AA.

DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE NodD2 protein.
 GN Name=nodD2;
 OS Rhizobium galegae.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 NC NCB1_TaxID=399;
 RX SEQUENCE FROM N.A.
 RC STRAIN=HAMB1;
 RA Suominen L., Roos C., Paulin L., Kaijalainen S., Lindstrom K.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 HTH LysR-type DNA-binding domain.
 DR EMBL: Y08963; CAA70157.1; -
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR000847; HTH_LysR.
 DR InterPro: IPR005119; LysR_subst.
 DR InterPro: IPR009058; Wng_hlx_DNA_bnd.
 DR Pfam: PF00126; HTH_1; 1.
 DR Pfam: PF03466; LysR_substrate; 1.
 DR PRINTS: PR00039; HTHLYSR.
 DR PROSITE: PSS0931; HTH_LysR; 1.
 KM DNA-binding; Transcription; Transcription regulation.
 SQ SEQUENCE 326 AA; 36373 MW; BBE9C32F6719E28B CRC64;

Query Match 57.5%; Score 42; DB 2; Length 326;
 Best Local Similarity 50.0%; Pred. No. 67;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGPTLRQWLAR 13
 :|||:|||||
 Db 204 KGBELQWLSSQ 215

RESULT 36
 Q7XPP6 PRELIMINARY; PRT; 375 AA.
 ID Q7XPP6
 AC Q7XPP6;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
 DE OSJNB0053K19.27 protein (OSJNB0060E08.2 protein).
 GN Name=OSJNB0053K19.27; Synonyms=OSJNB0060E08.2;
 OS Oryza sativa [aponia cultivar-group].
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocarideae; Oryzae; Oryza.
 NC NCB1_TaxID=39947;
 RX SEQUENCE FROM N.A.
 RP PubMed=12447439; DOI=10.1038/nature01183;
 RA Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
 RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 RA Wang Q., Zhang L., Lu Y., Wu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
 RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
 RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
 RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
 RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
 RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 RA Han B.;

RT "Sequence and analysis of rice chromosome 4.";
 RL Nature 420:316-320(2002).
 DR EMBL: AL606645; CAB03519.2; -
 DR EMBL: AL606649; CAB04739.1; -
 DR Gramene; Q7XPP6; -
 DR GO: GO:0005515; F:protein binding; IEA.
 DR InterPro: IPR000210; BTB_POZ.
 DR InterPro: IPR002083; MATF.
 DR InterPro: IPR008974; Traf_like.
 DR Pfam: PF00651; BTB; 1.
 DR Pfam: PF00917; MATF; 1.
 DR SMART: SM00225; BTB; 1.
 DR SMART: SM00061; MATF; 1.
 DR PROSITE: PSS0097; BTB; 1.
 DR PROSITE: PSS0144; MATF; 1.
 SQ SEQUENCE 375 AA; 41043 MW; 20FC6B99E4750816 CRC64;

Query Match 57.5%; Score 42; DB 2; Length 375;
 Best Local Similarity 61.5%; Pred. No. 77;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 IEGPTLRQWLAR 13
 :|||:|||||
 Db 138 MERPRRLQWLRR 150

RESULT 37
 Q9SLB9 PRELIMINARY; PRT; 450 AA.

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, last sequence update)
 DT 01-JUL-2004 (TrEMBLrel. 27, last annotation update)
 DE Expressed protein (At2g42400/MK10.12) (transcription factor
 DE AtVO22).
 GN Name=At2g42400; Synonyms=AtVO22;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCB1_TaxID=3702;
 RX SEQUENCE FROM N.A.
 RP Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
 RA Barnstead M.E., Mason T.M., Bowman C.L., Koning C.M., Benito M.-I.,
 RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Niernan W.C.,
 RA Fraser C.M., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

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RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee C.J., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.C., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shin P., Banh J., Bowser L.,
RA Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee C.J.,
RA Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M.,
RA Southwick A., Toriumi M., Yamada K., Yu G., Shinzaki K., Davis R.W.,
RA Theologis A., Ecker J.R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Mitsuda N., Hisebort T., Takeyasu K., Sato M.H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005956; AAD23723.2; -
DR EMBL; AY078048; AAL77749.1; -
DR EMBL; AF61831; AAK32843.1; -
DR EMBL; AB125257; BAD17858.1; -
DR PIR; E84853; E84853.
DR InterPro; IPR009105; Colicin_E3_cat.
SQ SEQUENCE 450 AA; 5056 MW; 44DBE7B4B69B95 CRC64;

Query Match 57.5%; Score 42; DB 2; Length 450;
Best Local Similarity 60.0%; Pred. No. 93;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 IEGETLRQWL 10
DB 320 VEGETIREWL 329

RESULT 38
Q9N6P9 PRELIMINARY; PRT; 586 AA.
ID Q9N6P9;
AC Q9N6P9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE L354.2.
GN Name=L354.2;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OC NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Fredlin;
RA Myler P.J., Sisk E., Cawthra J., Handley F., Vogt C., Robertson L.,
RA McDougall P., Ivens A., Nguyen D., Munden H., Stuart K.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC022473; AAF69566.1; -
SQ SEQUENCE 586 AA; 63594 MW; 208367C213896AF3 CRC64;

Query Match 57.5%; Score 42; DB 2; Length 586;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 IEGETLRQWLARA 14
DB 58 VEAPLILRQMTAA 71

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RESULT 39
ID_POL_SIVS4 STANDARD; PRT; 1019 AA.
AC P12502;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Pol polyprotein (Contains: Protease (Retropepsin) (RC 3.4.23.-);
DE Reverse transcriptase/ribonuclease H (EC 2.7.7.49) (EC 3.1.26.4) (RT);
DE Integrase (IN)).
GN Name=POL;
OS Simian immunodeficiency virus (P236/smh4 isolate) (sooty mangabey).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11737;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99262053; Pubmed=2786147; DOI=10.1038/339389a0,
RA Hirsch V.M., Olmstead R.A., Murphy-Cord M., Purcell R.H.,
RA Johnson P.R.;
RT "An African primate lentivirus (SIVem) closely related to HIV-2."
RL Nature 339:389-392(1989).
CC -1- FUNCTION: During replicative cycle of retroviruses, the reverse-
CC transcribed viral DNA is integrated into the host chromosome by
CC the viral integrase enzyme. RNase H activity is associated with
CC the reverse transcriptase.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphomonoester.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA}(N).
CC -1- PTM: Cleavage sites that yield the mature proteins remain to be
CC determined.
CC -1- SIMILARITY: Belongs to the retroviruses Pol polyprotein family.
CC -1- SIMILARITY: Contains 1 integrase-type zinc finger.
CC -1- SIMILARITY: Contains 1 peptidase A2 domain.
CC -1- SIMILARITY: Contains 1 reverse transcriptase domain.
CC -1- SIMILARITY: Contains 1 RNase H domain.
CC -----
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CC -----
DR EMBL; X14307; -; NOT_ANNOTATED_CDS.
DR HSSP; P04584; 1MU2.
DR MEROPS; A02.002; -.
DR HIV; X14307; POL_SSMH4.
DR InterPro; IPR001037; Integrase_C.
DR InterPro; IPR003308; Integrase_Zn_N.
DR InterPro; IPR001995; Peptidase_A2.
DR InterPro; IPR009007; Pept_AspArtic.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR004777; RVTse.
DR InterPro; IPR010659; RVT_connect.
DR InterPro; IPR010661; RVT_thumb.
DR Pfam; PF00552; Integrase_1.
DR Pfam; PF02022; Integrase_Zn_1.
DR Pfam; PF00075; RNaseH_1.
DR Pfam; PF00665; Rve_1.
DR Pfam; PF00077; RVP_1.
DR Pfam; PF00078; RVT_1.
DR Pfam; PF06815; RVT_connect_1.
DR Pfam; PF06817; RVT_thumb_1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS0175; ASP_PROT_RETROV; 1.
DR PROSITE; PS50878; RNASE_H; 1.
DR PROSITE; PS50879; RT_POL; 1.
DR PROSITE; PS50876; ZF_INTEGRASE; 1.
KW AIDS; Aspartyl protease; DNA integration; DNA recombination;

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KW Endonuclease; Hydrolase; Metal-binding; Multifunctional enzyme;
KM Nuclease; Polypeptide; RNA-directed DNA polymerase; Transferase; Zinc;
Zinc-finger.
FT CHAIN 1 167 Protease.
FT DOMAIN 211 401 Reverse transcriptase.
FT DOMAIN 600 723 RNase H.
FT ZN_FING 729 770 Integrase-type.
FT ACT_SITE 93 93 By similarity.
SQ SEQUENCE 1019 AA, 115465 MW, 8D3DE0B85FC92B1C CRC64;

Query Match 57.5%; Score 42; DB 1; Length 1019;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGPTLRQW 9
Db 184 EGPKLRQW 191

RESULT 40
P89154 PRELIMINARY; PRT; 1019 AA.
ID P89154
AC P89154;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pol polyprotein (Fragment).
Name=pol;
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
NCBI_TaxID=11723;
RN NAME=POL;
RP SEQUENCE FROM N.A.
RC STRAIN=SIVme543;
RA Hirsch V.M.;
RA Hirsch V., Adgey-Johnson D., Campbell B., Goldstein S., Brown C.,
RA Elkins W.R., Montefiori D.C.;
RT "A molecularly cloned, pathogenic, neutralization-resistant simian
RT immunodeficiency virus, SIVme543-3.";
RL J. Virol. 71:1608-1620 (1997).
[2]
RN NAME=POL;
RP SEQUENCE FROM N.A.
RC STRAIN=SIVme543;
RA Hirsch V.M.;
RA Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family A2.
DR EMBL: U72748; AAC56559.1; -.
DR PIR: T11560; T11560.
DR HSSP: P04584; 1MU2.
DR MEROP; A02.002; -.
DR GO: GO:0004190; F:aspartic-type endopeptidase activity; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0008907; F:integrase activity; IEA.
DR GO: GO:0008907; F:peptidase activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004523; F:ribonuclease H activity; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0015074; F:DNA integration; IEA.
DR GO: GO:0006310; P:DNA recombination; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO: GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro: IPR001037; Integrase_C.
DR InterPro: IPR003308; Integrase_Zn_N.
DR InterPro: IPR001995; Peptidase_A2.
DR InterPro: IPR009007; Pept_Aspartic.
DR InterPro: IPR001969; Pept_Asp_AS.
DR InterPro: IPR002156; RNaseH.
DR InterPro: IPR000477; RVTse.
DR InterPro: IPR010659; RVT_connect.
DR InterPro: IPR010659; RVT_chumb.
DR InterPro: IPR010661; RVT_chumb.

DR InterPro: IPR005829; Sug_transporter.
DR Pfam: PF02022; Integrase_Zn_1.
DR Pfam: PF00075; RNaseH_1.
DR Pfam: PF00665; rve_1.
DR Pfam: PF00077; RVP_1.
DR Pfam: PF00078; RVP_1.
DR Pfam: PF06815; RVT_connect_1.
DR Pfam: PF06817; RVT_chumb_1.
DR PROSITE: PS00141; ASP_PROTASE_1.
DR PROSITE: PS00175; ASP_PROT_RETROV_1.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
KW Aspartyl protease; Hydrolase; Polypeptide; Protease;
KM RNA-directed DNA polymerase; Transferase.
FT NON_TER 1 1
SQ SEQUENCE 1019 AA, 115595 MW, 26F1EF4594E59537 CRC64;

Query Match 57.5%; Score 42; DB 2; Length 1019;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EGPTLRQW 9
Db 184 EGPKLRQW 191

RESULT 41
Q7ZBR5 PRELIMINARY; PRT; 1019 AA.
ID Q7ZBR5
AC Q7ZBR5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pol (Fragment).
Name=pol;
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
NCBI_TaxID=11723;
RN NAME=POL;
RP SEQUENCE FROM N.A.
RC MEDLINE=22628501; PubMed=12743298;
RX DOI=10.1128/JVI.77.11.6405-6418.2003;
RA Debhani H., Puffer B.A., Doms R.W., Hirsch V.M.;
RT "Unique pattern of convergent envelope evolution in simian
RT immunodeficiency virus-infected rapid progressor macaques: association
RT with CD4-independent usage of CCR5.";
RL J. Virol. 77:6405-6418 (2003).
CC -1- SIMILARITY: Belongs to peptidase family A2.
DR EMBL: AY221515; AA067309.1; -.
DR HSSP: P04584; 1MU2.
DR GO: GO:0004190; F:aspartic-type endopeptidase activity; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0008907; F:integrase activity; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0004523; F:ribonuclease H activity; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0015074; F:DNA integration; IEA.
DR GO: GO:0006310; P:DNA recombination; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO: GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro: IPR001037; Integrase_C.
DR InterPro: IPR003308; Integrase_Zn_N.
DR InterPro: IPR001995; Peptidase_A2.
DR InterPro: IPR009007; Pept_Aspartic.
DR InterPro: IPR001969; Pept_Asp_AS.
DR InterPro: IPR002156; RNaseH.
DR InterPro: IPR001584; Rve.
DR InterPro: IPR000477; RVTse.
DR InterPro: IPR010659; RVT_connect.
DR InterPro: IPR010661; RVT_chumb.
DR InterPro: IPR005829; Sug_transporter.

DR Pfam; PF02022; Integrase_Zn; 1.
 DR Pfam; PF00075; RNaseH; 1.
 DR Pfam; PF00665; rve; 1.
 DR Pfam; PF00077; RVP; 1.
 DR Pfam; PF00078; RVP; 1.
 DR Pfam; PF06815; RVT_connect; 1.
 DR Pfam; PF06817; RVT_chumb; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR PROSITE; PS01175; ASP_PROT_RETROV; 1.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN 1.
 DR Aspartyl protease; Hydrolase; Protease; RNA-directed DNA polymerase;
 KM Transferase.
 FT NON_TER
 SQ SEQUENCE 1019 AA; 115613 MW; 6002D54F14648C6C CRC64;
 Query Match 57.5%; Score 42; DB 2; Length 1019;
 Best Local Similarity 87.5%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EGPTLRQW 9
 Db 184 EGPKLRQW 191

RESULT 42
 07ZBR7 PRELIMINARY; PRT; 1019 AA.
 AC 07ZBR7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Pol (fragment).
 GN Name=Pol;
 OS Chimpanzee immunodeficiency virus (SIV/cpz) (CIV).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirinae.
 NC NCBI_TaxID=11723;
 RX MEDLINE=22628501; PubMed=12743298;
 RX DOI=10.1128/JVI.77.11.6405-6418.2003;
 RA Deighan H., Puffer B.A., Dome R.W., Hirsch V.M.;
 RT Unique pattern of convergent envelope evolution in simian
 RT immunodeficiency virus-infected rapid progressor macaques: association
 RT with CD4-independent usage of CCR5.";
 RL J. Virol. 77:6405-6418(2003).
 CC -1- SIMILARITY: Belongs to peptidase family A2.
 DR EMBL; AY221514; AAC67307.1; -.
 DR HSPSP; P04584; IIMU2.
 DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0008907; F:integrase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004523; F:ribonuclease H activity; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
 DR InterPro; IPR001037; Integrase_C.
 DR InterPro; IPR003308; Integrase_Zn_N.
 DR InterPro; IPR001995; Peptidase_A2.
 DR InterPro; IPR009007; Peptidase_A2.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR InterPro; IPR00156; RNaseH.
 DR InterPro; IPR001584; RVE.
 DR InterPro; IPR000477; RVTse.
 DR InterPro; IPR010659; RVT_connect.
 DR InterPro; IPR010661; RVT_chumb.
 DR InterPro; IPR005829; Sug_transporter.
 DR Pfam; PF02022; Integrase_Zn; 1.

DR Pfam; PF00075; RNaseH; 1.
 DR Pfam; PF00665; rve; 1.
 DR Pfam; PF00077; RVP; 1.
 DR Pfam; PF00078; RVP; 1.
 DR Pfam; PF06815; RVT_connect; 1.
 DR Pfam; PF06817; RVT_chumb; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR PROSITE; PS01175; ASP_PROT_RETROV; 1.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN 1.
 DR Aspartyl protease; Hydrolase; Protease; RNA-directed DNA polymerase;
 KM Transferase.
 FT NON_TER
 SQ SEQUENCE 1019 AA; 115340 MW; A886525DF1BE26F CRC64;
 Query Match 57.5%; Score 42; DB 2; Length 1019;
 Best Local Similarity 87.5%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EGPTLRQW 9
 Db 184 EGPKLRQW 191

RESULT 43
 08P9L5 PRELIMINARY; PRT; 410 AA.
 AC 08P9L5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Valine-pyruvate aminotransferase.
 GN Name=avtA; OrderedLocNames=XCC1838;
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 NC NCBI_TaxID=340;
 RX MEDLINE=2202145; PubMed=12042217; DOI=10.1038/417459a;
 RX DOI=10.1128/JVI.77.11.6405-6418.2003;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Catarote G., Camavari F., Cardozo J., Chamberg F., Clapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Medeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Seubel J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.";
 RL Nature 417:459-463(2002).
 DR EMBL; AEO12286; AAM41127.1; -.
 DR GO; GO:0008483; F:transaminase activity; IEA.
 DR GO; GO:0016740; F:transaminase activity; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR InterPro; IPR004839; Aminotran_1_2; 1.
 DR Pfam; PF0015; Aminotran_1_2; 1.
 KM Aminotransferase; Complete proteome; Pyruvate; Transferase.
 SQ SEQUENCE 410 AA; 44530 MW; 441BEA9A9F04F553 CRC64;

Qy 3 GPT-----LQWLAAAR 13
 Query Match 56.8%; Score 41.5; DB 2; Length 410;
 Best Local Similarity 56.2%; Pred. No. 1e+02;
 Matches 9; Conservative 2; Mismatches 0; Indels 5; Gaps 1;

Db 78 GPTGYAPLREWVAAR 93

RESULT 44

08PLE2 PRELIMINARY; PRT; 427 AA.

AC 08PLE2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE Value-private aminotransferase.
 GN Name-avaA; OrderedlocusNames-XA1858;
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Ouaggo R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
 RA Camarotte G., Camavan F., Cardozo J., Chambergo F., Chapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spindola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RA "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities."
 RL Nature 417:459-463(2002).
 DR EMBL; AE011819; AAM36720.1; -.
 DR GO; GO:0008483; F:transaminase activity; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR InterPro; IPR004839; AminoTrans_I/II.
 DR Pfam; PF00155; AminoTrans_1_2; 1.
 DR Complete proteome.
 SK SEQUENCE 427 AA; 45926 MW; BBDC205BDA06B56E CRC64;

Query Match 56.8%; Score 41.5; DB 2; Length 427;

Best Local Similarity 56.2%; Pred. No. 1.1e+02;
 Matches 9; Conservative 2; Mismatches 0; Indels 5; Gaps 1;

Qy 3 GPT-----LRQWLAR 13
 ||| |||
 Db 95 GPTGYAPLREWVAAR 110

RESULT 45

098AJ1 PRELIMINARY; PRT; 75 AA.

AC 098AJ1;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, last annotation update)
 DE Transposase.
 GN OrderedlocusNames-msr5979;
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Watanabe A., Ideesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti."
 RL DNA Res 7:331-338(2000).
 DR EMBL; AP003008; BAB52338.1; -.
 KW Complete proteome.
 SK SEQUENCE 75 AA; 8363 MW; B76547C20DA52EAD CRC64;

Query Match 56.2%; Score 41; DB 2; Length 75;

Best Local Similarity 58.3%; Pred. No. 22;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EGPTLRQWLAR 13
 :| | | | |
 Db 3 QGKACREWLAR 14

Search completed: September 1, 2005, 16:21:19
 Job time : 55.0719 secs